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Prostate gene P510
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-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120

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Prostate gene PS10 cDNA sequence of a

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Human prostate-re

DR WPI: 2002-508560/54. P-PDB: ABB77575. XX Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity pracessed in patients with allergic hypersensitivity pracessociated with mast cell regranulation and allergic hypersensitivity pracessed in mast cells following corresponding to genes differentially expressed in mast cells following corresponding to genes differentially expressed in mast cells following corresponding to genes differentially expressed in mast cells following corresponding to genes differentially expressed in mast cells following corresponding to genes differentially expressed in mast cells following corresponding to genes deferentially september (II) is useful for identifying blinding patterns: (I) is useful for diancis or treating a disease corresponding to treating a disease corresponding to the level of expression of (I) or (II) is used as a marker to detect, diagnose or identifying the expression level in a tissue or at least one mast cell of (I), is useful for response in a patient. The protein can also serve as a target that condulate gene expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents that modulate expression of the protein or agents with a modulating activity and differential activity and differential activity and salergic hypersensitivity. XX Sequence 1662 BP; 259 A; 551 C; 511 G; 371 T; 0 other;	Alignment Scores: Pred
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The present invention relates to methods of detecting a prostate cancer-associated transcript in a cell from a patient. The method comprises contacting a biological sample from the patient with prostate cancer-associated polynucleotides (designated PC genes) that selectively hybridise to a sequence that is at least 80% identical to them. The prostate cancer-associated polynucleotide sequences are differentially expressed in prostate tumour tissue or in prostate cancer and are derived from the tissues of various organisms such as humans or other mammals (e.g. mice, sheep and dogs). The methods of the invention are useful for diagnosing and treating prostate cancer in mammals. The prostate cancer, as well as for identifying modulators of prostate cancer or agents that inhibit prostate cancer. The nucleic acid sequences are particularly useful in gene therapy, as a vaccine or in antisense applications.

ABR92115-ABK92263 represent prostate cancer-associated polynucleotide
1 CTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTC 1560
                                                            Jecting a prostate cancer-associated transcript in a cell in a cint, useful for diagnosing prostate cancer (PC) or screening Julators of PC, by determining if prostate cancer-associated genes expressed in a prostate tissue
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3-DEC-2000; 2000US-0733288.

3-DEC-2000; 2000US-0733742.

3-DEC-2000; 2000US-2659579.

5-MAR-2001; 2001US-276791P.
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Oy 301 TyrGlnGlyV 1210 TACCAGGGCG Qy 321 ValArgMetG Db 1270 GTTCGGATGG	Oy 341 ValMetAspA Db 1330 GTCATGGACC	Oy 361 AlaPheProV 	Qy 381 SerAlaAlaL 	401	1570	1630	461	1750	501 1810		Oy 541 ValValPhen. 	314 314	AAS14962; 14-FEB-2002	DE DNA encoding hux XX KW Human; PROST 03 KW Cytostatic; vac	OS Homo sapiens. XX FH Key	FT CDS . FT XX WO200181577-A2.
Sequence 2582 BP; 407 A; 822 C; 785 G; 566 T; 2 other; gnment Scores: ed. No.: cent Similarity: 100.00% 100.00	100.00% Indels: 0 24 Gaps: 0 (1-553) x ABK92217 (1-2582)	1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 	21 ValasnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlylleThrTyfValPro 40	41 ProLeuLeuGluvalGlyvalGluGluLySPheMetThrMetValLeuGly 60 	61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80	81 ArgTyrGlyArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100 	101 PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120	121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140 	141 ThrProLeuGlualaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnala 160 	180	181 IleaspTrpaspThrSeralaLeualaProTyrLeuGlyThrGlnGluGluCySLeuPhe 200	201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAladluGlu 220 	221 AlaalaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240	241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260 	261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280	281 SerTrpMetAlaLeumetThrPheThrLeuPheTyrThrAspPheValGlyGlyGlyGlyGlyGlyGlyGlyIn 110
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                                              21 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu
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tostatic; vaccine; ss.
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/*tag= a
/product= "PROST 03".
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01-NOV-2001
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26-APR-2001; 2001WO-US13323

27-APR-2000; 2000US-200065P. 20-APR-2001; 2001US-0200065.

(SCHD) SCHERING AG

Schneider DW, Steinbrecher R; Parkes D, Parry G, Wu J; T, Lin RJ, Heuit PT, W Lau T, Van

WPI; 2002-041404/05.

P-PSDB; AAU10324

Novel PROST 03 polypeptides and polynucleotides useful in research, diagnosis and therapeutic applications, particularly for use in cancer therapeutics

Claim 6; Fig 1; 77pp; English.

the polynuclectide (II) encoding PROST 03. (TII) is useful for selectively destroying a cell expressing (I), and for treating a disease-state associated with expression (I), and for treating a disease-state associated with expression (I), and for treating a disease-state sesful for diagnosing metastasis associated with (I), in a subject.

(I) is also useful for diagnosing and treating diseases of cell proliferation such as prostate cancers. (I) is also useful for generating antibodies to prostate cancers. (I) is also useful for generating antibodies to prost 03. (III) is useful in detecting the levels of PROST 03 on this prostate cancers. (I) is also useful for generating and metastatic tumours. (I) is also useful in diagnostic assays for detecting the levels of polypucleotides encoding prost 03 in cells and tissues. (II) is useful as DNA probes, as targets for antisense polymucleotides encoding prost or antisense polymucleotides. (II) are useful in research, biological, clinical and therapeutic purposes. (I) he present sequence represents the coding sequence of human PROST 03. invention relates to an isolated PROST 03 polypeptide (I) and to The

Sequence 3320 BP; 585 A; 1013 C; 944 G; 778 T; 0 other;

Alignment Scores: .. 9

3320 553 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 0 553.00 100.00% 100.00% 24 Best Local Similarity: Percent Similarity: Query Match: DB: Score:

US-09-593-793A-113 (1-553) x AAS14962 (1-3320)

- 282 ŏ
- 40 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 21 ò
- 342 g

ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly

41

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- 402 g
- 521 80 61 462 ŏ g
- 81 522

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MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu

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                                                                                                        ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
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                            LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal
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Similarity:

Best Local S Query Match:

Percent Similarity:

Alignment Scores:

Indels:

US-09-593-793A-113 (1-553) x AAV61201 (1-3410)

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the method of the invention. The method is for detecting and can the method of the invention. The method is for detecting ancer comprises contacting to biological sample with an agent of an immunogenic portion of a prostate protein (such as this sequence). An antibody which binds to an immunogenic the prostate protein, and the method can be used to detect, or treat prostate cancers. The antibody may injugated to a therapeutic agent for use in therapy of prostate
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Mismatches:
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CDNA; 3410

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The present sequence was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immunotherapy and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to
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                           cytostatic; immunotherapy;
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Matches:
Conservative:
Mismatches:
Indels:
tumour clone P501S
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                                                                                                                                                                                                                                                                                                                                                                              English.
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cDNA sequence of human breast
                           antigen;
                                                                                                                                                                                                                                                                                                                        A novel isolated polypeptide
breast cancer protein useful
cancer -
                                                                                                                                                      2000WO-US09688
                                                                                                                                                                                99US-0288950
99US-0346327
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                                         vaccine; ss
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                           tumour
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                      Xu J,
                                                                                                                                                                                                                                                                                              P-PSDB; AAB28527
                                         cancer;
                                                                                               WO200061756-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3410
                           breast
                                                                                                                                                   10-APR-2000;
                                                                                                                                                                                09-APR-1999;
02-JUL-1999;
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Pred. No.:
                                                                                                                           19-0CT-2000
                                                                                                                                                                                                                                                    SG,
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                            Human;
                                         breast
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No.:
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                                                                      Homo
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οy	101	LeuileProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 12
qq	584	TITCTCATCCCAAGGGCCGGCTGGCTAGCAGGGCTGCTGTGCCGGATCCCAGGCCCCTG 643
Oy Db	121	GluLeualaLeuLeuIleLeuGlyValGlyLeuLeuaspPheCysGlyGlnValCysPhe 140
Oy Dp	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160
Oy Dp	161 764	TyrservaltyralaPheMetileSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Qy Db	181 824	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe
Qy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
O _Y	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
oy og	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
O.y Db	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
QY Dp	281 1124	SerTrpWetalaLeuwetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
Oy Dp	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
Qy Dp	321	ValargMetGlySerLeuGlyLeuPheLeuGlnCysalalleSerLeuValPheSerLeu 340
Oy Dp	341	ValMetaspargleuValGlnargPheGlyThrargalaValTyrLeualaSerValala 360
Oy Dp	361 1364	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380
Qy Db	381 1424	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Oy Dp	401	SerLeufyrHisargGluLysGlnValPheLeuProLysTyrargGlyaspThrGlyGly 420
Qy Db	421 1544	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
Oy Db	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460

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The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polypruclectides encoding them have cytośtatic activity and can be used in vaccines and in gene therapy. The polypeptides and polypeptides and polypeptides and polypeptides, antibodies against the polypeptides and vaccines comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06241 to AAA06691 and AAY82000 to AAX82020 represent sequences used in the exemplification of the present invention.
1843
                                                   Human immunogenic prostate tumour protein cDNA sequence SEQ ID NO:110.
                                                                                                                                                         ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
                                                                                                                                                                                                                                                                                                                                                                                           Human; prostate cancer; diagnosis; tumour; gene therapy; detection; immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptide useful for treating and diagnosing prostate cancer comprises an immunogenic portion of prostate tumor protein .
                                                                                                                    LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitcham JL;
                                                                                                                                                                                                        Xu J,
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                                                                                                                                                                                                                                                                                      AAA06349 standard; cDNA; 3410 BP.
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98US-0116134.
98US-0159812.
98US-0159822.
99US-0232149.
99US-023880.
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14-JUL-1998;
23-SEP-1998;
23-SEP-1998;
15-JAN-1999;
09-APR-1999;
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Sequenc	ice 3410 BP;	667 A; 1015 C;	945 G; 782 T; 1	other;				Qy Db 1
O .4 o	Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match: DB:	0 553.00 100.00% 100.00% 21	Length: Matches: Conservative: Mismatches: Indels:	3410 553 0 0				
-79	93A-113 (1-9	553) x AAA06349	(1-3410)					T 00
$\underline{\mathbf{e}} - \mathbf{H}$	tValGlnArgi GGTCCAGAGGG	MetValGinargLeuTrpValSerArgLeuLeuArgHisArgLysAlaGinLeuLeuLeu 	euLeuArgHisArgLi TGCTGCGGCACCGGA	/SAlaGlnLeu		20 343		r da
	alAsnLeuLeu' 	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrÜVa 	alCysLeuAlaAlaG TGTGTTTGGCCGCAG	LylleThrTyr 	1Pro	40 403		Oy Db 1
	roLeuLeuLeu(ProLeuLeuLeuGluValGlyValGluGluLySPheMetThrMetValLeuGly ¹ 1eGl; 	luLysPheMetThrMe 	tValLeuGly 	>-6	60 463		Qy Db 1
	roValLeuGly: 	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArg 	euLeuGlySerAlaSe TCCTAGGCTCAGCCA	erAspHisTrp	31y 	80 523		oy Db 1
	rgTyrGlyArg SCTATGGCCGC	ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeu 	rpAlaLeuSerLeuG 	LylleLeuLeu 	uSerLeu 	100 583	,	Oy Db 1
	heLeuIlePro TTCTCATCCCA	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArg 	laGlyLeuLeuCysP: 	COASPPROARG	~ - rn	120 643	<u></u>	OY Db 1
	luLeuAlaLeul AGCTGGCACTGC	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPh 	lyLeuLeuAspPheCy 	sGlyGlnVal	0 - 0	140 703		D G
	hrProLeuGlu 	Thr ProLeugluala Leu Leuserasp Leu Pheargasp proasphiscysar gan. 	euPheArgAspProAs TCTTCCGGGACCCGG	SPHisCysarge	Ala 	160 763		Oy Db 1
	yrServalTyri 	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuLeUroAla 	euGlyGlyCysLeuG 	LYTYr Leu Leu 	at ()	180 823		Oy Dp 1
	leAspTrpAsp′ TTGACTGGGAC	IleasptrpaspThrSeralaLeualaproTyrLeuGlyThrGlnGluGJuCys	roTyrLeuGlyThrG] 	InGluGluCys \GGAGGAGTGC	0 - =	200 883		uy Db 1
	lyLeuLeuThri 	GlybeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlı 	ysValAlaAlaThrLe 	suLeuValAlae	3 0	220 943		AAS635 ID A
	laAlaLeuGly 	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 	luGlyLeuSerAlaP) 	coserLeuser	(n ()	240 1003		XEX
	ysCysProCysi 	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuPr ^o ArgLei 	heArgAsnLeuGlyA. TCCGGAACCTGGGCGG	laLeuLeuPro	3 – m	260 1063		XXX
	isGlnLeuCys(ACCAGCTGTGC	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCy. 	hrLeuArgArgLeuPh 	neValAlaGlu 	ro — r)	280 1123		XXXX
	erTrpMetalal GCTGGATGGCA(SerTrpMetalaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGl ^u GlyLeu 	euPheTyrThrAspP} TGTTTACACGGATT	neValGlyGluc 		300 1183		XX PY PF PR
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                         1484 TCCCTCTACCACCGGGAGAGCAGGTGTTCCTGCCCAAATACCGAGGGACACTGGAGGT
                                                                                                                                                                 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro
                                                                                                                                                                                     PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu
                                                                                                                                  SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                              immunostimulant; tumour
                                                                                                                                                                                                                                                                                                                    cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                 sequence #109.
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                                                                                                                                                                                                                                                                                                                                                           AAS63557 standard; cDNA; 3410
                                                                                                                                                                                                                                                                                                                                                                                                              cancer; ss;
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polymucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting calls expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polymucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polymucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polymucleotide of the invention.
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                                                                                                                                                                                                                                                                 Kalos M
Carter
                                                                                                                                                                                                                                                            , Mitcham JL, Harlocker SL, Jiang Y, sr MW, Stolk JA, Day CH, Vedvick TS, Skeiky XAW, Hepler WT, Henderson RA;
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                                                           20000S-0605783.
2000US-0636215.
2000US-0651236.
2000US-0657279.
2000US-067426.
2000US-0568100.
2000US-0570737.
2000US-0593793.
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09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
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10-AUG-2000;
29-AUG-2000;
06-SEP-2000;
02-OCT-2000;
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op 2	- Ŏ	CTATGGCCGCCGCCCTTCATCTGGGCACTGTCCTTGGGCATCTTGAGCTTC
2y 1	1 Ph	eLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 12.
.,	21 G1	uLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 14
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Oy 2 Db 8	201 G1y 	yLeuLeuThrLeuIlePheLeuThrCysVa ¹ AlaAlaAThrLeuLeuValAlaGluGlu 22)
Oy 2		aAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 24
5 qa	- 4 CC	ACCCTCCTCCTCCCACCAGCACAGCGCTGTCGCCCCCTCCTTGTCGCCCCAC 10
0y 2	241 Cys	SCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu
Db 10	4 TG	TOTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG 10
0y 2	61 Hi 	ysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys
-	4	AGCTGTGCTGCCGCATGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGC
	281 SerT	rpMetalaLeuMetThrPheThrLeuPheTyrThraspPheValGlyGluGlyLeu
0b 11	4	3GATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCTG
ργ 3	_	LnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly
Db 11	84 TP	AGGCCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGC
2y 3	21 Vē	rgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu
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Dp 13	_	SACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA
	61 Al	ProvalAlaAlaGlyAlaThrCysLeuSerHisServalAlavalValThrAla
Db 13	64 GC	CTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT
oy 3	81 Se	rAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400

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AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro
                                                        PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu
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patient a
                     SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly
                                                                                                         CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla
                                                                                                                                                                 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal
                                                                                                                                                                                                                                                                                                                             prostate cancer; prostate-specific; diagnosis; vaccine;
tic; gene therapy; metastasis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide encoding a prostate-specific protein, diagnosing, monitoring and treating prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                      Jiang Y,
                                                                                                                                                                                                                                                                                                              Human prostate-specific full length cDNA sequence L1-12.
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Retter MW, Stolk JA,
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Kalos MD, Fanger GR, Day
                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Kalos MD, Fanger GR
Wang A, Meagher MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for use in vaccines
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               and can be used in vaccine production and gene therapy. (1), (II), antibodies to (II), fusion proteins comprising (II), and isolated (II) are calls prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies of (I) can be used for monitoring the progression of cancer in a patient (I) and (II) can also be used to improve diagnostic and therapeutic
                                                                                                                                                                methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01118 represent polynucleotide and amino acid sequences used in the
prostate-specific proteins (II). (I) and (II) have cytostatic activity
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                                                                                                                                                                                                           AAM01318 represent polynucleotide and amino acid sequences used in exemplification of the present invention.
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Mismatches:
                                                                                                                                                                                                                                                                    Sequence 3410 BP; 667 A; 1014 C; 945 G; 783
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Matches:
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553.00
100.00%
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Best Local Similarity:
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polynucleotide and polypeptide sequences used in the exemplification of the present invention.
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Query Match:
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                              1604 TICCCIAAIGGACACGIGGGGCGTGGAGGCAGTGGCTGCTCCCACCTCCACCTCGGCGCTC
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                                                                1124 AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGGGGGCTG
                                                                                           SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla
                                                                                                                                                                                                                                                                                                                                     SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu
                                                                                                              ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu
                                                                                                                                                                                                                                               AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro
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1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu

G; 783 T; 1 other;

945

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3410 553 0 0 0

Matches: Conservative: Mismatches:

Indels:

553.00 100.00% 100.00% 100.00%

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463

80

09

523

ArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100

ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly

ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly

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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P774P, P775P and B305D are located in a genomic region on chromosome 22q11.2 known as the Cat Eye Syndrome region. Prostate specific antigen (PSA) P501S was located on chromosome 1. AAH84671 to AAH85143 and AAG99000 to AAG99077 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an immunogenic portion of diagnosis and therapy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG;
Wang A;
                                                          syndrome;
                                                      Human; prostate cancer; therapy; diagnosis; cat eye syndro chromosome 22q11.2; prostate-specific protein; chromosome prostate specific antigen; PSA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SL, Jiang Y,
Skeiky YAW,
prostate-specific cDNA sequence L1-12/P501S
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Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated polypeptide comprising at least prostate-specific protein, useful in the prostate cancer -
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MD, Retter MW, Stolk JA,
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99US-0443686
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Kalos P
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7 197 C	1		1724	Db 1784 C		1844	Oy 541 Va		102530 AAH02	AC AAH025: XX DT 14-JUN	Pro	Huma	XX OS Homo sa XX PN W020013		PF 04-OCT	AA PR 04-OCT XX PA (CORI-		DR WPI; 20	XX PT Prosta		CC at leas CC its val				xx SQ Sequend Alignment SG
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CCTGCTGAGCCTC	ProArgProLeu	GlnValCysPhe	CAGGTGTGCTTC	SCysArgGlnAla 	LeuLeuProAla	CTCCTGCCTGCC	GluCysLeuPhe	SGAGTGCCTCTTT	avalAlaGluGlu 	TeuSerProHis	TTGTCGCCCCAC	TheuProArgleu	AlaGluLeuCys 	GlyGluGlyLeu	GGCGAGGGGCTG	TyraspGluGly	WalPheSerLeu	GTCTTCTCTCTG	MlaServalAla 	ValValThrAla	OTYTThrLeuAla	AspThrGlyGly	GACACTGGAGGT	ProGlyAlaPro	ProProAlaLeu
GTCCTTGGGCAI	ulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 	uAspPheCysGly		Thr ProLeuGluala LeuLeuSerasp LeuPheàrgasp ProaspHisCysargGlnali 	yCysLeuGlyTy:		IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluGluCysLeuPhe	GGGCACCCAGGAC	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis	GTCGGCCCCCTCC	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 	rThrAspPheVal	AGCTGGATGGCACTCATGACGTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCT	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu	CGCCATCTCCCTG	ValMetaspargLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 	AlaPheProValAlaAlaGlyAlaThrCySLeuSerHisSerValAlaValValThrAla 	SeralaalaLeuThrGlyPheThrPheSeralaLeuGlnIleLeuProTyrThrLeuAla	Seried Tribital Series	CAAATACCGAGGG	AlaSerSerGludspSerLeumetThrSerPheLeuProGlyProLysProGlyAlaPro 	PheproasnGlyHissValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu
TCATCTGGGCACT	rpLeuAlaGlyLe 	lyValGlyLeuLe		erAspLeuPheAr 	leSerLeuGlyGl		euAlaProTyrLe	гесссстасст	euThrCysValAl rcACCTGCGTAGC	roAlaGluGlyLe	CAGCAGAAGGGCT	euAlaPheArgAs IGGCTTTCCGGAA	roArgThrLeuAr 	heThrLeuPheTy		luProGlyThrGl 	euPheLeuGlnCy	rgttcctgcagtg	rgPheGlyThrAr 	laThrCysLeuse 	hrPheSerAlaLe	InvalPheLeuPr	AGGTGTTCCTGCC	etThrSerPheLe GACCAGCTTCCT	laGlyGlySerGl
GCCGCCGGCCCT	roArgAlaGlyT 	Snellelleleng	TGCTCATCCTGG	lualaLeuLeus 	yralaPheMetI		AspThrSerAlaL	ACACCAGIGCC	hrteullePheL	lyProThrGluP	GCCCCACCGAGC	ysargalaargi 	yscysargmetP 	laLeuMetThrP	CACTCATGACCT	alProargalagi 	lySerLeuGlyLa	GCAGCCTGGGGC	rgLeuValGlnA: 	alalaalaglya.	euThrGlyPheT 	isArgGluLysG	ACCGGGAGAAGC	luaspserLeum 	lyhisvalglya.
4 CGCTATGGCC	PheLe	GluLe									4 GCAGCGCTGG							4 GTTCGGATGG					4 TCCCTCTACC	1 AlaserserG 	1 PheProAsnG
Db 524	Oy 101 Db 584	7	Db 644	Oy 141		Db 764	0y 181	Db 824	Oy 201 Db 884	0y 221	Db 944	Oy 241 Db 1004	Oy 261	1	Db 1124	Oy 301 Db 1184	Qy 321	Db 1244	Oy 341 Db 1304	Oy 361 Db 1364	38.	40	Db 1484	Qy 421 Db 1544	Qy 441 Db 1604

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The present invention describes an isolated polypeptide (I) comprising I least an immunogenic portion of a prostate tumour antigen protein or so variant. (I) have oylostatic activity and can be used in vaccine coduction. (I), prostate tumour antigen polynucleotides, an antigen resenting cell (APC e.g. a dendritic cell) that expresses (I), and a armaceutical composition containing (I) are useful for inhibiting the evelopment of cancer in a patient. Antibodies specific for prostate evelopment of cancer in a patient. Antibodies specific for prostate secific proteins and oligonucleotides that hybridise to a blynucleotide that encodes a prostate specific protein are useful by detecting the presence or absence of a cancer or monitoring the cogression the progression of a cancer, especially prostate cancer. ANG2422 to AAB74798 to AAB74821 and AAB74830 are sequences sed in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ite tumour antigen determined full length cDNA sequence for L1-12.
                                                                                                                                                                                                polynucleotide, useful for
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                                                                                                                                                                                                                                                                                                                                                                                                      ate specific protein and its encoding polyreatment and diagnosis of prostate cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        530 standard; cDNA; 3410 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              r-2000; 2000WO-US27464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-0157455.
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B; AAB74800.
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scores:

Pred. N Score: Percent Best Lo Query M	. No.: e: ent Si Local Y Matc	: imilarity: 1 Similarity: ch:	0 553.00 100.00% 100.00% 100.00%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	3410 5553 0 0		
03-09-5	593-	-793A-113 (1-5	53) х ААНО2530	(1-3410)			
Oy Db 2	1 284		JLeuTrpValSerArgLeuLeu 	ArgHisArg	LysalaginLeuteur 	eu 20 TG 34	В
Qy Db 3	21	ValAsnLeuLeuT 	uThrPheGlyLeuGluVal 	alCysLeuAlaAlaGly 	yllethrfyrvalp 	ro 40 CG 40	æ
Qy Db 4	41	ProteuteuteuG 	euGluValGlyValGluG 	GluLysPheMetThrMet 	ValLeuGlyile 	Gly 60 GGT 46	e
Qy Db 4	61 464	ProValLeuGlyL 	LeuvalcysvalProLe 	euLeuGlySerAlaS 	erasphistrpargd	1y 80 11 GA 52	m
Oy Db 5	81 524	ArgTyrGlyArgA: 	ArgArgProPhelleT 	rpAlaLeuSerLeuGl 	lylleLeuLeuSerLei 	eu 10 - 58	0 E
0y 1 Db 5	101 584	PheLeulleProa: 	coargalaGlyTrpLeual 	laGlyLeuLeuCysProAs 	spProArghre	Leu 12 CTG 64	O E
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Oy 1 Db 7	141	ThrProLeuGluAlai 	laLeuLeuSerAspLeuPhe 	euPheArgAspProAspHi 	pHisCysArgGlnAla 	la 16 CC 76	9 9
Oy 1 Db 7	161 764	TyrSerValTyrA	AlaPheMetIleSerLeuGlyGl 	ycysLeuGl crGccrGGG	YTYrLeuLeuProAla 	1a 18 	0 %
Oy 1 Db 8	181 824	IleAspTrpAspT 		coTyrLeuGlyThrGlnG 	nGluGluCysLeuPho 	he 20 T 88	0 %
Oy 2 Db 8	201	GlyLeuLeuThrLd 	GlyLeuLeuThrLeuTlePheLeuThrCysValalaala' 	Thrle ACACT	Leuvalalaglug 	lu 22 AG 94	0 %
Qy 2 Db 9	221 944	AlaAlaLeuGlyP:	yProThrGluProAlaG] 	laGluGlyLeuSerAlaPr 	ProserteuserProH	is 24 	0
Qy 2, Db 10	241	CysCysProCysA: GCTGTCCATGCC	ArgAlaArgLeuAlaPhe 	neArgAsnLeuGlyAlal CCGGAACCTGGGCGCCC	aLeuLeuProArgLe 	eu 26 10	0
Oy 2 Db 10	61 64	HisGlnLeuCysCy 	/sArgMetProArg 	ThrLeuArgArgLeuPh 	PhevalalaGluLeuc 	ys 28 CC 11	0 23
Qy 2 Db 11	281	SerTrpMetalaL	LeuMetThrPheThrLeu 	PheTyrThraspPh TTTTACACGGATTT	ValGlyGluGlyL 	eu 30 TG 11	0 83
Oy 3 Db 11	301	TyrGlnGlyValP TACCAGGGCGTGC	/alProargalagluProGl 	roGlyThrGluAlaargArg 	HisTyrAspGluG CACTATGATGAAG	1y 32 GC 12	4 3

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                                                                          1844 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTACTTTGCTACACACAG
      ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln
ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu
                                                                                                                             AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro
                                                                                                                                                                                CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla
                                                                                                                                                                                                                                   LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal
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97US-0904804.
98US-0020956.
98US-0030607.
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01-AUG-1997;
09-FEB-1998;
25-FEB-1998;
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A, Day CH, Vedvick TS,
spler WT, Henderson RA;
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Skeiky YAW, Hepler
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GR, Retter MW, Stolk J.
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DAY C H.
VEDVICK T S.
CARTER D.
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KALOS M D.
FANGER G R.
RETTER M W.
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for treating
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                                          TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT 1543
                                                                                                                1604 TTCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGGGCTC 1663
                                                                                                                                                                                                          AGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783
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SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly
                                                                                           PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu
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2000US-0687507.
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cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that bind to a breast tumour polypeptide, detecting in the sample an amount of polypeptide that binds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient.isquences ABK28920-ABK29025 represent cDNA clones encoding human breast tumour polypeptides of the
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The present sequence is that of a triple gene fusion comprising, from the 5' end, the trax thioredoxin gene from Escherichia coli, the human ubiquitin coding sequence, the prostate antigen P501S (amino acids 55-55) coding sequence, and pNA encoding a histidine tail. The triple fusion was constructed in plasmid pRITI5063, which included the Saccharomyces cerevisiae CUP1 promoter and yeast alpha prepro signal sequence. The triple fusion protein (see AMM50661) was production of friple fusion proteins of the production of triple fusion proteins of the invention comprising ubiquitin fused between thioredoxin and a notein of interest, in this case P501S(aa55-553). A claimed method of producing a recombinant protein of interest involves: culturing a host cell (preferably E. coll) under conditions which allow for co-expression of the triple fusion and a ubiquitin specific endoprotease (especially UBP1 from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel DNA sequence encoding triple fusion protein comprising ubiguitin fused between thioredoxin and polypeptide of interest, useful for producing recombinant polypeptide of interest suitable for medicinal
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Chimeric - Homo sapiens.
Chimeric - Escherichia coli.
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                                                                   GlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAla
                                                                                     AlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeu
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                                                                                         AlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P501S; tumour; prostate; antigen;
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Escherichia coli
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the invention comprising ubiquitin fused between thioredoxin and a protein of interest, in this case P501S(aal 320). A claimed method of producing a recombinant protein of interest involves: culturing a host cell (preferably E. coli) under conditions which allow for co-expression of the triple fusion and a ubiquitin-specific endoprotease (especially UBP1 from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the ubiquitin-specific endoprotease in vivo. In the present case, expression was controlled by addition of tryptophan. The recombinant protein can used as a vaccine for cancer therapy.
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241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260

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The invention relates to isolated prostate specific polynecteds, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful, for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nseful for
                                                                                                                        1503
                                       1324 TGCTGTCCATGCCGGCCCGCTTGCCTTTCCGGAACGTGGGCGCCCTGCTTCCCGGCTG 1383
                                                                                             300
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Carter D;
                                                                                                           1444 AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGGCTG
                                                                                                                                                SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prostate cancer
                                                                                                                                                                                                                                                                                                                                            cancer; ss; cytostatic; immunostimulant; tumour.
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                                                                                                                                                                                                                                                                                                                  Human prosate cDNA P553S splice variant #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New human prostate-specific polypeptides the diagnosis and treatment of cancer, es
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 483-484; 579pp; English.
                                                                                                                                                                                                                                   BP.
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2000US-0558100.
2000US-0570737.
2000US-0593793.
2000US-065583.
2000US-0651236.
2000US-0651236.
2000US-0651236.
2000US-0651236.
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                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                               Human; prostate
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T; 0 other;	4034 320 0 0 0 0	-	sAlaGlnLeu	CGGAAAGCCCAGCTC	AlaGlyIleThrTyr'	ATCACCTAT	ValLeuGly 	rAspHisTrp	телссисте	rLeuGlyIleLeuLeuS(***************************************	SFICASPFICATG	sGlyGlnVal	тесссяесте	AsphisCysarg	LeuGlyTyrLeuLeuPro	CTACCT	lythrGlnGluGluCys)	\laThrLeuLeuValAlaC	стестесст	erAlaProSerLeuSerP	corcorrer	AlaLeuLeuPr 	Phevelalagi	CTCTTCGTGGCTGAGC	hevalGlyGlu	rtcgtgggcgAg	ArgArgHisTyrAsp(
C; 1141 G; 946	Length: Matches: Conservativ Mismatches Indels:	40 (1-4034)	euLeuArgHis	TGCTGCGGCAC	luValCysLeuAla	AGGTGTTTTGGCC	GluGluLySPhemetThrmet 	ProLeuLeuGlySerAlaSe	. ~	PrpAlaLeuSe	o Inc Int Oak	eunidely beubeucy 	ValG1yLeuLeuAspPheCy	16666	ASPLeuPheArgAspPrc 	erLeuGlyGlyCysLeuGl	GGGGCTC	rLeug] CCTGGC	ThrCysValAlaAla7	rgcgragcad	luGlyLeus	AAGGGCTGT	rgLeuAlaPheArgAsnLeuGly 	Argare	CCGCACCCTGCGCCGGC	hrLeuPheTyrThrAsp		ProGlyThrGluAla#
; 721 A; 1226	9.75e-288 320.00 100.00% : 100.00% 57.87%	-553) x AAS640	euTrpVals	GCTGTGGGTGAGCCGC	LeuThrPheGlyLeuG]	ACCTTT66CCT6	G uVa G yVa GAAGTGGGGGT	yLeuValCysVal	ccreercrerer	gArgArgProPheIle	Je I d D T de	OALGATAGIYIIPEEU 	uLeuIleLeuGly	тсстевесс	euLeuSer# 	YrAlaPheMetIleSerLeuG	TGCCTTCATGATCA	pAspThrSerAlaLeuAlaProTy 	LeuThrLeuIlePheLeuT	TTCCTC	lyProThrGluProAlaG	cccaccaagccag	1aA)	SArdMe	CCGCATGCC	tAlaLeuMetThrPheThrLeuPheT	ACTCATGACCTTCA	lProArgAlaGlu
ence 4034 BP	Scores: : imilarity: I Similarity ch:	-793A-113 (1	MetValGlnArgL	- 55	ValAsnLeuLe	AACC I	Proteuteuteu 	roValLeuGl	AGTGCTGGG	ArgTyrGlyArc	Tollob	TTCTCATCCC	GluLeuAlaLe	CTGGCACT	ThrProLeuGluAlaL	TyrSerValTy	CTCTGTCT	Ileaspirpas 	GlyLeuLeuTh	CCTC	AlaAlaLeuGl	SCGCTGG	CysCysProCysArgA TGCTGTCCATGCCGGG	- 1	CACCAGCTGTGCTG	SerTrpMetAl	AT	TyrGlnGlyVa
Sedne	ynment 1. No. re: cent S c Loca ry Mat	-09-593	н.	281	21	,	41	61	461	81		S 60	121	4	141	y v	761	181	201	881	221	941	241	261	9	281	1121	301
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (II) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated (II), to the antibodies are also used in the detection of cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. It can be used for monitoring the progression of cancer in a patient. (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate value. AMM913157 to AMH93144 and AAM01115 to AMM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encode
1181 TACCAGGGCTGCCCAGAGCTGAGCCGGGCACCAGGCCCGGAACACTATGATGAAGGT 1240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                          Reed SG;
Skeiky YAW;
                                                                                                                                                                                                     Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss.
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Retter MW, Stolk JA, S
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 460-461; 543pp; English.
                                                                                                                                                                           P553S cDNA splice variant P553S-10.
                                                                                 AAH93868 standard; cDNA; 4034 BP
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4D, Fanger GR, Day CH,
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320.00
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                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang A, Meagher MJ;
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                                                                                                                                                                                                                                                        Homo sapiens.
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GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTTGGCCGCAGGCATCACCTATGTGCCG 400
                                                                                                                                                                                                                                                                                                                                                        prostate cancer; vaccine; cytostatic; immunostimulant;
          9
                              80
         {\tt TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla}
                                                                                                                                                       ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla
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                                                                                          GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA
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Carter
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H, Vedvick TS,
Henderson RA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate-specific polynucleotides for mases, in particular prostate cancer, a
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G
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GR, Retter MW, Stolk
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2000us-0605783.
2000us-0651236.
2000us-0651236.
2000us-0651279.
2000us-0659426.
                        9705-0806099.
9705-0020804.
9805-0020956.
9805-0030607.
9805-0155812.
9905-0232149.
9905-0232149.
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2000US-0536857.
2000US-0568100.
2000US-0570737.
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 2001US-0759143
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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MITCHAM J L.
HARLOCKER S I
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DAY C H.
VEDVICK T S.
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RETTER M W.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                             JIANG Y.
KALOS M I
                                                                                                                                                                                            09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
29-AUG-2000;
06-SEP-2000;
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14-JUL-1998
23-SEP-1998
15-JAN-1999
13-JUL-1999
13-JUL-1999
12-NOV-1999
18-NOV-1999
12-JAN-2001;
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(first entry)

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                     MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu
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                                    21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro
                                          ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly
                                                                                    ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla
                                                                                                                                                                                        TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla
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                                                                                                                                                                                                                   AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis
                                                                                                                                                                                                                                                              ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGly,IleGly
                                                                                                                                              GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe
                                                                                                                                                                                                                                                                                                                       SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyGlyLeu
                                                                                                                                                                                                                                                                                                                                            TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly
     (1-4034)
    (1-553) x ABL95411
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    US-09-593-793A-113
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polynucleotides, polypetides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer! Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer - \,
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Carter D;
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                                               tumour.
                                             Human; prostate cancer; ss; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1203 BP; 175 A; 415 C; 368 G; 245 T; 0 other;
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tuberculosis fusion protein RA12-P501S-E2
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Matches:
Conservative:
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                                                                                          Chimeric - Homo sapiens.
Chimeric - Microbacterium tuberculosis.
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2000US-0570737.
2000US-059793.
2000US-0636218.
2000US-0657283.
2000US-0657279.
2000US-0672796.
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Best Local Similarity:
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                                                                                                                                                          WO200173032-A2.
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09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
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06-SEP-2000;
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                                                                                                                                      176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
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     IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro
                                      652 GATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGT
                                                                                                             HisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer; prostate-specific; cytostatic; gene therapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                 Ral2-P501S-E2 construct cDNA sequence,
                                                                                                                                                                                                                                                                                                                                          BP
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                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                   ValGlyGlu 298
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                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to exemplification of the present invention.
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SG;
YAW;
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, Reed S
Skeiky
                                                                                         for
                                                                                                      diagnosing, monitoring and treating prostate cancer in a for use in vaccines
                                                                                           protein,
 , Jiang Y,
Stolk JA,
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Matches:
Conservative:
Mismatches:
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Harlocker
Retter MW,
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                                                                                                                                                      8; Page 504; 543pp; English.
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GE,
                                                                                         New polynucleotide encoding a
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263.00
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 Mitcham GR, Day
                            Meagher MJ;
                                                            WPI; 2001-425873/45
Dillon DC,
MD, Fanger
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Best Local Similarity:
Query Match:
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 Xu J,
Kalos
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DB:
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TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
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                                                                                               HENDERSON R A.
                                                                            SKEIKY Y A W. HEPLER W T.
KALOS M D.
FANCER G R.
RETTER M W.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
                                                                                                                                               WPI; 2002-255649/30.
                                                                                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
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 (KALO/)
(FANG/)
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(WANG/)
(SKEI/)
(HEPL/)
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(DAYC/)
(VEDV/)
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                          1012 TCCTTGTCGCCCCCACTGCTGCTCCAFGCCGGCCCCCTTGCCGAACCTGGGCGCC 1071
                                                                                                                                         1132 GTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTC 1191
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                                                            SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255
                                                                                              LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
 Human; cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                276 ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPhe
                                                                                                                                                                                                                                                                        NO 851.
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    Mycobacterium tuberculosis,
    Homo sapiens.

                                                                                                                                                                                                                     ABL95524 standard; cDNA; 1203 BP.
                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1997; 97US-0806099.
01-AUG-1997; 97US-0804804.
02-FEB-1998; 98US-0020956.
23-FEB-1998; 98US-0115453.
23-SEP-1998; 98US-0115453.
15-JAN-1999; 99US-02149.
09-APR-1999; 99US-0288946.
13-JUL-1999; 99US-0352616.
13-JUL-1999; 99US-035887.
09-MAY-2000; 2000US-043813.
14-JAN-2000; 2000US-0588100.
12-MAY-2000; 2000US-0588100.
13-JUN-2000; 2000US-0588100.
13-JUN-2000; 2000US-058810.
13-JUN-2000; 2000US-058810.
13-JUN-2000; 2000US-058810.
13-JUN-2000; 2000US-058810.
13-JUN-2000; 2000US-058810.
29-AUG-2000; 2000US-058136.
06-SEP-2000; 2000US-0655136.
06-SEP-2000; 2000US-0657426.
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                                                                                                                                                                                                                                                       (first entry)
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MITCHAM J L.
HARLOCKER S L.
JIANG Y.
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  36 IleThrTyrValProProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMet
 Kalos M
Carter
                                                                                                       for
                                                                                      New prostate-specific polynucleotides for diagnosing and diseases, in particular prostate cancer, and as markers f progression of cancer
Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler'WT, Henderson RA;
                                                                                                                                                                                                                                                             G; 245 T; 0 other;
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Conservative:
Mismatches:
Indels:
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/transl_except= (pos:209..211, aa:Xaa)
/note= "Xaa corresponds to any of the naturally occurring
                                                                                                                                                                                                                                                                                                               foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis, diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kindney disorder; allergy; pregnancy related disorder; endocrine disorder; allergy; pregnancy related disorder; endocrine disorder; allergy; cell culture; chemotaxis; vulnerary; binding partner identification;
                                                                                                                                                                                                                                                                                       Human secreted protein-encoding gene 11 cDNA clone HWBAR14, SEQ ID NO:21
                                                                                             1071
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               GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu
                                        LeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro
                                                                                                                                              ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPhe
                                                                                                                                                                                                                                                                                                        secreted protein; proliferative disorder; cancer; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baker KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "Mature human secreted protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ruben SM, Komatsoulis GA, Wei P, Fiscella M,
                                                                                                                                                                                                                                                                                                                                                                                                                       Socation/Qualifiers
                                                                                                                                                                                                                                    BP.
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                                                                                                                                                                                                                                  AAD05230 standard; cDNA; 3878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0164835
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                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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AAD05220-AAD05282 represent CDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE01413 represent the proteins they encode.

CC AAE01415-AAE01433 represent human secreted protein fragments or variants.

CC AAE014123 represent human secreted protein fragments or variants.

CC AAE014123 represent human secreted protein fragments or variants.

The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy.

CC parhological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 21 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, AIDS, autoimmune of diseases (e.g., rheumatoid archiritis), inflammation, allergies, neurological disorders, schizophrenia, asthma, skin disorders (e.g., nourological disorders, atherosclerosis, cardiovascular disorders, cognitive disorders, fidney disorders, gastrointestinal disorders, proteins can also be used to aid wound healing and epithelial cell corrections in to prevent skin aging due to subbran, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding to process.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preservative to modify storage properties. Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein-encoding cDNA of
                                                                                         New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
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                                                                                                                                                                                                                                                                         Claim 1; Page 388-389; 490pp; English.
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                            P-PSDB; AAE01362
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ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
                           LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalos MD;
Carter D;
                                                                              SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu
                                CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal
                                                                                                                        785 TCGCCCCACTGCTGTCCATGCCGGGCCCGCTTTGCGGAACCTGGGCGCCCTGCTT
                                                                                                                                                                                          298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr
                                                                                                                                                                                                                                                                                                                   tumour.
                                                                                                                                                                                                                                                                                                                   Human; prostate cancer; ss; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                      P553S splice variant #1
                                                                                                                                                                                                                                                             AAS64038 standard; cDNA; 4894
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                                                                                                                                                                                                                                                                                        (first entry)
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Li SX,
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polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
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                                                                                     prostate cancer
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                                                               es and polynucleotides especially prostate ca
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263
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                                                                                                                                                                           The invention relates to isolated prostate-specific
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Conservative:
Mismatches:
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                                                          New human prostate-specific polypeptides the diagnosis and treatment of cancer, es
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                                                                                                                              Claim 1; Page 480-482; 579pp; English
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263.00
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47.56%
WPI; 2001-639232/73.
N-PSDB; AAU69874, AAU69875.
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Best Local Similarity:
Query Match:
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Conservative: Mismatches: Matches:

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4894

Length:

1.52e-234

Pred. No.:

Human P553S splice variant SEQ ID NO 702.

BP.

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LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
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                                                                                     (1-553) x AAH93866 (1-4894)
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         Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                    ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla
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Retter MW,
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Kalos MD, Fanger GR, Day CH,
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Wang A,

AAH93866;

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Length:

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AspGluGly 320
               Percent Similarity:
Best Local Similarity:
                                Query Match:
Pred. No.:
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        cancer; vaccine; cytostatic; immunostimulant;
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Carter
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A, Day CH, Vedvick TS,
epler WT, Henderson RA;
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GR, Retter MW, Stolk JA, Day CH,
Wang A, Skeiky YAW, Hepler WT,
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m for}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New prostate-specific polynucleotides for diseases, in particular prostate cancer, progression of cancer
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                                                                                                                                                                       990S-0439313
990S-0443686.
20000S-0483672
20000S-0536857.
20000S-0568100.
20000S-057737.
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2000US-0636215.
2000US-0651236.
2000US-0672779.
2000US-0679426.
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97US-0904804.
88US-0020956.
98US-0010607.
98US-0115453.
98US-0159812.
99US-0232149.
99US-0388946.
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KALOS M D.
FANGER G R.
RETTER M W.
STOLK J A.
DAY C H.
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               gene therapy; gene;
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HARLOCKER S
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DILLON D C.
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WANG A.
                                               JS200202248-A1
        cancer;
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09-APR-1999;
12-NOV-1999;
12-NOV-1999;
14-JAN-2000;
27-MAR-2000;
27-MAR-2000;
27-MAY-2000;
27-MAY-2000;
27-MAY-2000;
27-MAY-2000;
27-MAY-2000;
27-AUG-2000;
28-AUG-2000;
202-OCT-2000;
10-OCT-2000;
10-OCT-2000;
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                                Homo sapiens
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23-SEP-1998,
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                                                               21-FEB-2002
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25-FEB-1998
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01-AUG-1997
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(CART/)
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Li SX,
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other;

Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1

Alignment Scores:

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                                                                                             ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln
                                                                                                                                                                                     ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys
                                                                                                                                                                                            298 GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr
                                                                                                                                                                                                                                                                                                                                                                                                                                   2031 GAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCAGAGCCCGGAGACAAT
                                                                                                                                                                                                                                                                                                                                                                   ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla
                                                                                                                                                                                                                                                                                                                                                                                                GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly
4894
263
0
0
0
       Matches:
Conservative:
Mismatches:
                              Indels:
                                                   US-09-593-793A-113 (1-553) x ABL95409 (1-4894)
                                     Gaps:
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1.52e-234
263.00
100.00%
100.00%
47.56%
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2091 GATGAAGGT 2099
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1322 CTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCTAGGAGGGCTGCTGCTGCTGCCGGATCCC 1381
                                                        ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
                                                                                                                                                                                                                                                                                                                                                                                                       LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 ProargLeuHisGlnLeuCysCysArgMetProargThrLeuArgArgLeuPheValAla 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCCGGCTGCACCAGCTGTGCTGCTGCCATCCCCCGCACCCTGCGCCCGGCTCTTCGTGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harlocker SL, Jiang Y, Reed SG;
Retter MW, Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnosis; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prostate cancer; prostate-specific; cytostatic; gene therapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P553S cDNA splice variant P553S-6.
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Kalos MD, Fanger GR, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA; 6976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to isolated prostate-specific polymerical antibodies raised against the polymeptides for antigenic epitopes antibodies raised against the polymeptides for antigenic epitopes derived from them) and antigen presenting cells expressing the polymeptides. The antigen-presenting cells expressing the prospecially prostate cancer. The polymeptides, polymerications and the antigen-presenting cells are useful for stimulating and/or expanding the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. Compositions comprising the polymerication and for inhibiting an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polymerical for the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGCGTGGACGCTATGGCCGCCGCCGGCCCTTCATCTGGGCACTGTCCTTGGGCATCCTG 1321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TrpArgGlyArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlylleLeu 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human prostate-specific polypeptides and polynucleotides useful the diagnosis and treatment of cancer, especially prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kalos M
Carter
                                                           prostate cancer; ss; cytostatic; immunostimulant; tumour.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        illon DC, Mitcham JL, Harlocker SL, Jiang Y, R. Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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263
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Matches:
Conservative:
Mismatches:
  splice variant #4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 484-486; 579pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dillon DC, Mitcham JL,
                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-2000; 2000US-0570737.
13-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0505783.
10-MG-2000; 2000US-0565215.
29-MG-2000; 2000US-0551236.
06-SBP-2000; 2000US-05779.
02-CCT-2000; 2000US-057426.
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                                                                                                                                                                                                                                                                                                                                               2000US-0536857.
2000US-0568100.
                                                                                                                                                                                                                                                                                      27-MAR-2001; 2001WO-US09919
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100.00%
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47.56%
  Human prosate cDNA P553S
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                                                                                                                                                                                                                                                                                                                                         27-MAR-2000;
09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
29-AUG-2000;
29-AUG-2000;
06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6976
                                                                                                                    Homo sapiens
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                                                           Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li SX,
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10-AUG-2000; 2000US-0636215.
29-AUG-2000; 2000US-0651236.
06-SEP-2000; 2000US-0657279.
02-OCT-2000; 2000US-069426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           970S-0904804.
980S-0020956.
980S-0130607.
980S-01159812.
990S-0232149.
990S-0288146.
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2000US-0570737.
2000US-0593793.
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2000US-0536857.
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                                                                                                                                                                                                                                                                                                                    (first entry)
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DILLON D C.
MITCHAM J L.
HARLOCKER S 1
                                                                                                                                                                                                                                                                                                                                                                               gene therapy; gene;
                                                                                                                                                                                                                   1982 GATGAAGGT 1990
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KALOS M D.
FANGER G R.
RETTER M W.
                                                                                                                                                                                           318 AspGluGly 320
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                                                                                                                                                                                                                                                                                                                                                                                                                            US200202248-A1.
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12-MAY-2000; 2
13-JUN-2000; 2
                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-72N-1999;
09-APR-1999;
13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
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                                                                                                                                                                                                                                                                                                                   19-JUL-2002
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14-JUL-1998
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                                                                                                                                                                                                                                                                                            ABL95412;
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(MITC/)
(HARL/)
(JIAN/)
(KALO/)
(FANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (XC11X)
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                                                                                                                                                                                                                                                                                                                                                                   Human;
                                                                                               278
                                                                                                                                                                                                                                            RESULT 29
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                                                                                                                                                                                                                                                                               The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and each be used in vaccine production and gene therapy. (I); (II), and isolated antibodies to (II), inson proteins comprising (II), and isolated [II], and the antibodies are also used in the detection of cancer in a patient. (I) and the antibodies are also used on treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. Analysis7 to Anign3944 and AAM01115 to exemplification of the present invention.
                                                                                                                       which encode
                                                                                                                                                                                                           or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
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                                                            and
                                   New polynucleotide encoding a prostate-specific protein, for
diagnosing, monitoring and treating prostate cancer in a patient
for use in vaccines
                                                                                                                                                                                                                                                                                                      Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
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                                                                                             Claim 1; Page 461-463; 543pp; English.
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  Meagher MJ;
                       WPI; 2001-425873/45
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Best Local Similarity:
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1862 GAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC
                                                                                     258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla
                                                                                                                                    GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human P553S splice variant SEQ ID NO 1705
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Query Match:
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                                                                                                                                               their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention.
                                                                                                                                                                                                                                                                                                                                                1561
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                                                                                                                                                                                                                                                                                                                                                                                                  157
                                                                                                                                                                                                                                                                                                                                                                                                         LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 117
                                                                                                                                                                                                                                                                                                                                                                     118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
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                                                                                                                                                                                                                                                                               Gly11eGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis
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                                                                                                                                                                                                                                                                                                            TrpArgGlyArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlyIleLeu
                                                                                                           New prostate-specific polynucleotides for diagnosing and treating diseases, in particular prostate cancer, and as markers for the progression of cancer
                                                                  Kalos MI
Carter I
                                                                                                                                                                                          Sequence 6976 BP; 1312 A; 1996 C; 1961 G; 1706 T; 1 other;
                                                                 Harlocker SL, Jiang Y,
A, Day CH, Vedvick TS,
spler WT, Henderson RA;
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Matches:
Conservative:
Mismatches:
                                                                 Mitcham JL, Harlocker
er MW, Stolk JA, Day CH
Skeiky YAW, Hepler WT,
                                                                                                                                                                                                                                             Indels:
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WANG A.
SKEIKY Y A W.
HEPLER W T.
                                                 HEND/) HENDERSON R A.
        s.
                                                                                             WPI; 2002-255649/30.
                                                                        Retter
       VEDVICK T
                                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
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               CARTER D.
                                                                               Wang A,
DAY C H.
                                                                                                                                                                                                        Alignment Scores:
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                            (WANG/)
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Li SX,
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The present invention is related to a number of partial coding and protein sequences for the human prostate tissue protein PS108. These sequences can be used in the diagnosis and prognosis of prostate diseases, particularly prostate cancer. They can also be used to product antibodies which can be used in treatment. The present sequence is one of the PS108 partial coding sequences.
                                                                                                                                                                                   1921
                                                                                                                                                                                                                      277
                                                                                                                                                297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methods for detecting target prostate-specific polynucleotides or diseases of the prostate (e.g. prostate cancer), comprising detecting the presence of any of PS108 nucleic acid sequences in a test sample .
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                   GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly
                                                                                                                                                                   SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu
                                                                        ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla
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Yu P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer; PS108; antibody; tumour; metastasis; ds.
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Stroupe SD,
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Mismatches:
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A, Klass MR, Roberts-Rapp L,
Russell JC, Hodges SC;
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Matches:
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Gaps:
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                                                                                                                                                                                                                                                                                                  AspGluGly 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; prostate
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               GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp
                                                                                                            SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer
                                                                     ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal
                                                                                            PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln
                                                                                                                                                                                                                                                           GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly
                                                                                                                                                                                 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProPro
                                                                                                                                                                                                                                                                                                                                                                                  Prostate; PS108; immunogen; drug screening; image localisation; diagnostic; therapeutic; prostate tissue disease; cancer; metas expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                       Prostate gene PS108-specific cDNA (EST) consensus sequence
                                                                                                                                                                                                                                                                                                  ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
     (1-2133)
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     (1-553) x AAC64928
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    US-09-593-793A-113
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The sequence represents the prostate gene PS108-specific expressed sequence tag (EST) consensus sequence. The sequence was produced from overlapping PS108 ESTs sequences to produce a full length consensus sequence. This sequence was then used to produce PS108 polypeptides which sequence antibodies. The polypeptide is useful for screening compounds which specifically bind to the polypeptide and for screening for drugs, compounds, or any other agent which can be used to treat of diseases associated with PS108. The antibody is useful to detect, or for image localisation of, PS108 antigen in a patient, for detecting or diseases or conditions associated with PS108, especially cancer. The antibody is also cuseful for generating chimeric antibodies for therapeutic useful for generating chimeric antibodies for therapeutic useful for generating chimeric antibodies for therapeutic use, for inhibiting the biological activity of PS108, in therapy (for e.g. to treat prostate tissue disease including prostate cancer and its test metastases), and to detect the presence of any polypeptide in a test and part and the ps108.
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Klass MR, ¡Kratochvil JD, Roberts-Rapp L;
Yu H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel PS108 polypeptide useful in assays for detecting antibodies prostate tissue, and as immunogens to produce PS108 antibodies \,
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97US-0850713.
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Stroupe SD,
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Best Local Similarity:
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                                                                                                                                                                                                              01-MAY-1998;
02-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                              Granados EN,
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182 GTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACACACGTGTGGCCGTGGTG

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                                                         GlyGlyalaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
                                                                       362 GGAGGIGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGA 421
                                                                                                                478
                                                                                                                                                        601
                                                                                                                                                                     518
                                                                                                                                                                                   661
                                                                                                                                                                                                538
                                                                                                                                                                                                       gene derived from overlapping clones.
    499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln
                                                                                                                                                                                                SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla
                                                                                                                      LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr
                                                                                                                AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr
                                                                                                                                          GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla
                                                                                                                                                                                                                                                                                                                       PS108 gene; prostate disease; benign prostatic hyperplasia; BPH; prostatitis; prostatic intraepithelial neoplasia; PIN; cancer; drug screening; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kratochvil JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Friedman PN;
MR, Kratoch
                                                                                                                                                                                                                         M, Colpitts TL,
Hodges SC, Klass
JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 2..769 /*tag= a
                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                          sequence of the PS108
                                                                                                                                                                                                                                                                  CDNA; 2152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gordon J, Granados EN, Hodg
Roberts-Rapp L, Russell JC,
                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US08930
                                                                                                                                                                                                                                                                                                                                                                                                                                          97US-0850713
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                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                                                                                                                                                                  AAV71181 standard;
                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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The present sequence represents the consensus sequence for a PS108 gene. The sequence is derived from overlapping clones AAV71166-79. The clone sequences are PS108 gene-specific. They are used in the method of the invention. The specification describes a method for detecting the presence of a target PS108 polynucleotide in a test sample. The method comprises contacting the test sample with at least 1 PS108-specific polynucleotide or complement, and detecting the presence of the target PS108 polynucleotide. The products can be used for detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (BPH), prostatits, prostatic intraeplihalial neoplasia (PIN) and cancer. In particular the products can be used in drug screening and gene therapy.
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eases, e.c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 GTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 TCTCTGGTCATGGACCGGCTGGTGGAGCGATTCGGCAGTCGAGCAGTCTATTTGGCCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         379 ThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             302 CTGGCCTCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGGCCCAAATACCGAGGGGACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 359 ValAlaAlaPheProValAlaAlaGlyAlaThrCySL&uSerHisSerValAlaValVal
                                            New isolated prostate-specific polynucleotides - used to develo products for the diagnosis and treatment of prostate diseases, benign hyperplasia, prostatic or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2152
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
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                                                                                                                                     Claim 1; Fig 1A-E; 122pp; English.
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255.00
100.00%
100.00%
46.11%
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Best Local Similarity:
P-PSDB; AAW85068
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Pred. No.:
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The present invention is related to a number of partial coding and protein sequences for the human prostate tissue protein PS108. These sequences can be used in the diagnosis and prognosis of prostate diseases, particularly prostate cancer. They can also be used to produce antibodies which can be used in treatment. The present sequence is one of the PS108 partial coding sequences.
                                                 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methods for detecting target prostate-specific polynucleotides or diseases of the prostate (e.g. prostate cancer), comprising detecting the presence of any of PS108 nucleic acid sequences in a test sample
                          661
                                                                         721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341
                                               PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln
                       602 Trccrccrccrccrccrccrccrcrrrrrggccrccarrcragcrccagcrcagcrcag
                                                                                                                                                                                                                                                                            ds.
                                                                                                                                                                                                                                                                           cancer; PS108; antibody; tumour; metastasis;
                                                                                                                                                                                                                                                   Human prostate-related PS108 partial coding sequence SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Granados EN
Stroupe SD,
                                                                                               Sequence 2124 BP; 411 A; 616 C; 558 G; 539 T; 0 other;
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Matches:
Conservative:
Mismatches:
Indels:
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Billing-Medel PA, Klass MR, Roberts-Rapp L, S
Kratochvil JD, Russell JC, Hodges SC;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Column 75-78; 55pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                               (ABBO ) ABBOTT LAB.
                                                                                                                                                                          AAC64927 standard;
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Best Local Similarity:
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                                                                                                                                                                                                                          07-FEB-2001
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Prostate; PSIO8; immunogen; drug screening; image localisation; diagnostic; therapeutic; prostate tissue disease; cancer; metastasis; expressed sequence tag; EST; ss.
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543 GTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTG
                                                                                                                                                                                                                     PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer
                                                             SerSerGluaspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe
                                                                                                                                                                                                                                                                           502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr
                                                                                                                                                                                                                                                                                   603 TCCCAGGTGGCCCCATCTTTTTTGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACT
                                                                                                                                                                                                                                            482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu
                                                                                                                                                                                                              GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate gene PS108-specific cDNA clone 1711346IH
                                                                                                                                                                                                                                                                                                                                      AAS07601 standard; cDNA; 2124 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0071710.
97US-0850713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6252047-B1.
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02-MAY-1997;
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GlyAlaSerAlaCysAspValSerValArgValValValVblGlyGluProThrGluAlaArg

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The sequence represents the coding sequence of prostate gene PS108-
specific expressed sequence tag (EST) cDNA clone 1711346IH. The sequence
cas used along with other overlapping cDNA clones to produce a full
clength consensus sequence (see AASO/155). This sequence could then be
length consensus sequence (see AASO/155). This sequence could then be
consecuting antibodies to prostate tissue, and as immunogens to produce
cantibodies. The polypeptide is useful for screening compounds which
specifically bind to the polypeptide and for screening for drugs,
compounds, or any other agent which can be used to treat diseases
cascociated with PS108. The antibody is useful to detecting or diagnosing a
compounds, or any other agent which can be used to treat diseases
cascociated with PS108 antigen in a patient, for detecting or diagnosing a
closalisation of PS108 antigen in a patient, for detecting or diagnosing
condition, as delivery agents for therapeutic agents as well
cas for diagnostic tests and for screening for diseases or conditions
cassociated with PS108, especially cancer. The antibody is also useful for
conditional activity of PS108, in therapeutic use, for inhibiting the
conditional activity of PS108, in therapeutic use, for inhibiting the
clissue disease including prostate cancer and its metastases), and to
detect the presence of any polypeptide in a test sample which shares one
conditionally activity the PS108 polypeptide.
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                       Friedman PN, Gordon J;
shvil JD, Roberts-Rapp
                                                                                                                                                                            Novel PS108 polypeptide useful in assays for detecting antibodies prostate tissue, and as immunogens to produce PS108 antibodies \,
                       M, Colpitts TL, Friedman
Klass MR, Kratochvil JD,
Yu H;
                                                                                                                                                                                                                                                       Example 1; Fig 1; 55pp; English.
                       Cohen
                                               Hodges SC,
Stroupe SD,
                                                                                                                          WPI; 2001-424488/45.
                          PA,
                          Billing-Medel
                                                  Granados EN,
Russell JC,
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411 A; 616 C; 558 G; 539 T; 0 other;

Sequence 2124 BP;

123 ATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCT 182 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321 AlaalaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401 402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421 MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 362 PheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 2124 252 0 0 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels: US-09-593-793A-113 (1-553) x AAS07601 (1-2124) Gaps: ..19e-224 252.00 100.00% 100.00% 45.57% Similarity: Percent Similarity: Alignment Scores: Query Match: .. Q Best Local 302 382 243 322 342 Score: ò g g qq ΩD g qq ò οy ò ò ò

242

381

442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCys 461

SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441

422

ŏ g ò

361

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The present sequence represents the full length contig of the PS108 gene, as represented by clone 171346fH. This clone is the contig of overlapping clones AAV1166-79. The clone sequences are PS108 gene-specific. They are used in the method of the invention. The specification describes a method for detecting the presence of a target PS108 polynucleotide in a test sample. The method comprises contacting the test sample with at least 1 PS108-specific polynucleotide or complement, and detecting the presence of the target PS108 polynucleotide. The products can be used for detecting, diagnosing, staging, monitoring, producting, in vivo imaging, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (BPH), prostatitis,
                                                          501
                                                                                        602
                                                                                                                       521
                                                                                                                                                     662
                                                                                                                                                                                541
                                                                                                                                                                                                 ValValProG1yArgG1yI1eCysLeuAspLeuAlaIµeLeuAspSerAlaPheLeuLeu
                                                                          SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr
                                                                                                                                      522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated prostate-specific polynucleotides - used to develop products for the diagnosis and treatment of prostate diseases, e. benign hyperplasia, prostatic or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene; prostate disease; benign prostatic hyperplasia; BPH; atitis; prostatic intraepithelial neoplasia; PIN; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kratochvil JD;
                                                                                                                                                                                                                                                                                                                                                                                                                                Clone 1711346IH, the PS108 gene contig full length sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Friedman PN;
MR, Kratoch
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                                                                                                                                                                                                                                                                          258
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s EN, Hodges SC, Klass
ussell JC, Stroupe SD;
                                                                                                                                                                                                                                                          723 GTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG
                                                                                                                                                                                                                                            ValPheAspLysSerAspLeuAlaLysTyrSerAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug screening; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                       AAV71180 standard; cDNA; 2143 BP.
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Roberts-Rapp L,
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   In particular
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prostatic intraepithelial neoplasia (PIN) and cancer. In products can be used in drug screening and gene therapy
                                              541 T; 0 other;
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252
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Matches:
Conservative:
Mismatches:
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                                              Sequence 2143 BP; 418 A; 621
                                                                                           1.2e-224
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Best Local Similarity:
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The invention relates to isolated prostate-specific polypeptides, polypeptides, fusion proteins of the polypeptides, artibodies raised against the polypeptides for antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding T cells specific for a tumour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the oplynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific protein invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human prostate-specific polypeptides and polynucleotides useful the diagnosis and treatment of cancer, especially prostate cancer - \,
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Carter D
                                            Human; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 A; 875 C; 773 G; 714 T; 0 other;
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Matches:
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prosate cDNA P553S splice variant #2.
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                                                                                                                                                                                                                                                                              27-MAR-2000; 2000US-0536857.
09-MAY-2000; 2000US-0568100.
12-MAY-2000; 2000US-0570737.
13-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0653783.
10-AUG-2000; 2000US-0651236.
29-AUG-2000; 2000US-0657279.
02-OCT-2000; 2000US-0657279.
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Best Local Similarity:
                                                                                                                                          WO200173032-A2.
                                                                                              Homo sapiens
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Alignment Scores:
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                                                                                       1410 TCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGCCATTTACTTTGCT 1469
                                                           GAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCC 1349
                                                   418
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                                                                                                                                                                         498
                                                                                                                                                                                                                                   538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -
GlualaargValValProGlyArgGlyIleCysLeuaspLeualaIleLeuaspSerala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Reed SG;
Skeiky YAW;
                      ThralaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr
                                                  399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr
                                                                                GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly
                                                                                                                                                                                                                                   SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla
                                                                                                                                                                                                                                                                                                                                                                         prostate cancer; prostate-specific; diagnosis; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SL, Jim.
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Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                therapy; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                          P553S cDNA splice variant P553S-12.
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CH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon DC, Mitcham
4D, Fanger GR, Day
, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                           entry)
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                                                                                                                                                                                                                                                                                                                                                                                cytostatic; gene
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or
                                                       prostate-specific proteins (II). (II) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and the bear of (II), fusion proteins comprising (II), and isolated T cells prepared using (I) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies of (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH03157 to AAH9344 and AAM01115 to AAM01118 represent polynucleotide and amino acid sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ThralaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr
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                                          sednences
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235
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Mismatches:
Indels:
                                          present invention describes polynucleotide
                                                                                                                                                                                                                                                                                                                                                    Sequence 2904 BP; 542 A; 875 C; 773 G; 714
                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
Matches:
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                                                                                                                                                                                                                                                                                                              exemplification of the present invention
  543pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              1.12e-208
235.00
100.00$
100.00$
42.50$
Page 459-460;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
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other

2904 235 0 0 0

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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention.
                                                                                                                                                                                                                                                                                                                                for diagnosing and treating
                                                                                                                                                                                                                                                                                             ValAlaAlaPheProValAlaAlaGlyAlaThrCySLeuSerHiSSerValAlaVal
                                                                                                                                                                                                                                                                                                                930 GTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                          GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly
New prostate-specific polynucleotides for diagnosing and treatin
diseases, in particular prostate cancer, and as markers for the
progression of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Matches:
Conservative:
Mismatches:
Indels:
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G; 714 T; 0
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                                       Claim 1; SEQ ID NO 703; 87pp; English.
                                                                                                       542 A; 875 C; 773
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Best Local Similarity:
Query Match:
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                                                                                                                                          Human; cancer; prostate cancer; vaccine; cytostatic; immundstimulant; gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kalos MD;
Carter D;
         Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                       ID NO 703
                                                                  ABL95410 standard; cDNA; 2904 BP
                                                                                                                       Human P553S splice variant SEQ
                                                                                                                                                                                                                                                                                                                                                                 09-MAY 2000; 20000S-058100; 12-MAY 2000; 20000S-0581100; 13-JUN-2000; 20000S-059793; 27-JUN-2000; 20000S-058783; 10-AUG-2000; 2000US-0551236; 29-AUG-2000; 2000US-0551236; 06-SEP-2000; 2000US-0551236; 06-SEP-2000; 2000US-0551279; 02-OCT-2000; 2000US-0651279; 10-OCT-2000; 2000US-065126;
                                                                                                                                                                                                                                             970S-0806099.
9778-0904804.
980S-0020956.
980S-0115453.
980S-012912.
990S-0232149.
99US-0232146.
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2000US-0536857
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MITCHAM J L.
HARLOCKER S L.
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WANG A.
SKEIKY Y A W.
HEPLER W T.
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DAY C H.
VEDVICK T S.
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KALOS M D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARTER D.
                                                                                                                                                                                       JS200202248-A1.
                                                                                                                                                                                                                                             25-FEB-1997;
01-AdC-1997;
02-FEB-1998;
14-7dL-1998;
14-7dL-1998;
15-JAN-1999;
15-JAN-1999;
13-JUL-1999;
12-NOV-1999;
14-JAN-2000;
27-MAR-2000;
                                                                                                                                                                       Homo sapiens
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                                                                                                      19-JUL-2002
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                                                                                    ABL95410;
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(MITC/)
(HARL/)
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LeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerVal

340 427 AlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThr 399 909 419 999

380 547

360 487 607

400

AAZ45677 standard; cDNA; 2462

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RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying biomolecules for the diagnosis and treatment of diseases
                                                                                                                                            Prostate cancer-associated gene; Incyte clone 1864683; bone cancer; cell proliferation; cancer; adrenal gland cancer; bladder cancer; prostate cancer; ss.
                                                                                                                                                                                                                                                                                                                                          /product= "prostate cancer-associated protein" 376..516
/*tag= b
                                                                                              cDNA sequence of a novel prostate cancer-associated gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sprinzak EA;
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                                                                                                                                                                                                                                                                                      Location/Qualifiers
376..1071
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US13524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0102615
                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (INCY-) INCYTE PHARM INC
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                                              06-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                             sig_peptide
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AAZ45677;
                                                                                                                                                                                                                                                                                           Key
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ProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAla 459

727

440

LeuCysGlyAlaSerAlaCysAspValSerValArgValValValValGlyGluProThrGlu 479

787 480 847 500

460

786

499 906 519 996

967 GTCACTGCCTATATGGTGTCTGCCGCA 993 ValThrAlaTyrMetValSerAlaAla 528

520

ABN81320 standard; cDNA; 3663 BP

ABN81320;

LeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSer

AlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPhe

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Human; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic;
vasotropic; dermatological; allergy; hypersensitivity; rhinitis; asthma;
                                                                                                                                                                                                                                                                    Human mast cell related gene MC14 SEQ ID NO 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
294..746
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/product= "MC14-2"
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2001US-275479P.
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/product= "1
1238..2218
/*tag= a
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14-MAR-2001;
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US-09-593-793A-113 (1-553) x AAZ45677 (1-2462)

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Length:
Matches:
Conservative:
Mismatches:
Indels:

1.6e-184 209.00 100.00% 100.00% 37.79%

Percent Similarity: Best Local Similarity:

Query Match:

Alignment Scores:

.. No

Score:

Gaps:

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The invention relates to isolated nucleic acid (ABNB1319-ABNB1324), corresponding to genes differentially expressed in mast cells following activation or in paintents with allergic hypersensitivity disease, (I) that encodes proteins (ABB7756) (II) or a protein fragment of partners. (I) or (II) is useful for diagnosing or treating a disease state (e.g. allergic hypersensitivity, seasonal rhinitis, actima disease state (e.g. allergic hypersensitivity, seasonal rhinitis, actima, urticaria or atopic dermatitis or mastocytosis) in a subject which involves determining the level of expression of (I) or (II). A computer system, comprising a database containing information identifying the expression level in a tissue or at least one mast cell of (I), is useful or presenting information to identify the relative expression level of (I). (II) is used as a marker to detect, diagnose or identify an allergic modulate gene expression or activity and as an antiget that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as agents that modulate expression of the protein or agents, such as a general antibodies. (II) and thus are useful for a pativity and function of (II) and thus are useful for a pativity and function of (II) and thus are useful for a pativity.
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                                                                                                                                                                                                                                           differentially expressed in mast
                                                                                                                                                                                                                                      Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 98-102; 119pp; English
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28-MAR-2001; 2001US-279115P, 02-APR-2001; 2001US-280143P.
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                                                                                                                                                                  WPI; 2002-508560/54
                                                                                                                     K, Pirozzi
                                                                      (UNIO ) UCB SA
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Sequence 3663 BP; 740 A; 1058 C; 985 G; 880 T; 0 other; 3663 187 0000 Conservative: Mismatches: Matches: Length: Indels: 7.44e-164 187.00 100.00% 100.00% 33.82% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: Score:

US-09-593-793A-113 (1-553) x ABN81320 (1-3663)

1331 GGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCAGTGACCAC 1390 58 GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 86 a g g δ ò õ

1451 CTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGCTAGCAGGGCTGCTGTGCCCGGATCCC 1510 118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln g ö

137

117

11

157

138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys

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of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library. 1751 TGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTG 1810 1811 GCTGAGGAGGCAGCGCTGGCCCCACCGAGCAGAGAGAGGCTGTCGGCCCCCTCTTG 1870 1631 CGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGGTGCTGGGCTACCTC 1690 The present sequence is a new DNA which encodes an immunogenic portion 237 Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu Prostate; cancer; tumour; vaccine; immunogen; clone; 3' cDNA sequence of prostate tumour clone L1-12 Claim 3; Page 38-39; 130pp; English BP 1871 TCGCCCCACTGCTGTCCATGC 1891 SerProHisCysCysProCys 244 AAV61144 standard; cDNA; 789 98WO-US03492. 98US-0020956. 97US-0806099. 97US-0904804 (first entry) (CORI-) CORIXA CORP. WPI; 1998-609886/51 ., , × Homo sapiens. WO9837093-A2. 01-AUG-1997; 25-FEB-1998; 09-FEB-1998; 25-FEB-1997; 06-JAN-1999 27-AUG-1998 Dillon DC, AAV61144; 178 198 218 238 RESULT 41 AAV61144 QC qq Dp g ò ò

789 122 0 0 0 0 Conservative: Mismatches: Indels: Length: Matches: Gaps: 6.07e-104 122.00 100.00% 100.00% 22.06% Similarity: Percent Similarity: Alignment Scores: Match: .. Q Best Local Score: Query

Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;

US-09-593-793A-113 (1-553) x AAV61144 (1-789)

AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376 357 δλ 14 other;

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G; 182

221

BP; 122 A; 250 C;

us-09-593-793a-113.olig.rng

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Sequence 789
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                                                                                                     396
                                    397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
                                                                           ProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGlu 476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human prostate specific tumour protein and fragments – useful for detecting and treating prostate cancers
ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro
                                                                                                                                                                                                                                                                                                                                                            Prostate tumour specific gene; human; prostate cancer; detection;
                                                                                                                                                                                                                                                                                                                                         3' fragment of prostate tumour specific gene L1-12.
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01-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; diagnosis; tumour; gene therapy; detection;
                                                                                        TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly
                                                                                                                                                                                                    AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys
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22.06%
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98US-0116134.
98US-0159812.
98US-0232149.
99US-0232149.
99US-023880.
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                         Percent Similarity:
Best Local Similarity:
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23-SEP-1998;
23-SEP-1998;
15-JAN-1999;
15-JAN-1999;
09-APR-1999;
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Alignment Scores
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                                                                                                          polynucleotides encoding them, antigen presenting cells which express polynucleotides encoding them, antigen presenting cells which express comprising the molyneptides against the polypeptides and vaccines comprising the mean be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polynucleotides encoding the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06641 to AAA06691 and AAX82000 to AAX82020 represent sequences used in the exemplification of
                                                                              immunogenic portion of a prostate tumour profein (PTP). The polypeptides and polynucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and
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                                                                     The present invention describes isolated polypeptides, comprising an
                     cancer
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                    prostate
protein
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                   and diagnosing prostate tumor
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                   New polypeptide useful for treating comprises an immunogenic portion of
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                                                  263pp; English
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                                                                                                                                                                                              the present invention.
WPI; 2000-171268/15
                                                  Claim 1; Page 99;
                                                                                                                                                                                                                                                                 Similarity:
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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for polynucleotide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human prostate-specific polypeptides and polynucleotides useful for the diagnosis and treatment of cancer, especially prostate cancer -
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Carter i
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A, Day CH, Vedvick TS,
Epler WT, Henderson RA;
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Fanger GR, Retter MW, Stolk JA, Day CH
Li SX, Wang A, Skelky YAW, Hepler WT,
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2000US-056100.
2000US-0593793.
2000US-0593783.
2000US-0651235.
2000US-0651236.
2000US-0651236.
2000US-0651236.
                                                                                 27-MAR-2001; 2001WO-US09919
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Best Local Similarity:
WO200173032-A2.
                                                                                                                                                               12-MAY-2000;
13-JUN-2000;
                                                                                                                                                                                                           27-JUN-2000;
10-AUG-2000;
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397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnyalPheLeuProLysTyrArgGly
         AspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys
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Job time : 306 secs
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                          311
                                          Novel polynucleotide encoding polypeptide comprising a portion of prostate tumour protein useful for inhibiting development of prostate cancer or for treating prostate cancer in a patient \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIJeLeuPro 396
      G; 182 T; 14 other;
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Matches:
Conservative:
Mismatches:
Indels:
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97US-0904804.
98US-0020956.
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Best Local Similarity:
Query Match:
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01-AUG-1997;
09-FEB-1998;
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US-09-525-397-15
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US-09-160-110
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                                                                                                                              nucleic search, using frame_plus_p2n model
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Copyright (c) 1993
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	21 ValasnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40	LeuGlu 	ProvalLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 8	81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100 	101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120	121 GluLeualaLeuLeuIleLeuGlyvalGlyLeuLeuaspPheCysGlyGlnValCysPhe 140	141 ThrProLeuGlualaLeuLeuSerAspLeuPhargAspProAspHisCysArgGlnAla 160 	161 TyrSerValTyrAlaPheMetIleSerLeug yGlyClysLeuGlyTyrLeuLeuProAla 180 	181 IleaspTrpaspThrSeralaLeualaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200 	201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220 	221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240 HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260 	261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280	281 SerTrpMetalaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300	301 TyrGlnGlyValProArgAlaGluProGly [†] hrGluAlaArgArgHisTyrAspGluGly 320 	21 ValargMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 3 	341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360	361 AlaPheProValAlaAlaGlyAlaThrCysteuSerHisSerValAlaValValThrAla 380
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		77	US-08-261-206A-36 US-09-605-785-485 US-09-439-313-485 US-08-298-073-20		09020956	1982 MATION: Au Jiangchun Dillin, Davin C.	UNDS FOR IMMUNOTHERAPY OF P	bsJU COlumbia Center, 701 Fifth Avenue eattle A.A. USA	k ible	S/MS-DOS ase #1.0, Version #1.30 09/020,956	φ	31,392 5R: 210121.427C2 AMTION: 4900	110: s			Length: 3410 Matches: 553 Conservative: 0 Mismatches: 0	Indels: Gaps:	/938-113 (1-353) X US-U9-U2U-956-11U (1-341U) MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLe
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нын			7 1.3	-	6-110 10, Appli	NFORMATION Xu, NT: Dill	S OM EM		ZIF: 98104 COMPUTER READABLE MEDIUM TYPE: FI COMPUTER: IBM	OPERATING SYSTEM: SOFTWARE: PATENTI RRENT APPLICATION NUMBER	FILING DATE: O CLASSIFICATION: ATTORNEY/AGENT IN NAME: MAKI, DA	REGISTRATION NUMBER: REFERENCE/DOCKET NUM LLECOMMUNICATION INFO	ည္≨ကု	nucler EDNESS: GY: li TYPE:	<u>.</u>	Scores: milarity: Similarity	,	3A-113 (1 tValGlnAr
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		ი ი 9 9 9 2 9 5 4 3	96 98 99	100	RESULT 1 US-09-020-956-110 ; Sequence 110, Application US/09020956	GENERAL INFOI GENERAL INFOI APPLICANT: APPLICANT:	TITLE C NUMBER CORRESP	STREET: CITY: S STATE: COUNTRY:	COMPUTE	CURRENT CORRENT APPLI	CLASS CLASS ATTORNE	REGIS REFER TELECOM TELEP	TELEFAX: INFORMATION I SEQUENCE CI	TYPE: D STRANDED TOPOLOGY MOLECULE	; OKIGINAL SOU ; ORGANISM: US-09-020-956-110	Alignment Scores: Pred. No.: Score: Percent Similarity Hest Foreal Similarity	Matc	US-U9-593-/93A-113 , Qy 1 MetValG1

PRE: nucleic acid RRANDEDNESS: single POLOCY: linear SCULE TYPE: cDNA SINAL SOURCE: RGANISM: Homo sapiens 0-607-110	Pred. No.: 0	Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20	41 ProLeuLeuGluValGlyValGluCluLySPhemetThrMetValLeuGly1leGly 60	Db 464 CCAGTGCTGGCCTGGTCTGTGTCCCCTCCTAGGCTCAGTGACCACTGGCGTGGA 523 Qy 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100	101
Db 1364 GCTTTCCCTGTGGCTGCCGACATGCCTGTCCCACAGTGGGCCGTGGTGACAGCT 1423 Qy 381 SeralaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400 1111111111111111111111111111111111	Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440	Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480	501 LeuserGlnValalaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 52	Db 1844 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903 Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553	Sequence 110 Sequence Characters Sequence Characters Sequence Characters Sequence Characters Sequence Characters Sequence Characters Sequence Sequence 110 Sequence Characters Sequence Sequence 110 Sequence Characters Sequence Sequence Sequence 110 Sequence Characters Sequence Se

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281 SerTrpMetalaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300	y 320	21 ValargmetelySerLeuGlyLeupheLeuGlnCysAlaIleSerLeuValpheSerLeu 340	ValmetaspargLeuValGlnargPheGlyThrargalaValTyrLeualaserValala 360 	380	381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400 S	401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420 LIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440	441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProProPalaLeu 460	461 CysGlyalaSerAlaCysAspValSerValArgValValValGlyGluProThirGluAla 480 111111111111111111111111111111111111	481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSeraläPheLeu 500 	501 LeuSerGinValalaProSerLeuPhemetGlySerIleValGinLeuSerGihSerVal 520	521 ThralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540	541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553	09605785		r L. L.	t A.		
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JICANT: Vedvick, Thomas S.

JICANT: Carter, Darrick
JICANT: Li, Samuel
JICANT: Li, Samuel
JICANT: Wang, Aljun
JICANT: Skeiky, Yasir A.W.
JICANT: Skeiky, Walliam
JICANT: Skeiky, Walliam
JICANT: COMPOSITIONS AND METHODS FOR THE
JE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
JE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
JENT APPLICATION NUMBER: US/09/605,785
JENT FILING DATE: 2000-06-27
JENT FILING DATE: 2000-06-27
JENT FILING DATE: 2000-06-27
JENT FILING SAFE FOR WINDOWS VERSION 3.0
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Xu, Jiangchun

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221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240 	241 CyscysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260 	261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280	281 SerTrpWetalaLeuWetThrPheThrLeuPheTyrThrAspPheValGl) 	301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320 	. 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340 	341 ValMetaspargLeuvalGlnargPheGlyThrargalavalTyrLeuAlaSerValala 360 	361 AlapheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380 	381 SeralaalaLeuThrGlyPheThrPheSeralaLeuGInIleLeuProTyrThrLeuala 400 	401 SerleuTyrHisargGluLysGlnValPheLeuProLysTyrargGlyAspThrGlyGly 420 	421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440	441 PheproAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460 	461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480 	481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500 	501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520 	521 ThralaTyrMetValSeralaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540 	541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553	CAAATACTCAGC	CO I U	Tent No. 6329505 NERAL INFORMATION:	
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Read, Steven G.
APPLICANT: Ralos, Michael
APPLICANT: Ranger, Garry
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THEF
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
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URRENT FILING DATE: 1999-11-12
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RESULT 5 US-09-352-	; Sequence ; Patent N		; APPLICA! ; APPLICA! ; TITLE O! ; TITLE O	; FILE RE; CURRENT; CURRENT; CURRENT; NUMBER	5, E	; ORGANI; US-09-352-	s: Snt Loc	Query Matcl DB: US-09-593-	Qy 1 1 Db 284		Qy 41	4	Oy 81 Db 524 O	Qy 101 Db 584	Oy 121 O	Qy 141 ?	Qy 161 7	Oy 181 Db 824	
201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220		221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSe [†] ProHis 240 	241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260 	261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlacluLeuCys 280 	281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyGlyLeu 300 	301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHiSTyrAspGluGly 320 	321 ValargMetGlySerLeuGlyLeuPheLeuGlnCysalalleSerLeuValPhèSerLeu 340 	341 ValMetaspargLeuValGlnargPheGlyThrargalaValTyrLeuAlaSerValAla 360 	361 AlaPheProvalAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla 380 	40	401 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrargGlyAspThrGlyGly 420 	421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440 	441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460 	461 CysGlyalaSeralaCysAspValSerValArgValValValGlyGluProThrGluala 480 	481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500 	501 LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGl ^h SerVal 520 	521 ThralaTyrMetValSeralaalaGlyLeuGlyLeuValalalleTyrPhealaThrGln 540 	541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553 	
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uence 110, Application US/09352616A

EEAL INFORMATION:

PLICANT: Dillon, Davin C.

PLICANT: Jangchun

PLICANT: Jangchun

PLICANT: Mitcham, Jennifer Lynn

TILE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE

RRENT APPLICATION NUMBER: US/09/352,616A

RRENT FILING DATE: 1999-07-13

MERRY FILING DATE: 1999-07-13
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euThrCy:	TCACCTG	CAGCAGA	euAlaPh TGGCTTT	roargTh: 	heThrLe TCACGCT	luProGly AGCCGGG	euPheLei 	rgPheGly GATTCGG	lathrCy:	hrPhese	CCTTCTC	lnvalPho AGGTGTT	etThrSe	TGACCAG	11111111111111111111111111111111111111	alServa	TCTCCGT	leCysLet	TCTGCCT	euPhemet	TGTTTATO	laglyLet	euAlaLys	=
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GlyLeuL	GGCCTGC	GCAGCGC	CyscysP GCTGTC	HisGlnL	SerTrpM AGCTGGA	TyrGlnG TACCAGG	ValArgM GTTCGGA	ValMetA: GTCATGG	AlaPheP: 	SerAlaA	TCAGCCG	SerLeuT) TCCCTCT	AlaSerS	GCTAGCA	PheProA	CysGlyA.	TGCGGGG	Argvalva	AGGGTGG	LeuSerG	CTGTCCC.	Thralat	ValValP	=
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7A ID METHOD OF BREAST 02,877A ion 3.0	th: nes: erva atch ls:	793A-113 (1-553) x US-09-602-877A-100 (1-3410) METValGIDARGLeuTrpValSerArgLeuLeuAcutghisArgLysAlaGIDLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuL	ATGSTCCAGAGGCTGTGGGTGAGCCGCTGCTGCGCGGCCCGGAAAGCCCAGCTCTTGCT ValasnLeuLeuThrPheGlyLeuGluValCySLeuAlaalaGly1leThrTyrValPr 	ProLeuLeuLeuGluValGlyValGluGluLysPhemetThrmetValLeuGlyIleGl. 	ProvalLeuGlyLeuvalCysValProLeuLeuGlySė́ralaSerAspHisTrpArgGl; 	ArgTyrG1yArgArgArgProPhe11eTrpAlaLeuS ^è rLeuG1y11eLeuLeuSerLeu 	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspFroArgProLeu 	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCy 	Thr ProLeuglu Ala Leu Leu Ser Asp Leu Phe Arga proAsp His CysArg Gln Al 	aPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAl. 	ASPTrpASPThrSerAlaLeuAlaProTyrLeuG 	yLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu
Sequence 100, Application US/0960287 Patent No. 6432707 GENERAL INFORMATION GENERAL INFORMATION APPLICANT Xu, Jiangchun TITLE OF INVENTION COMPOSITIONS TITLE OF INVENTION AND DIAGNOSIS FILE REFERENCE 210121 4465 CURRENT APPLICATION NUMBER US/09/6 CURRENT FILING DATE 2000-06-22 NUMBER OF SEQ ID NOS 107 SSOFTWARE FastSEQ for Windows Vers SSOFTWARE FastSEQ for Windows Vers SSOFTWARE TYPE DAN TYPE DAN TYPE DAN ORGANISM HOMO Sapien S-09-602-877A-100	ment Scores: No.: it this in the similarity: Local Similarity: Match:	93-	28 ATGGTCCAGAGGCTC 21 ValAsnLeuLeuTh 111111111111111111111111111111111111	41 ProteuteuteuGlu 	61 ProvalLeuGlyLeu 	81 ArgTyrGlyArgArg 	101 PheLeulleProArg	121 GluLeuAlaLeuLeu -	141 ThrProLeuGluAla 	161 TyrServalTyrAla 	181 IleaspTrpaspTh 	201 GlyLeuLeuThrLeu
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Sequence 110, Application US/09232149A Patent No. 6465611

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                       ICANT: Xu, Jiangchun
ICANT: Dillon, Davin C.
ICANT: Mitcham, Jennifer Lynn
ICANT: Mitcham, Jennifer Lynn
ICONT: CONCOUNDS FOR THEIR USE
REFERENCE: 210121.427C6
INTELLING DAME: 1999-01-15
INTELLING DATE: 1999-01-15
INTELLING DATE: MITCHAM
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Matches:
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR T
FILLE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILLING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FASTSEQ for Windows Version 3.0
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Oy 58 GlylleGlyPr	1311 78 1371	Oy 98 LeuSerLeuPh 	Qy 118 ArgProLeuGl 	Qy 138 ValcysPheTh	Qy 158 ArgGlnAlaTy	Qy 178 LeuProAlail.	Oy 198 CysteuPheGl.	1791	1851	1911	OY 278 GluteuCysSe 	Qy 298 GluGlyLeuTy.	Oy 318 AspGluGly 3 	RESULT 10 US-09-605-785-705 ; Sequence 705, Appli. ; Patent No. 6321716 ; GENERAL INFORMATION ; APPLICANNT: XV, JIA	APPLICANT: MICCANT: APPLICANT: HATLOC. APPLICANT: Jang, APPLICANT: Kalos, APPLICANT: Fanger APPLICANT: Fanger APPLICANT: Fater
Oy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCluCysLeuPhe 200	201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu	Qy 221 AlaalaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240 111111111111111111111111111111111111	Oy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260	Oy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280	Oy 281 SertrpMetalaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300 	Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320	RESULT 9 US-09-605-785-702 ; Sequence 702, Application US/09605785 ; Patent No. 6321716 ; GENERAL INFORMATION:	; APPLICANT: Xu, Jiangchun ; APPLICANT: Dlllon, Davin C. ; APPLICANT: Mitchan, Jennifer L. ; APPLICANT: Harlocker, Susan L.		Retter, Marc W. Stolk, John A. Day, Craig H.	; APPLICANT: Carter, Darrick ; APPLICANT: L1, Samuel ; APPLICANT: H1, Samuel ; APPLICANT: Wang, Aljun	; APPLICANT: Skeiky, Yasir A.W. ; APPLICANT: Hepler, William ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER	; FILE REFERENCE: 210121.427C16 ; CURRENT APPLICATION NUMBER: US/09/605,785 ; CURRENT FILING DATE: 2000-06-27 ; NUMBER OF SEQ ID NOS: 835	; SOFTWARE: FastSEO for Windows Version 3.0 ; SEO ID NO 702 ; LENGTH: 4894 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-605-785-702	Alignment Scores: Pred. No.: 263.00 Matches: 263.00 Percent Similarity: 100.00% Mismatches: 0 Query Match: 47.56% Indels: 0 US-09-593-793A-113 (1-553) x US-09-605-785-702 (1-4894)

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Locker, Susan L.
Locker, Susan L.
Ty Yuqui Robert A.
Ser, Michael D.
Ser, Gary R.
Ler, Marc W.
Lk, John A.
Craig H.
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278 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
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APPLICANT: GORDON, JULIAN
APPLICANT: GRANDOS, EDWARD N
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                           Sequence 16, Application US/09071710 Patent No. 6130043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                 COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
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LENGTH: 2152 base pairs
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STRANDEDNESS: single
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STATE: IL
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Best Local Similarity:
Query Match:
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US-09-071-710-16
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       APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427016
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 705
                                                                                                                                                                                                                                                                                                                                                                          US-09-593-793A-113 (1-553) x US-09-605-785-705 (1-6976)
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Conservative:
Mismatches:
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Vedvick, Thomas
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US-09-605-785-705
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Best Local Similarit
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                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-09-525-397-16
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Best Local Similarity:
Query Match:
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                                                  GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
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                        (1-2152)
                        US-09-593-793A-113 (1-553) x US-09-071-710-16
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COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
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Patent No. 6252047
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRANADOS, EDWARD N. HODGES, STYPEN C. KLASS, MICHAEL R. KRATOCHVIL, JON D. ROBERTS-RAPP, LISA RUSSELL, JOHN C. STROUPE, STEPHEN D.
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62 GAAGGCGTTCGGATGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTC
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Mismatches:
Indels:
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MEDIUM TYPE: Diskette
COMPUTER: TBM Compatible
OFBRATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.(
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397,
ELLING DATE:
CLASSIFICATION:
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                  REAGENTS AND METHODS
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TITLE OF INVENTION: FOR DETECTION INVENTED OF SEQUENCES: 41 CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

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CORRESPONDENCE ADDRESS:
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APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                     STREET: 100 Abbott Park Road CITY: Abbott Park STATE: IL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 847/935-1729
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SEQUENCE CHARACTERISTICS:
LENGTH: 2152 base pairs
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                                                   Length:
Matches:
Conservative:
Mismatches:
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252.00
100.00%
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45.57%
TION FOR SEQ ID NO: 15
TION FOR SEQ ID NO: 15
TOTE CHARACTERISTICS:
TH: 2143 base pairs
TH: nucleic acid
THOMBEDNESS: single
TLOGY: linear
TOTE CHARACTERISTICS:
TOTE CHARACTERISTICS
THOMBEDNESS: 100-15
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421

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462 GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 481
 123 ATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCCAGCT 182
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                           482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT APPLICATION NUMBER: US/09/605,785
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 703, Application US/09605785 Patent No. 6321716
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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Henderson, Robert A.
Kalos, Michael D.
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Vedvick, Thomas S
Carter, Darrick
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Retter, Marc W.
Stolk, John A.
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LENGTH: 2904
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APPLICANT: GORDON, JULIAN N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HONGES, STEVEN C.
APPLICANT: HONGES, MICHAEL R.
APPLICANT: KRAYOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
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Mismatches:
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SOFTWARE: FRSALSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
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Matches:
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                                             BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                SEE: Abbott Laboratories
: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
, Application US/09525397
6252047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.58e-235
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TELEFAX: 847/938-2623
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LENGTH: 2143 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Sequence 15, Applicat.
Patent No. 6252047
GENERAL INFORMATION:
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Best Local Similarity:
Query Match:
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CITY: Ab
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APPLICANT:
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 6300 Columbia Center, 701 Fifth Avenue
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Mismatches:
Indels:
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                                                                   MEDIUM TYPE: Floppy disk Compartible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version
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Matches:
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APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
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                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTARION UNBER: 31,392
REFERENCE/DOCKET WUMBER: 21012
REFERENCE/COCKET WUMBER: 21012
REFERENCE/COCKET WOMBER: 21012
REFERENCE/COCKET WOMBER: 21012
REFERENCE/COCKET WOMBER: 21012
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDENESS: SINGLE
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MEDIUM TYPE: Floppy
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Best Local Similarity:
Query Match:
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 STREET: (CITY: Sea STATE: WARE
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Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS :
NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
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                                                                                          Best Local Similarity:
Query Match:
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                                                                               Percent Similarity:
; TYPE: DNA
; ORGANISM: HOMO
US-09-605-785-703
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                                             Alignment Scores:
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357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla
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                                                                                                                                                                                                                                                                                               APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
                                        Sequence 10, Application US/09605785 Patent No. 6321716
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                                                                                                                                                Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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; OTHER INFORMATION: n = A,T,C or
US-09-605-785-10
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122.00
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                                                                  GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer
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Skeiky, Yasir A.W.
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Vedvick, Thomas
Carter, Darrick
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                                                                                                                                     Jiang, Yuqui
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Best Local Similarity:
Query Match:
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LENGTH: 789
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TILLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS INUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                377 ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly 416
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122
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                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
                                                                3: SEED and BERRY LLP 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative:
Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                          210121.427C3
                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REPERENCE/DOCKET NUMBER: 2101;
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.67e-109
122.00
100.00%
100.00%
22.06%
                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 789 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-030-607-10
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Best Local Similarity:
Query Match:
                                                                              STREET: 6300 C
CITY: Seattle
                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                      USA
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                                                                ADDRESSEE:
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US-09-593-793A-113 (1-553) x US-09-352-616A-10
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                                                  Sequence 10, Application US/09352616A Patent No. 6395278 GENERAL INFORMATION: APPLICANT: Dillon, Davin C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-232-149A-10; Sequence 10, Application US/09232149A; Patent No. 6465611; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                          DUCATION: (1)...(789); OTHER INFORMATION: n = A,T,C or GUS-09-352-616A-10
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122.00
100.00%
100.00%
22.06%
                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapien
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Best Local Similarity:
Query Match:
  372 CCCACC 377
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                                       US-09-352-616A-10
                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
                                                                                                                                                                                                                                                   SEQ ID NO 10
LENGTH: 789
                                                                                                                                                                                                                                                                              TYPE: DNA
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                                                                                                                        APPLICANT: Dilon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Redo, Steven G.
APPLICANT: Redo, Michael
APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Bay, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT APPLICANT: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
LENGHH: 789
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Conservative:
Mismatches:
Indels:
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                                                                           Sequence 10, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
                                                                                                                APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
                                                                                                                                                                                                                                                                                                                                                                                                                       : NAME/KEY: misc_feature

: LOCATION: (1)...(789)

: OTHER INFORMATION: n = A,T,C or G

US-09-439-313-10
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122.00
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Best Local Similarity:
Query Match:
477 ProThr 478
                        372 CCCACC 377
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                                                  SULT 19
-09-439-313-10
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357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla 376
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APPLICANT: Dillon, Davin C.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Jiang, Yuqui
APPLICANT: Jiang, Yuqui
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OP PROSTATE CANCER AND METHODS FOR THEIR USE
CURRENT FILING DATE: 1999 07-13
NUMBER OF SEQ ID NOS: 472
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122
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Mismatches:
Indels:
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Matches:
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Sequence 1, Application US/09525397
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Pred. No.:
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US-09-525-397-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               377 ValvalThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIlèLeuPro 396
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              APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
TITLE OF INVENTION: CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.427C6
CURRENT APPLICATION NUMBER: US/09/232,149A
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FASTSEQ for Windows Version 3.0
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Mismatches:
Indels:
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APPLICANT: COHEN, MAURICE
APPLICANT: COLPTITS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KRANDOS, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRASS, MICHAEL R.
APPLICANT: ROBERTS-RAPP, LISA
                                                                                                                                                                                                                                                                                                      G
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COTHER INFORMATION: n = A,T,C
US-09-232-149A-10
APPLICANT: Xu, Jiangchun
                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                          SEQ ID NO 10
LENGTH: 789
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                                                                                                                                                                                                                                                  FEATURE:
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299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE About Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: 1L
COUNTRY: USA
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-593-793A-113 (1-553) x US-09-071-710-1 (1-258)
                                                                                                                                                                                                                                                           SOFTWARE: FASESEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,710
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                                                                                                                                                                                                                                                                                    APPLICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILLING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
NAME: Becker, Cheryl L.
JOHN C.
STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9.47e-74
85.00
100.00%
100.00%
                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                            ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 ThralaSerAlaAla 383
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
Query Match:
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61

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359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 378
                   TITLE OF INVENTION: REAGENTS AND METHODS USEFUL ITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastESD for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
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                                                                                                                                                                                                                         BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILLING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                      ; Sequence 4, Application US/09071710; Patent No. 6130043; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                            GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
                                                                                                                                                                                                                                                                                                                                                                                 ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BECKEr, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 608
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
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82.00
100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 247 base pairs
TYPE: nucleic acid
                                                                                        242 ACAGCTTCAGCCGCC 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                  379 ThrAlaSerAlaAla 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 847/938-2623
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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APPLICANT:
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APPLICANT:
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APPLICANT:
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                                                                                                                                                      US-09-071-710-4
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                                                                                                                                       RESULT
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TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
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Matches:
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                BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
THORA PAPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
                           THE COLPITYS, TRACEY L.
TO FRIEDMAN, PAULA N.
TO GORDON, JULIAN N.
TO GARANDOS, EDWARD N.
TO GRANADOS, EDWARD N.
TO GRANADOS, EDWARD N.
TO GRANADOS, TEVEN C.
TO GRANADOS, TEVEN C.
TO GRANADOS, TEVEN C.
TO GRANADOS, TEVEN C.
TO GRANADOS, TEVEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFRENCE/DOCKET NUMBER: 6083
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
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85.00
100.00%
15.37%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                     Diskette
                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                          CITY: Abbott Park
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ZIP: 60064-3500
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
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                                                                 APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
APPLICANT:
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; TOPOLOGY: linear	Qy 439 AlabroPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProPro 458	Oy 479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498	RESULT 26 US-09-071-710-2 ; Sequence 2, Application US/09071710 ; Patent No. 6130043 ; GENERL INFORMATION: APPLICANT: COHEN, MAURICE ; APPLICANT: COLPITS, TRACEY L. APPLICANT: GOLDON, JULIAN ; APPLICANT: GORDON, JULIAN ; APPLICANT: GRANDOS, EDWARD N.	HORES	STATE: IL COUNTRY: USA ZIP: GO064-350 COMPUTER READALE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEO for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,710 FILING DATE: CLASSIETCATION DATA: PRIOR APPLICATION DATA: PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/09/071,710 FILING DATE: APPLICATION NUMBER: 08/09/071,710 APPLICATION NUMBER: 08/09/071,710 APPLICATION NUMBER: 08/09/071,710
439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProPro 458	499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerTleValGlnLeuSerGln 518	4 APP	APPLICANT: HODGES, STEER C. APPLICANT: KLASS, MICHAEL R. APPLICANT: KRATOCHVIL, JON D. APPLICANT: ROBERTS-RAPP, LISA APPLICANT: ROBERTS-RAPP, LISA APPLICANT: ROSSELL, JOHN C. APPLICANT: STROUPE, STEPHEN D. TITLE OF INVENTION: REAGENTS AND METHODS USEFUL TITLE OF INVENTION: POR DETECTING DISEASES OF THE PROSTATE NUMBER OF SEQUENCES: 41 CORRESPONDENCE ADDRESS: ADDRESSEE: Abbott Laboratories STREET: 100 Abbott Park Road CITY: Abhott Park Road	STATE: IL. COUNTRY: USA ZIP: 60064-3500 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/525,397 FILING DATE: CLASSTFICATION:	PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/071,710 FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441 REFERENCE/DOCKET NUMBER: 35,401 TELEPHONE: 847/935-1729 TELEPHONE: 847/935-1729 TELERAX: 847/935-1729 TELERAX: 847/936-2623 TELEX: 41/938-2623 TELEX: 25Q ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 247 base pairs TYPE: nucleic acid STRANDEDNESS: single

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CURRENT APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321
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Sequence 2, Application US/09525397

Patent No. 6252047

GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MAURICE
APPLICANT: COLPITTS, TRACEY L.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: MOGES, STEVEN C.
APPLICANT: KRATOCHULL, JON D.
APPLICANT: RATOCHULL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES:
ADDRESSEE: AND APPLICANT:
ADDRESSEE: AND APPL
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71
0
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Mismatches:
Indels:
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FastSEQ for Windows Version 2.0
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Matches:
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                                                                6083.US.P1
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1: 100 Abbott Park Road
Abbott Park
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1229
TELEFAX: 847/938-2623
                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
JGPOLOGY: linear
US-09-071-710-2
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71.00
100.00%
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RY: USA
60064-3500
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Best Local Similarity:
Query Match:
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CITY: AL
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GENERAL INCORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COLENT'S, TRACEY L.
APPLICANT: COLENT'S, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHEL R.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: RRAGENTS AND METHODS USEFUL
TITLE OF INVENTION: RRAGENTS AND WETHODS USEFUL
TITLE OF INVENTION: RRAGENTS AND WETHODS USEFUL
TITLE OF INVENTION: RRAGENTS AND WETHODS USEFUL
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                  217
71
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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                                                                                                                                                6083.US.P1
US/09/525,397
                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 3, Application US/09071710 ; Patent No. 6130043
                                                                                                            NAME: BECKEr, Cheryl L.
REGISSRATION NUMBER: 35,41
REFERENCE/DOCKET NUMBER: 6083
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                 3.04e-60
71.00
100.00%
100.00%
                                                                                                ATTORNEY/AGENT INFORMATION:
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LENGTH: 217 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: linear
US-09-525-397-2
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                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
Query Match:
                               CLASSIFICATION:
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STREET: 10
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US-09-071-710-3
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US-09-525-397-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 ACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
Indels:
                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
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Matches:
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CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY,AGENT INFORMATION:
NAME: BECKEY, Cheryl L.
REGISTRATION NUMBER: 35,441
TELECOMMUNICATION INFORMATION:
TELECHHONE: 847/935-1729
TELEFRAX: 847/938-2623
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Patent No. 6522047
GENERAL INFORMATION:
APPLICANT: BILLING MEDEL, PATRICIL
APPLICANT: COLENT, MAURICE
APPLICANT: COLETTS, TRACEY L.
APPLICANT: FRIEDMAN, PAULA N.
APPLICANT: GRRON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: base_polymorphism
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71.00
100.008
100.008
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LENGTH: 255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 215
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
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Best Local Similarity:
Query Match:
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399 LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
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APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCES: ADDOLT Laboratories
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= " N' represents an A or G or
T or C polymorphism at this position"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/525,397 FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       439 AlaProPheProAsnGlyHisValGlyAlaGly 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.Pl
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
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COCATION: 215
OTHER INFORMATION: /note= "OTHER INFORMATION: T or C po
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71.00
                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                STALL.
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
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100.00%
12.84%
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LENGTH: 255 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        CITY: Abbott Park
STATE: IL
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63 CTCAGCCAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGG-CTGGGTCTGGTCGCCATT 121
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                                      OF THE PROSTATE
                                                                                                                                                                                                                               APPLICANT: COHEN, MURICE
APPLICANT: COLPITS, TRACEY L.
APPLICANT: GORDON, PULAN PALLA N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE B.
NUMBER OF SEQUENCES: 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2:0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
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                                                                                                                                                                                                                    BILLING-MEDEL, PATRICIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
                                                                                                                                                      Sequence 5, Application US/09525397
Patent No. 6252047
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: BECKEY, CHEYL L.
REGISTRATION NUMBER: 35.41
REFERENCE/DOCKET NUMBER: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2.54e-24
34.00
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98.28%
6.15%
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SEQUENCE CHARACTERISTICS:
LENGTH: 231 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 847/938-2623
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Best Local Similarity:
Query Match:
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                                                                                                                                      US-09-525-397-5
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                                                                                                                                                                                                                                                                                                                                                                     REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      231
57
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSep for Windows Version 2.0
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/071,710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
Matches:
182 GCTCCCTTCCCTAATGGACACGTGGTGCTGGA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6083.US.P1
                                                                                                                              NT: BILLING-MEDEL, PATRICIA
NT: COHEN, MAURICE
NT: COLPITY, TRACET L.
NT: GORDON, JULIAN
NT: GRANADOS, EDWARD N.
NT: GRANADOS, EDWARD N.
NT: KLASS, MICHAEL R.
NT: KLASS, MICHAEL R.
NT: KRATOCHVIL, JON D.
NT: ROBERTS-RAPP, LISA
NT: STROUPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Abbott Laboratories 100 Abbott Park Road
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                                                                        Sequence 5, Application US/09071710 Patent No. 6130043 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
CLASSIFICATION CATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.54e-24
34.00
98.28%
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                APPLICANT:
                                                        US-09-071-710-5
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REPERENCE: 2.0121.427C9
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Benson, Darin R.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Ming, Gordon E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR OVARIAN
TITLE OF INVENTION: CANCER THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.466C2
CURRENT FILIAG DATE: 1999-09-16

NUMBER OF SEQ ID NOS: 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-593-793A-113 (1-553) x US-09-397-787-331 (1-176)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-593-793A-113 (1-553) x US-09-439-313-488 (1-33)
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Mismatches:
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Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227 GluProAlaGluGlyLeuSerAlaPro 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 GAACCTGCGGAGGACTGAGTGCCCCT 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 LeuLeuProArgLeuHisGlnLeuCys 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 CTTCTTCCCCGGCTGCACCAGCTGTGC 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 331, Application US/09397787 Patent No. 6468758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 11, Application US/08658639 ; Patent No. 5914238
                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Made in a lab
                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.47
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      Fanger, Gary
                     Retter, Mark
Solk, John
Day, Craig
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US-09-397-787-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                     US-09-439-313-488
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US-09-397-787-331
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US-08-658-639-11
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LENGTH: 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                      516 LeuSerGinServalThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIle 535
                                                             63 CTCAGCCAGTCTGTCACTACTATATGGTGTCTGCCGCAGG-CTGGGTCTGGTCGCCCATT 121
3 GATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTGTTTATGGGCTCCATTGTCCAG 62
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Handerson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Renger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Thomas S.
APPLICANT: Carter, Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Hepler, William W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                             536 TyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 CTTCTTCCCCGGCTGCACCAGCTGTGC 33
                                                                                                                                                                                                                                             Sequence 488, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-439-313-488
; Sequence 488, Application US/09439313
; Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harlocker, Susan Louise
Jiang Yuqui
Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Made in a lab
US-09-605-785-488
                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                         US-09-605-785-488
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APPLICANT: APPLICANT: APPLICANT:

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                              APPLICANT: KEESE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
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APPLICANT: KEESEE, SUSAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-YE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF
TITLE OF INVENTION: BEEAST CANCER
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Testa, HURWILZ & Thibeault
STREET: 125 High St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,639
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Matches:
Conservative:
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NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REGISTRATION NUMBER: 36,989
REERENGE/DOCKET NUMBER: MTP-021 (8395/24)
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-593-793A-113 (1-553) x US-08-658-639-11 (1-613)
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Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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Best Local Similarity:
Query Match:
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                           Abbas
STREET: 12.
TTV: Boston
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02110
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; LOCATION: 1...
US-08-658-639-11
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COUNTRY: U
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Pred. No.:
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US-08-944-604-15
Sequence 15, Application US/08944604
Patent No. 6218131
GENERAL INFORMATION:
APPLICANT: REESEE, SUGAN
APPLICANT: OBAR, ROBERT
APPLICANT: WU, YING-JYE
TITLE OF INVENTION: MATERIALS AND METHODS FOR DETECTION OF TITLE OF INVENTION: 24
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentul Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,604
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                                                                                                                                                                                                                                                         MTP-021 (8395/24)
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NAME: MEYERS, THOMAS C
REGISTRATION NUMBER: 36,989
REFERENCE/DOCKET NUMBER: MTP-021 (8395/24)
TELECOMMUNICATION:
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Indels:
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STREET: 125 High St.
CITY: Boston
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                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: MEYERS, THORAS C
REGISTRATION NUMBER: 36,989
REPRENCE/DOCKET NUMBER: MTP-O
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 248-7000
INFORMATION FOR SEQ ID NO: 11:
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100.00%
1.63%
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 613 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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US-08-944-604-11
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Score:

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APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Helpler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT PILLIG DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 487
LENGTH: 36
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Red, Steven G.
APPLICANT: Ranger, Garven G.
APPLICANT: Retter, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Dalk, John
APPLICANT: Dillon, Didnost Sof PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C9
CURRENT FILING DATE: 1999-11-12
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 575
SEQ ID NO 487
SEQ ID NO 487
LENTH: 36
MANDER OF SELENTH
APPLICATION OF SECONO 
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-593-793A-113 (1-553) x US-09-605-785-487 (1-36)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 487, Application US/09439313
Patent No. 6329505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
COTHER INFORMATION: Made in a lab
US-09-605-785-487
  Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Made in a lab US-09-439-313-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                          Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.7
8.00
100.00%
100.00%
                                                                                                                      Stolk, John A.
                                                                                                                                                                                                                                 Li, Samuel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-439-313-487/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
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                                                                                      APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score:
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US-09-1995-3/C
US-09-1995-3/C
Sequence 3, Application US/09729995
Patent No. 6426206
GENERAL INFORMATION:
APPLICANT: WELL MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC |
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO00904
CURRENT FILICATION NUMBER: US/09/729,995
CURRENT FILICATION NUMBER: US/09/729,995
CURRENT FILICATION NUMBER: VOICE OF WINDOWS VERSION 4.0
SOFTWARE: Fastes of or Windows Version 4.0
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Matches:
Conservative:
Mismatches:
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Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                               ; LOCATION: 130..795
; OTHER INFORMATION: /product= "BC-2"
US-08-944-604-15
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Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitchan, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227 GluProAlaGluGlyLeuSerAlaPro 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 GlyLeuSerAlaProSerLeuSerPro 239
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 903 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.00%
100.00%
1.63%
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100.00%
1.63%
                                                                                                                                                                 STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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ORGANISM: Human
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Query Match: DB:

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Pred. No.:

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E: Finnegan, Henderson, Farabow, Garrett & Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: 0.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/673,190A
FILING DATE: 27-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
   980000
                                                                                                                                                                                                                                          Sequence 5, Application US/08673190A

Patent No. 5985668

GENERAL INFORMATION:
APPLICANT: Mattes, Ralf
APPLICANT: Ricain, Kathrin
TITLE OF INVENTION: Sucrose Metabolism Mutants.
TUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                              US-09-593-793A-113 (1-553) x US-09-439-313-487 (1-36)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Forman, David S.

REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 06473.0001-00000
TELECOMUNICATION INFORMATION:
TELEPRONE: (202)408-4400
TELEFRAX: (202)408-4400
TELEFRAX: (202)408-4400
SEQUENCE CHARACTERISTICS:
                                                                                 Gaps:
                                                                                                                                              ORGANISM: Enterobacter species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
6.7
8.00
100.00%
100.00%
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8.00
100.00%
100.00%
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                 .458
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                               Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: line
MOLECULE TYPE: D
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                             US-08-673-190A-6
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                                                                 Query Match:
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Pred. No.:
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RESULT 42 US-09-328-111-46/C

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GENERAL INFORMATION:
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBPTITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
FILE REFERENCE: GENSET. 031A
CURRENT APPLICATION NUMBER: US/09/345,882
CURRENT FILING DATE: 1999-06-30
                                                         APPLICANT: Bardege, Wilson O.
APPLICANT: Steinman, Kathleen E.
APPLICANT: Steinman, Kathleen E.
APPLICANT: Steinman, Kathleen E.
APPLICANT: Burgess, Christopher C.
APPLICANT: Bushnell, Steven E.
APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
APPLICANT: Cathon, Theodore J.
APPLICANT: Derti, Adnan M.
APPLICANT: Derti, Adnan M.
APPLICANT: Lewis, Marcia E.
APPLICANT: Schiegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: NOWBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER APPLICATION NUMBER: US 60/088,801
MUMBER OF SEQ ID NOS: 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              633
0
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Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 46 LENGTH: 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
PRIOR FILING DATE: 1998-12-10
PRIOR FILING DATE: 1998-12-10
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patent.pm
Sequence 46, Application US/09328111 Patent No. 6262333 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            231 GlyLeuSerAlaProSerLeuSer 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(633); OTHER INFORMATION: n = A,T,C or GUS-09-328-111-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/09345882 Patent No. 6399373
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100.00%
1.45%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens US-09-345-882-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 999
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US-09-345-882-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
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APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS NUMBER OF SEQUENCES: 224 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607,
FILING DATE: 25-FEB-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 210121.427C3
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFACE (206) 622-4900
TELEFACE (206) 622-4900
TELEFACE (206) 622-6031
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-593-793A-113 (1-553) x US-09-030-607-175 (1-1167)
                                                                                                             ADDRESSEE: SEED and BERRY LLP . STREET: 6300 Columbia Center, 701 Fifth Avenue CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches:
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                                                                                                                                                                                                           ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            447 GlyAlaGlyGlySerGlyLeuLeu 454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 836 GGGCTGGGGGGTCTGGACTCCTG 813
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100.00%
100.00%
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-030-607-175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM:
                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                Sequence 175, Application US/09020956
Patent No. 6261562
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FO NUMBER OF SEQUENCES: 178
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STRRET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
80000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,956
FILING DATE: 09-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative:
Mismatches:
Indels:
                 Conservative:
                                                                                                         US-09-593-793A-113 (1-553) x US-09-345-882-3 (1-999)
                                   Mismatches:
Indels:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACTERISTICS:
LENGTH: 1167 base pairs
Matches:
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10S-09-3030-607-175/c
Sequence 175, Application US/09030607
Patent No. 6262245
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STRANDEDNESS: single
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Best Local Similarity:
Query Match:
             Percent Similarity:
Best Local Similarity:
Query Match:
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US-09-020-956-175/c
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BM914562 AGENCOURT
BG950805 AGENCOURT
BG469520 602532833
BF972601 602243025
AA112574 zm28c12.s
AF109299 AF109299
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AW787124 120845 MA
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AW175665 RC3-BT004
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BW915527 AGENCOURT
BM915527 AGENCOURT
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BF233285 602023647
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B1345407 374221 MA
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BB627844 E
BB627667 E
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BB850079 B
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-MODEL-framet-p2n.nodel -DEF-xlh
-MODEL-framet-p2n.nodel -DEF-xlh
-Og/cgn2_1/USPTO_spool/US09593793/runat_13022003_161426_21829/app_query.fasta_1.711
-Og-/cgn2_1/USPTO_spool/US09593793/runat_13022003_161426_21829/app_query.fasta_1.711
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    (without alignments)
5418.091 Million cell updates/sec
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         GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                             - nucleic search, using frame_plus_p2n model
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BB627844 BB627667 dab86b09. 602909416

us-09-593-793a-113.olig.rst

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BM192568 dai19906. AL262608 Tetraodon BB848279 BB848279 AL293075 Tetraodon BG221458 RST41270 BG193346 RST41260 AW022261 df36a12.y AW185227 se681603.y BE690088 uwdxb10.y BE690088 uwdxb10.y BE690088 uwdxb10.y R90985 yp93b01.r1 AL707231 DKF2p686K BM75284 UTE-E-JO-BM67725 UT-E-E-JO-BM67725 UT-E-E-JO-BM67727 UT-E-E-JO-BM67727 UT-E-E-JO-BM67727 UT-E-E-JO-BR6949 WC17400.x AI826426 WC17400.x AI826425 WK344a11.x BE762344 RCO-DTOO7 AW104168 xd71a06 x BE762344 RCO-DTOO7 BH867320 M4394004.y AI650794 W419903.x BI491393 df08b11.w	BG469889 BG469889 BG46989 BG4698 BG46989 BG46989 BG46989 BG46989 BG46989 BG46989 BG4698 BG4698
3 BM192568 7 CNS03VMF 8 CNS03VMF 10 BB848279 CNS04J40 2 BG221458 2 BG193546 AM185227 0 BE137141 0 BE13739 ALT 0 BE13730	ALIGNMENTS SFI NIH_MGC_15 Homo sapiens cDNA uence1 GI:13402164 iens a; Metazoa; Chordata; Craniata; V Eutheria; Primates; Catarrhini; s 1 to 946) http://mgc.nci.nih.gov/. Institutes of Health, Mammalian hed (1999) Robert Strausberg, Ph.D. Robert Strausberg, Ph.D. Brobert Strausberg, Ph.D. Brobert Strausberg, Ph.D. Brobert Strausberg, Ph.D. Brobert Strausberg, Ph.D. COUTEMBOL: ANC. Drary Arrayed by: The I.M.A.G.E. uencing by: NH Intramural Sequence in the I.M.A.G.E. councing by: NH Intramural Sequence Stop: 798. Location/Qualifiers 1. 946 //Organism="Homo sapiens" //db_xref="taxon:9606" //clone="IMAGE:4661075" //clone="IMAGE:4661075"
2.4 4 865 17 2 2.2 4 4 100 2 2.2 4 4 110 2 2.2 2 2.2 4 4 110 2 2.2 2 2.2 4 4 110 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2 2.2 2	BG469889 602533345F1 NIH_MGC_15 mRNA sequence. BG469889 BG469889.1 GI:13402164 BEST. human. Homo sapiens Eukaryota; Metazoa; Chc Mushanalia; Eutheria; Pri 1 (bases 1 to 946) NIH-MGC http://mgc.nci. NIH-MGC http://mgc.nci. NIH-MGC http://mgc.nci. NIH-MGC http://mgc.nci. NIH-MGC http://mgc.nci. NIH-MGL is contact: Robert Strausb Email: cgapbs-remail.nci. Contact Strausb DNA Sequencing by: NIH- DNA Sequencing by: NIH- Clone distribution: MG found through the I.M.A http://image.llnl.gov Plate: LLCM1459 row: i High quality sequence s //oraclen/Qualii. //clone="IMAGE:"HAGE: //clone="IMAGE:"HAGE:"
65 65 67 67 73 73 73 74 74 74 75 75 75 75 75 75 75 75 75 75	RESULT 1 EG46989 EG46989 EG46989 EGG46989

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/tissue_type="adenocarcinoma cell line"
/lab_host="DNIOB (phage=resistant)"
/note="Organ: colon; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; CDNA made by oligo-dT priming. Directionally
cloned into ECORI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size_selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
california, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"
20 a 331 c 296 g 199 t.
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601442309F1 NIH_MGC_65 Homo sa
mRNA sequence.
BE867241
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1, Chases 1 to 718)
                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. a column: 04
High quality sequence stop: 693.
Location/Qualifiers
1. 718
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: capabs-rémail.nih.gov
Tissue Procurement: Arca
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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E. I. (bases 1 to 885)

I. (bases 1 to 885)

I. Onpublished (1999)

L. Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13611 row: b column: 08

High quality sequence stop: 615.
                                                                                                     B85 bp mRNA linear EST 21-AUG-2002 AGENCOURT 8803099 Lupskl sciatic_nerve Homo sapiens cDNA clone IMAGE:6198823 5', mRNA sequence.
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5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected >
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                                                 AlaLeuCysG1yAlaSerAlaCysAspValSerValArgValValValG1yG1uProThr
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US-09-593-793A-113 (1-553) x BM914562 (1-1060)
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1. 1060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1060 bp mRNA linear EST 12-MAR-2002
AGENCOURT_6615475 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480245
BM914562
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II HMGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
clone distribution: MCC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Phttp://mage.lln.gov
Plate: LLCM2002 row: m column: 14
High quality sequence stop: 485.
                                                    438
                                                                                                                         81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
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                           499 GGCTATGGCCGCCGCCCCTTCATCTGGCCACTGTCCTTGGGCATCCTGCTGAGCCTC
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                                                                                                61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly
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FEATURES

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602532833F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:4660496 5', mRNA sequence.
BG469520
BG469520.1 GI:13401795
EST.
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing Dy: NIH Intramural Sequencing Center
Clone distribution: MCC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLCM1458 row: a column: 09
High quality sequence stop: 671.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                               Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbS-r@mail.ih.gov
Tissue Procurement: ATCC

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLCM196 row: a column: 08

High quality sequence stop: 675.

Location/Qualifiers

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Accation/Qualifiers

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Accation/Qualifiers

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Accation/Qualifiers

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Accation/Qualifiers

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Account through the Income sapiens a location of the laboratory of Gerald M. Rubin (University of California, Berkeley)

Clone="In-WHYD stee using the following 5" adaptor:
EcoRI: CDNA made by oligo-dr priming. Directionally cloned into Boorly Constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)

Library.

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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.
Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

(bases 1 to 228)

Hillar, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,
Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins
M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore,
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,
Schellenberg, K., Soares, M.B., Tran, F., Thierry-Meg, J. Trevaskis, E.,
Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Washington University School of Medicine
4444 Forest Park Parkway, Box,8501, St. Louis, MO 63108
Tel: 314 286 1800
Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
kept in mind should you use this clone.
                                                                                                                            p mRNA linear EST 23-DEC-1997 (#937208) Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40M13 fwd. from Amersham.

Location/Qualifiers
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                                                                                                                                228 bp
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IMAGE:526966 3', mRNA sequence.
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Januara "Homo sapiens"

Laref="taxon:9606"

Laref="taxon:9606"

Laref="taxon:9606"

Laref="NIH MGC.15"

Sue_type="adenocarcinoma cell line"

Sue_type="adenocarcinoma cell line"

Sue_type="adenocarcinoma cell line"

Sub_lost="Blil0B (phage-resistant)"

te="lorgan: colon; Vector: porB7; Site_1: XhoI; Site_2: tell. congan: colon; Vector: porB7; Site_1: XhoI; Site_2: RI; cDNA made by oligo-dr priming. Directionally need into EcoRICXAho! sites using the following 5' ptor: GGCACGAGG(G). Size-selected >500bp for average ert size 1.8kb. Library constructed by Ling Hong in laboratory of Gerald M, Rubin (University of library of library constructed by Ling Hong in libraria, Berkeley) using ZAP-cDNA synthesis kit ratagene) and Supersoript II RT (Life Technologies)"
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Arrayed by: The I.M.A.G.E. Consortium (LLNL)
1 by: NIH Intramural Sequencing Center
Ition: MGC clone distribution information can be
1.M.A.G.E. Consortium/LLNL at:
n1.gov
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@mail.nih.gov
ent: ATCC
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/dv.stage="Adult"
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Magai,M.A., da Silva,W. T., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souzà,S.J. and
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV2&t2=QV2-NT0147-
191100-482-h07&t3=2000-11-19&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 418.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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ValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAla
                                                                     63 GTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGGGGCTCTGCGGGGGCCTCTGCC
                                                                                                                                                                                                                                                                                                                                                                     182 CGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTTCCCAGGTGGCC
                                                                                                                                              CysAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGly
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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/lab_host="DH10B (phage-resistant)"
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/note="Corgan: muscle; Vector: potential of Canterial of Cant
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Brarryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1035)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: gapba-r@mail.nih.gov
Email: ARCC |
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLCM1807 row: i column: 03
High quality sequence start: 3
High quality sequence stop: 602.
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11 (bases 1 to 342).
11 (bases 1 to 142).
12 (bases 1 to 342).
13 (bases 1 to 342).
14 (bases 1 to 342).
15 (bases 1 to 342).
16 (bases 1 to 342).
17 (bases 1 to 342).
18 (bases 1
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  RT (Life Technologies)."
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
TEA: 314 286 1800
Fax: 314 286 1810
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/db_xref="GDB:3918395"
/db_xref="taxon:9606"
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BF371417 24-NOV-2000 mRNA linear EST 24-NOV-2000 RCO-FN0140-040800-023-h03 FN0140 Homo sapiens CDNA, mRNA sequence. BF371417
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Bukaryota, Matazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Merata; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 265)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Buchdr, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
Shotgun sequencing of the human transcriptome with ORF expressed
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Fear; 314 286 1800
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RCO&t2=RCO-FN0140-040800-023.h03&t3=0200-08-04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 8
High quality sequence stop: 265.
Location/Qualifiers
1. 265.
/Organism="Homo sapiens"
/Ob_xref="Laxon:9606"
/Gb_xref="Laxon:9606"
/Gb_xref="Laxon:9606"
/Gev_stage="Adult"
                                                                                                                                                                                                             /note="Organ: prostate_normal; Vector: pucl8; Site_1: Smal Site_2: Smal; A mini-library was made by cloning products derived from ONESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pucl8 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
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This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1041916
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uq13g05.yl Ren Stubbs mouse thymus Mus musculus cDNA clone
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Contact: Smith TPL
Contact: NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 537)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone, R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 09-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AW787124 537 bp mRNA linear
120845 MARC 1PIG Sus scrofa cpNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Ren Stubbs mouse thymus"
/sex="mixed"
/dev_stage="3 weeks"|
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Conservative:
Mismatches:
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Seq primer: Primer name ambiguous
High quality sequence stop: 474.
·Location/Qualifiers
                                                                                                                                                                                 /organism="Mus musculus"
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                                                                                                                                                                                                                                  /strain="C3H"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                /clone="IMAGE:2802392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AW787124.1 GI:7843900
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59.00
100.00%
100.00%
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BI145201 630 bp mRNA linear EST 05-JUL-2001
602909395F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5050583 5',
                                                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.n column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        401 TGGATGGCACTTATGACTTTCACACTGTTCTACACGGACTTCGTGGGAGGGGGCTGTAC 460
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NIH WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThraspPheValGlyGluGlyLeuTyr
                                                                                                                                                                                                                                                                                                                              592
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                                                                      /clone="IMAGE:2648691"
/clone_lib="NCI_CGAP_Man1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                  Matches:
Conservative:
Mismatches:
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/db_xref="taxon:10090"
/clone="IMAGE:5050583"
/clone_lib="NCI_CGAP_Li9"
                    /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-593-793A-113 (1-553) x AW412402 (1-592)
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High quality sequence stop: 630.
Location/Qualifiers
                                      /strain="FVB/N"
/db_xref="taxon:10090"
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Best Local Similarity:
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DB:
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LOCUS
DEFINITION
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TITLE
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COMMENT
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technolgies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-GGAP clone distribution information can be
Kound through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                           /note="Vector: pCMV SPORT6; Site_1: Not1; Site_2: Sall; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPheGly 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGly 47
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Outpublished (1997)
Other ESTS: u078h02.x1
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-593-793A-113 (1-553) x AW787124 (1-537)
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High quality sequence stop: 421.
Location/Qualifiers
              FORWARD: AGGAAACACTATGACCAT
BACKWARD: GTTTCCCAGTCACGACG
Plate: 45 row: C column: 12
Seg primer: ATTTAGGTACACTATAG.
                                                                                                               1. .537
/organism="Sus scrofa"
                                                                                                                                                  /db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                           186 g
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AW412402.1 GI:6938274
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59.00
100.008
100.008
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PCR PRimers
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Query Match:
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AW412402
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TITLE
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KEYWORDS
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BB627667
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bladder Mus
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
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URL:http://genome.gsc.riken.go.jp/
URL:http://genom
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
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                                                      Oligo dT
                               NotI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                         /note-"Organ: liver; Vector: pCMV-SPORT6; Site_1
Site_2: SalI; Cloned unidirectionally. Primer: O
Average insert size 1.9 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BB627844 RIKEN full-length enriched, adult male urihary musculus cDNA clone 9530042D02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal
/lab_host="DH10B (Tl phage-resistant)"
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Unpublished (2001)
Contact: Yoshihide Hayashizaki
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Y. and Hayashizaki,Y. Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
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bladder"
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Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Site_1: Sall; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5] of the primed with a primer [6] of the primer [7] of
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Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
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/tissuc_type="urinary bladder"
/dev_stage="adult"
/lab_host="DH10B"
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3'j. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from
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Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda
, M., Koya, S., MarEuyama, T., Miyazaki, A., Nomura, K., Ohno, M.,
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, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H.,
Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T.,
Muramatsu, M. and Hayashizaki, Y., et al. 2001)
Contact: Yoshihide Hayashizaki, T., et al. 2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9216
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URL: http://genome.ggc.riken.go.jp,
URL: http://genome.ggc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
A., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/dew_stage="adult"
/lab_host="bH108"
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ISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. CE 1 (bases 1 to 759)

RS NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MCC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

Plate: LLAM9810 row: 1 column: 07

High quality sequence start: 3

High quality sequence start: 3

Location/Qualifiers

Location/Qualifiers

Location/Qualifiers

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Location/Qualifiers BF789072 759 bp mRNA linear EST 12-JAN-2001 602104930F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4222998 5', mRNA sequence. /clone_lib="NCI_CGAP_Kid14"
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/nab_nost="DHIOB (TI phage_resistant)"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
1 218 c 243 g 167 t 193 CTGGAGGTGCCTGGCTGCCGCATTACCTATGTGCCACCCTTCTGCTGGAAGTCGGG 452 27 28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuGluValGly 47 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPheGly 1 others 692 0000 0000 Length:
Matches:
Conservative:
Mismatches:
Indels: 143 /organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone="IMAGE:422998" US-09-593-793A-113 (1-553) x BB627667 (1-692)

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US-09-593-793A-113 (1-553) x BI107873 (1-858)
                                                                                                                                                                                                                                                                                                                                                                                                                                BI650119.1 GI:15564355
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59.00
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100.008
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BI650119
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Best Local Similarity:
Query Match:
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ORIGIN
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BI650119
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TITLE
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COMMENT
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No
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KEYWORDS
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NIH-WGC http://mgc.nci.nh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: Gappas-remail.nh.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.

Contact: Robert Strausberg, Ph.D.

Tissue Procurement: Lothar Hennighausen Ph.D., Cho-xia Deng Ph.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at:

Http://inage.llnl.gov

Plate: LLAM11088 row: o column: 04

High quality sequence stop: 810.

Location/Qualifiers

//clone | Location/Qualifiers

//clone | Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI107873 858 bp mRNA linear EST 26-JUN-2001 602901816F1 NCI_CGAP_Mam3 Mus musculus CDNA clone IMAGE:5031771 5',
                                                                                                                                                                        363 CTGGAGGTGCCTGGCTGCCGCGTTACCTATGTGCCACCCCTTCTGCTGGAAGTCGG 422
                                                                                                                                                                                                                                                       47
                                                                                                                                                                                                                                                                                                                             28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuGluValGly
  759
59
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/dev_stage="10 months"
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                      Matches:
Conservative:
Mismatches:
Indels:
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Conservative:
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      Length:
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                                                                                                                                    US-09-593-793A-113 (1-553) x BF789072 (1-759)
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3.23e-43
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BI107873
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                                        Percent Similarity:
Best Local Similarity:
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Best Local Similarity:
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      Pred. No.:
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BI107873
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TITLE
JOURNAL
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KEYWORDS
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Site_2: NotI; Cloned unidirectionally Primer: Oligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH
Reference for transgenic model: Xu et al., Nature Genetics
22, 37-43 (1999) "
26 c 288 g | 202 t
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house mouse.

ISM Mus musculus.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Muridae; Murinae; Mus.

ICE 1 (bases 1 to 901)

SRS NIH-MGC http://mgc.nci.nih.gov/.

3 National Institutes of Health, Mammalian Gene Collection (MGC)

NAL Unpublished (1999)

T Contact: Robert Strausberg, Ph.D.

Fmail: Gapbs-rfemail.nih.gov

Tissue Procurement: Lohar Hennighausen Ph.D., Chu-xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: MGC Colne distribution information can be http://image.llnl.gov

Plate: LiAnl1855 row: p column: 02

High quality sequence stop: 778.

Location/Qualifiers .

Location/Qualifiers .
                                                                                                                                                                                                                                                                                                                                                                                                   BI650119 901 bp mRNA linear EST 12-SEP-2001 603296208F1 NCI_CGAP_Mam3 Mus.musculus cDNA clone IMAGE:5337073 5',
SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPheGly 27
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Mismatches:
Indels:
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/strain="129,C57BL/6J,FVB/N"
/db_xref="taxon:10090"
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                901 bp
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387 CAGGGIGIACCCAGAGCCGAGCCACCGAGGCCCGGGAGACACIAIGAIGAAGGC 443
                                           mRNA sequence.
BG242597
                                                                EST.
house mouse.
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Best Local Similarity:
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Query Match:
                                                                                                                                                                                                                     source
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                                  DEFINITION
            RESULT 25
BG242597
                                                                              ORGANISM
                                                                                                                TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
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                                                 ACCESSION
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KEYWORDS
SOURCE
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                                                                                                          AUTHORS
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                                                                                                                                                929 bp mRNA linear EST 12-JAN-2001 60212437F1 NCI_CGAP_Kidl4 Mus musculus cDNA clone IMAGE:4240617 BF785813
                   302 GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
                                                 48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal 66
                                                                                                                                                                                                                                                                                                                                                                                             9229
0 0 0 0
0 0 0
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Matches:
Conservative:
Mismatches:
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59.00
100.00%
100.00%
10.67%
                                                                                                                                     house mouse.
Mus musculus
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                                                                           RESULT 24
BF785813
LOCUS
DEFINITION
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No..
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AUTHORS
TITLE
JOURNAL
COMMENT
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ORIGIN
      339
                    28
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KEYWORDS
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BG242597 1116 bp | mRNA linear EST 13-FEB-2001 602354010F1 NCI_CGAP_Maml Mus musculus CDNA clone IMAGE:4482362 5',
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$11 Homo sapiens CDNA clone
                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

LU Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAMM0319 row: c column: 03

High quality sequence stop: 666.

Location/Qualifiers

Irce

Location/Qualifiers

Irce
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                                                                                                                                                                                   Mus musculus
Eukaryota; Metazoa; Chordata; Cranjata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
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59
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Mismatches:
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am84a12.s1 Stratagene schizo brain
IMAGE:1629790 3', mRNA sequence.
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                                                                                                       BG242597.1 GI:12752412
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59.00
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100.00%
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mкиA linear EST 21-AUG-2002
Mus musculus cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_rref="taxon:10090"
/clone="IMAGE:6396564"
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/lab_host="blost="The phage resistant)"
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Technologies. Note: chis is a NCI_CGAP Library."
a 278 c 273 g 219 t
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 934)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Uppublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: The Cepko, Laboratory
ConA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13892 row: i column: 05
High quality sequence stop: 634.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPheGly
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                     934
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Mismatches:
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                                                                                                                                              934 bp
AGENCOURT_8881033 NCI_CGAP_CO24 P
IMAGE:6396364 5', MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /strain="FVB/N"
                                                                                                                                                                                                                               BQ934815.1 GI:22350198
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9.228
                                                                                                                                                                                                                                                                                                  Mus musculus
                                                                                                                                                                                                                                                                            house mouse.
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BF854825/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_rype="schizophrenic brain S-11 frontal lobe"
/dev.stage="34 years old"
/dev.stage="34 years old"
/lab_host="304 years old"
/lab_host="Solk (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Library
constructed from S-11 frontal lobe, male, 34 years old,
50% caucasian, 50% Aleutian. Schizophrenic suicide.
Random primed into EcoRI site of ZAP II Vector. Mass
excised. Custom library. Avg insert length 1.4kb.
Material obtained by Johnston N., Torrey, Er., Yolken R.,
and the Stanley Neuropathology Consortium - Analysis of
RNAs from the Brains of Individuals with Psychiatric
Diseases (Unpublished) Stanley Neurovirology Laboratory,
Johns Hopkins School of Medicine, Baltimore MD."
                                                                                                                                      E I (bases I to 348)

S Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le.N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wyla,T., Waterston,R. and Wilson,R.
Contact: Wilson RK
Washigton University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@watson.wustl.edu
                                                                                                          Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: polyT not found
Seq primer: -40ml3 fwd. ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      326 LeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 crededererrecrecadrececcarcrecredererrerrerrerangeaceaerg 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                228 GCCGGTGCCACATGCCTGTCCCACACTGTGGCCGTGACAGCTTCAGCCGA-CCTCAC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                169 CGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCTACACACTGGCCTCCCTTACACC 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          366 AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAla-LeuTh 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405
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                                                                                Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="Stratagene schizo brain S11"
/sex="male"
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/db_xref="taxon:9606"
/clone="IMAGE:1629790"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     quality sequence stop: 348.
Location/Qualifiers
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AA984323.1 GI:3162848
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                                                                                         human.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-FN0202-
271000-011-A03&t32-2000-10-27&t4-1)
Seq primer: puc 18 forward
High quality sequence start: 12
High quality sequence start: 12
High quality sequence stop: 321.

Location/Qualifiers
1. 322
/Organism="Homo sapiens"
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/dev_stage="Addlt"
/clone_lib="FN0202"
/dev_stage="Addlt"
                                                                                                                                   Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: prostate_normal; Vector: puc18; Site_1: SmaI ste_2: SmaI; A mini-library was made by cloning products derived from ONESPEC PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                              Shotgun sequencing of the human transcriptome with ORF expressed
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BF854825
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48.00
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100.00%
8.68%
                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 322)
                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
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                                                                     Homo sapiens
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AW175665/c
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/ 1. 412
/ Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Br0046"
/dev_xtage="Adult"
/note="Organ: breast; Vector: pucl8; Site_l: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196; 716 - Ludwig Institute for Cancer Research) profiles into the puC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low
414 DP mRNA linear EST 16-NOV-1999
AW175665 AW17565.1 GI:6441806
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57, mRNA sequence.
BM915082
                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-BT0046-310899-002-F07&t3=1999-08-31&t4=1)
Seq primer: puc 18 forward
                                                                                                                              Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                          Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342
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HCGP http://www.ludwig.org.br/ORESTES.

The FAPESP/LICR Human Cancer Genome Project
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Conservative:
Mismatches:
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                                                                                                                                                                                                                                                     Unpublished (1999)
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Aliqnment Scores:
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                                                                                                                                                                                                                       Context: Robert Strausberg, Ph.D.
Tissue Procurement: DCTD/TIP
Tissue Procurement: DCTD/TIP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov f column: 03
High quality sequence start: 35
High quality sequence store: 657.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NIH wGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Best Local Similarity:
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ORIGIN
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EcoRI, cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
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AGENCOURT_6701857 NIH_MGC_41 | Homo sapiens cDNA clone IMAGE:5481717
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library."
                                                                                          Contact: Rocket Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt' Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Hitph://image.llnl.gov
Plate: LLCM1985 row: 1 column: 17
High quality sequence stop: 448.
1 (bases 1 to 1667)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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1. .1667
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665 c 258
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BM915527
BM915527.1 GI:19365906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AspLeuAlaLysTyrSerAla 553
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1. 341
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; Site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the pucl 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                                                                                                 Email: asimpsoneludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6st2=RC6-FN0202-080101-014-F018t3=2001-01-086t4=1)
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RCG-EN0202-271000-011-E04 FN0202 Homo sapiens CDNA, mRNA sequence.
BF854834
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Dias Neto.E., Garcia Correa, R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Coldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
Simpson,A.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
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Mammalia, Eutheria, Primates, Catarr¦hini, Hominidae, Homo.
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Mismatches:
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Matches:
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High quality sequence stop: 279.
Location/Qualifiers
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Fax: +55-11-2707001
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Best Local Similarity:
Query Match:
                                                                                                             Brazil
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                            /tissue_type="amelanotic melanoma, cell line"
/lab_host="DH10B (phage-resistant)"
/nab_host="DH10B (phage-resistant)"
/note="Organ: skin; vector: poTB7; site_1: Xho1; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGGG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo saplens
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 341)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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RC6-FN0202-080101-014-F01 FN0202 Homo sapiens CDNA, mRNA sequence.
BI045233
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                                 CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloseience Corporation
Clone distribution: MG clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2006 row: j column: 22
High quality sequence start: 131
High quality sequence store: 308.
Location/Qualifiers
1. 1063
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
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                      Tissue Procurement: DCTD/DTP
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283 c 261 g
3mail: cgapbs-r@mail.nih.gov
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Best Local Similarity:
Query Match:
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DEFINITION
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VERSION
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                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9666"
/clone_lib="Fr00202"
/dev_stage="Adult"
/note="Organ: prostate_normal; Vector: pucl8; Site_l: SmaI
/site_2: SmaI; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196/716 - Ludwig Institute for Cancer
Research) profiles into the pUC 18 vector: Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
11 a 11 c 137 g 68 t lothers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 242)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA647708 242 bp mRNA linear | EST 28-OCT-1997 vq77h04.sl Knowles Solter mouse 2 cell Mus musculus cDNA clone IMAGE:1108375 5', mRNA sequence.
                                                                                                                                                                Email: asimpsofelludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC6&t2=RC6-FN0202-
271000-011-E04&t3=2000-10-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence stop: 423.
                                                                                                    Sao Paulo-SP
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                                                   Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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Conservative:
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                    97
sequence tags
Proc. Natl. Acad. Sci. U.S.A.
20202663
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Best Local Similarity:
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/tlssue=Lype="embryo"
/dev_stage="0-cell"
/lab_host="DH10B"
/note="0rgan: embryo; Vector: pBluescribe (modified);
/note="organ: embryo; Vector: pBluescribe emorios:
/note="organ: embryo; Vector: pBluescribe emorios: Site_1: Mlu1; Site_2; Sal1; Cloned unidirectionally from mRNA prepared from 13,500 2-cell stage embryos. Primer: Sal1(dT): 5'-CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'. cDNAs were cloned into the "Mlu1/Sal1 sites of a modified pBluescribe vector using commercial linkers (NEB).
Average insert size: 1.2 kb."
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                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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601667874F1 NCI_CGAP_Mam1 Mus' musculus cDNA clone IMAGE:3967.
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Waterston, R.
The WashJ-HHMI Mouse EST Project
Unpublished (1996)
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
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Matches:
Conservative:
Mismatches:
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/strain="057BL/6J x DBA/2J Fl"
/db_xref="taxon:10090"
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High quality sequence stop: 213.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence.
BE914848
BE914848.1 GI:10413891
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Best Local Similarity:
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National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549 bp mRNA linear EST 26-JAN-2001
H3066G04-5 NIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
BG081576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kargul,G.J., Dudakula,D.B., Qian,Y., Lim,M.K., Jaradat,S.A., Tanaka,T.S., Carter,M.G. and Ko,M.S.H.
Verification and initial annotation of NIA mouse 15K cDNA clone set Other_ESTS: H3066G04-3
                                                                                                                                                                                                                                                                                                                                    /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH" 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 549)
                                                             DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. c column: 19
High quality sequence stop: 564.

I. 1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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43
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/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
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Mismatches:
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Matches:
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                                                                                                                                                                                              /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
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BG081576
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/note="Neeton: pSPORT1; Site_1: Sal1; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo. CDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary CDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT).Not primers. References include: (1) Genome-wide expression profilling of mid-gestation placenta and embryousing a 15,000 mouse developmental CDNA microarray, 2000, proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale CDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1745; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
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Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                         /clone_lib="NIA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
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visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3066 row: G column: 04
Seg primer: -21M13 Reverse
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                                                                                                                                                                                                                            /strain="C57BL/6J"
/db_xref="niaEST:H306G04-5"
/db_xref="taxon:10090"
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/organism="Mus musculus"
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                                                       Seq primer: -21M13 Reverse
High quality sequence stop: 549
POLYA-No.
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                                                                                                                                                                                                                                                                                                                  /clone="H3066G04"
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BF581244
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Best Local Similarity:
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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/clone="Inb="NOI_CGAP_CGAP"
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/lab_host="DH10
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                                                                                                                                                 Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.lni.gov
Plate: LLAM9603 row: p column: 16

High quality sequence start: 2

High quality sequence start: 2

High quality sequence stop: 680.

Location/Qualifiers

Free
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Bmall: cgapbs-remail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
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Best Local Similarity:
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ORGANISM
                                   AUTHORS
TITLE
JOURNAL
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BG173136
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/clone='IMAGE:445602"
/clone='IMAGE:445602"
/clone='IPAGE:45602"
/clone='IPAGE:45602"
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/note="taxon: mammary; Vector: pCMV-SPORT6; Site_1: Sall;
/site_2: Not1; cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
99 a 289 c 287 g 194 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 786)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.e. column: 05
Plate: LLAM10254 row: e column: 05
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Liffe Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution info
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAMN0257 row: e column: 03
High quality sequence stop: 608.
Location/Qualifiers
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/strain="FVB/N"
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BUKATYOGE, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 317)

Kimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Imotani, K., Ishii, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Sata, R., Sakazi, C., Sakai, K., Sakazi, R., Sakazi, C., Sakai, K., Sakazi, C., Sakai, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length CDNAS (Akimura, T., et al.
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Site_2: NotI: Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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URL:http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayasu,N., Sugahara,Y., Shibata,K., Itoh
,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BB707065 BIKEN full-length enriched, in vitro fertilized eggs Mususculus CDNA clone 7420496I01 3', mRNA sequence.
BB707065.1 GI:16055900
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339
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Conservative:
Mismatches:
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                                            /organism="Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                 6.38e-25
39.00
100.00%
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7.05%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST.
house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity:
Query Match:
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                       source
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BB707065
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FEATURES
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RÍKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2000) (2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BG246497 844 bp mRNA linear EST 13-FEB-2001 602360526F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4488895 5',
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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GAGAGAGAAGATCCAAGAGCTCTŢTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Site_1: Sal1: Site_2: BamHI: cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in
                                                                                                                                                                                                                                                                                                                                                                                                                                      Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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/clone="7420496101"
/clone=_1b="RxEN full-length enriched, in vitro fertilized eggs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="in vitro fertilized eggs"
/dev_stage="egg"
/lab_host="DH10B"
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Conservative:
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BG246497.1 GI:12756312
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81
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BG068547/c
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                                                                                                                 Contact: Robert Strausberg, Ph.D.
Email: Gapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium;(LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM1036 row: c column: 08
High quality sequence stop: 655.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gibbert Smith, NIH"
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 844)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 430) Walker, M.G., Volkmuth, W., Sprinzak, E., Hodgson, D. and Klingler, T. Prediction of gene function by genome-scale expression analysis: Genome Res. 9 (12), 1198-1203 (1999)
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                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:1000"
/clone="IMAGE:448895"
/clone_Lib="NCI_CGAP_Mam1"
/tissue_type="tunor, biopsy sample"
/dev_stage="10 months, virgin"
/lab_host="DH108"
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37
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Matches:
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Incyte Pharmaceuticals
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                                                                                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                               1. 844
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Best Local Similarity:
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                                                   REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
TITLE
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MEDLINE
COMMENT
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AF109303
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3174 Porter Drive, Palo Alto, CA 94304, USA

co-expressed with known prostate-cancer genes.

Location/Qualifiers

1. 430

/organism="Homo sapiens"
/db_xref="taxon:9606"

/clone="IPCA-8"
/clo
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Email: cdna@figun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: #13066 row: G column: 04
Seq primer: -21M13 Forward
High quality sequence stop: 466
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Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

Mus musculus.

I (bases I to 466)

Rargul, G.J., Dudekhla, D.B., Qian, Y., Lim, M.K., Jaradat, S.A., Tanaka, Y.T.S., Carter, M.G. and Ro, M.S.H.

Verification and initial annotation of NIA mouse 15K cDNA clone set Unpublished (2001)

Other_ESTS: 10066604-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGCGCACCGGAAAGCCCAGCTCTTGCTG 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu
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Mismatches:
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/db_xref="taxon:10090"
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/organism="Mus musculus"
/strain="C57BL/6J"
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             /note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7:5 embryos.

part of E7:5 embryos, extraembryonic part of E7:5 embryos.

, and E12:5 female mesonephros/gonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT) > Not primers. References include: (1) Genome-wide expression pofiling of mid-gestation placenta and embryo using a 15,000 mouse developmental cDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale cDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5 day mouse embryos reveals enrichment in the t-complex and under-representation on the x chromosome, 1998, Hum MoI Genet 7: 1967-1978.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. Mus. I, Chases 1 to 564)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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/lab_host="DH10B"
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/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/dlone="IMAGE:4984191"
/clone="IMAGE:4984191"
/clone="IMAGE:4984191"
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/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: sall; cloned unidirectionally. Primer: Oligo dT.
/strage insert size 1.6 kb]. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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Seg 16 2-7700 -> encodes 254 AA 257-553 553 554

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Qy 401 SerLeutyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420 Db 1482 TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGAACTGGAGGT 1541 Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		501 LeuserGlnValAlaProSerLeuPheMetGlySerIleVal 	Oy 541 VALVAIPheAspLysSerAspLeuAlaLysTyrSerAla 553	ONO ND	CURRENT APPLICATION NUMBER: US/09/232,880 CURRENT FILING DATE: 1999-01-15 NUMBER OF SEQ ID NOS: 338 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 110 LENGTH: 3410 TYPE: DNA ORGANISM: Homo sapien US-09-232-880-110	Alignment Scores: Pred. No.: Score: Score: Score: Forcent Similarity: 100.008 Conservative: Conservative: 0 Query Match: 100.008 Indels: 0 Gaps: 0 US-09-593-793A-113 (1-553) x IIS-09-232-880-110 (1-3410)	A TOTAL TO THE TOT

useralaproserLeuserProHis 240 nnLeuGlyAlaLeuLeuProArgLeu 260 1183 uGinileLeuProTyrThrLeuAla 400 unAspPheCysGlyGlnValCysPhe 140 9AspProAspHisCysArgGlnAla 160 YCYSLEUGIYTYLLEULEUProAla 180 200 883 943 OLYSTYTATGGLYASPTHTGLYGLY 420 userLeuGlyIleLeuLeuSerLeu 100 220 463 523 583 80 CATGACCATGGTGCTGGGCATTGGT

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11.1	DD 1484 TCCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT 1543	Oy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440	Oy 441 PheproAsnGlyHisValGlyAlaGlyGlyGevGevLeuFroProProAlaLeu 460	Db 1604 TICCCIAAIGGACACGIGGGIGCIGGAGGCAGIGGCCIGCICCCACCICCACCCGCGCGCTC 1663	CysGlyalaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla	1004 19CGGGGCCTCTGCCGTGATGTCTCCGTACGTGGTGGTGGGTG	481 AIGVATVALIONELYANGENTICOYSCHUASPHOUAILILEHUININIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		1784 CTGTCCCAGGTGGCCCCATCCCTGTTATGGGCTCCATTGTCCAGCTCAGCCAGC	Oy 521 ThralaTyrMetValSeralaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540	Db 1844 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903		Db 1904 GTAGTATTTGACAAGGGGACTTGGCCAAATACTCAGCG 1942	RESULT 3 US-10-102-896-110	; Sequence 110, Application US/10012896 ; Publication No. US20020183251A1	Xu, Jiangchun	APPLICANT: DILLON, DAVIN C. APPLICANT: Mitchen, Jennifer L. APDITCANT: Harlocker, Ginear I	. Jiang, Yuqi . Kalos Mich		APPLICANT: Day Craig H.	APPLICANT: Carter, Darrick	Wang			Houghton, Raymond	Foy, Teresa Fander Gary B	APPLICANT: Funger, 2017 N.; APPLICANT: Mantanabe, Yoshihiro	TILL OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND THESE OF INVENTION: PLACEMENT OF PROCESSED AND THESE OF INVENTION: PLACEMENT OF PROCESSED AND THE OF INVENTION.	FILE REFERENCE: 20121.42720. FILE REFERENCE: 20121.42720. FILE REFERENCE: 20121.42720.	Ď	Northware: FastSEO for Windows Version 3.0	CLE IL NO 110 ; LENGTHIN 3410 mydd: DHIN	IIFE: UNA OCANISM: Homo sapiens	

Alignment Scores:

		343	40	403	0		523	100	583	120	643	140	703	160	763	180	823	200	883	220	943	4	1003	260	1063	280	1123	300	1183	20	1243
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APPLICANT: Fanger, Gary R.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.53422
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF EQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 110
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Conservative:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Matches:
Conservative:
Mismatches:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR 'TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C26
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UNDRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: PASLSEQ for Windows Version 3.0
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Jiang, Yuqiu
Kalos, Michael D
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas
Carter, Darrick
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US-09-895-814-110
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Best Local Similarity:
Query Match:
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	TITLE OF INVENTION: COMPOUNDS FOR IMMUNOINEMARY AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND TOTAL AND	Alignment Scores: Pred. No.: Score: Score: Score: Fercent Similarity: Best Local Similarity: 100.00% Mismatches: Ouery Match: 10 00% Mismatches:	US-09-593-793A-113 (1-553) x US-09-745-288-100 (1-3410 Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLy Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLy Db 284 ATGGTCCAGAGGCTGTGGGTGAGCCGCTGCTGCGGACCGGAA Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGl	344 41 404 61	464 81 524 101	Db 584 TTCTCATCCCAAGGCCGGCTGGCTAGCAGGCCTGCTGCTGCTGCTGCTGCTGCTGCCTGC	Oy 141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAs
161 TyrSerValfyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180	y 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260	y 301 TyrGlnGlyValProArgalaGluProGlyThrGlualaArgArgHisTyrAspGluGly 320	y 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360	y 381 SeralaalaLeuThrGlyPheThrPheSeralaLeuGlnIleLeuProTyrThrLeuala 400	y 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440	y 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480	SerGln CCCAG

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AND
AND METHODS FOR THEIR USE ATTTACTTTGCTACACAG 1903 AGCATCACCTATGTGCC 40 MetvalLeuGlyIleGly 60 SerAspHisTrpArgGly 80 ProAspProArgProLeu 120 CysGlyGlnValCysPhe 140 ||||||||||||||||||||||||| TGTGGCCAGGTGTGTTC 703 AspHisCysArgGlnAla 160 10) 42 m

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31 8	81 IleaspTrpaspThrSeralaLeualaProTyrLeuGlyThrGluGluGluCysLeuPhe 200 	
25	01 GlyLeuLeuThrLeu11ePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220 	
9 23	21 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240 	
24	41 CyscysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProargLeu 260 	
106	61 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280 	
26	81 SerTrpWetalaLeuWetThrPheThrLeuPheTyrThraspPheValGlyGlyGluGlyLeu 300 	
3(01 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320 	
33	21 ValargMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340 	
34	41 ValMetaspargLeuValGlnargPheGlyThrargAlaValTyrLeuAlaSerValAla 360 	
36	61 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380 	
38	81 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThileuAla 400 	
148	01 SerLeuTyrHisargGluLysGlnValPheLeuProLysTyrargGlyaspThrGlyGly 420 	
42	21 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440 	
44	41 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460 	
46	61 CysGlyalaseralacysAspValSerValArgValValValGlyGluProThrGluAla 480 	
172	81 ArgValValProGlyArgGlyIleCysLeuAspLeuAalaIleLeuAspSerAlaPheLeu 500 	
50	01 LeuserGlnValalaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520 	
184	21 ThralatyrMetValSerAlaAlaGlyLeuGlyLeuValAlaileTyrPheAlathrGln 540 	

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ArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlylleLeuLeuSerLeu 100
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                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 110
LENGTH: 3410
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            1904 GTAGTATTTGACAAGAGGGACTTGGCCAAATACTCAGCG 1942
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Matches:
Conservative:
Mismatches:
541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Gaps:
                                                           5-09-759-143-110
Sequence 110, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
                                                                                                                                                               Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
                                                                                                             Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
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Vedvick, Thomas S
Carter, Darrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                             Li, Samuel
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Best Local Similarity:
Query Match:
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Q Op	141	ThrProLeuGlualaLeuLeuSerAspLeuPheargaspProAspHisCysargGlnala 160	Oy Dp 1	78
çy O	161	TyrSerValtyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 18 	Qy Db 1	84
Q Dp	181	IleaspTrpaspThrSeralaLeualaProTyrLeuGlyThrGlnGluGluCysLeuPhe 20	Qy Db 1	90
Qy Db	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 	ESUL S-09 Seq Pat	T 8 -78 uen
Qy Db	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240 	GENE APP	LICER
Oy Db	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260 	; APPLIC ; APPLIC ; APPLIC ; APPLIC	EEEE
Oy Dp	261 1064	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280 		EEEE
Oy Dp	281	SerTrpWetalaLeuMetThrPheThrLeuPheTyrThraspPheValGlyGluGlyLeu 300 		iiiii
Qy Db	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320 		EEEE
Oy Dp	321	ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlalleSerLeuValPheSerLeu 340 		LEE!
Oy Dp	341	ValMetAspargLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360 		TWE
Qy Dp	361	AlaPheProValAlaAlaGlyAlaThrCySLeuSerHisSerValAlaValThrAla 380 		ID NGJ
Qy Dp	381	SeralaalaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400 	US-09-78(Alignment Pred. No.	78(No.
Qy Db	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420 	Score: Percent Best Loc Query Ma	t s oca Mat
Qy Dp	421	AlaSerSerGluaspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440 		593
Oy Dp	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460 		284
o d	461	CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480 		344
οy	481	ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 500	δŏ	4

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CCTCTGCTGCAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGGATTGGT	ProvalLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 	pAlaLeuSerLeuGlyIleLeuLe 	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCySProAspProArgProLeu 	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe	ThrProLeuGlualaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnala	TyrSerValtyralaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuPeroala 	IleaspTrpaspThrSeralaLeualaProTyrLeuGlyThrGlnGluGluCySLeuPhe 	GlyLeuLeuThrLeullePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 	CysCysProCysArgAlaargLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 	HisGinLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGlüLeuCys	SerTrpMetalaLeuMetThrPheThrLeuPheTyrThraspPheValGlyGlüGlyLeu 	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 	ValargMetGlySerLeuGlyLeuPheLeuGlnCysalaIleSerLeuValPheSerLeu 	ValmetaspargLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 	AlaPheProValAlaAlaGlyAlaThrCySLeuSerHisSerValAlaValValThrAla 	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGly
404	61	81 524	101	121	141	161 764	181 824	201	221	241 1004	261 1064	281 1124	301 1184	321	341	361 1364	381 1424	401
q	oy Og	Qy Db	o do	oy Op	Qy Dp	Oy Db	Qy	Qy Db	Qy Dp	Oy Dp	Oy Dp	Qy	Oy Db	Qy Db	Qy Db	Qy Db	Oy Dp	Oy Op

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Sequence 110, Application US/09030606

Patent No. US20020081580A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wi, Jiangchun

APPLICANT: Dillon, Davin C.

TITLE OF INFUNITION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHOD NUMBER OF SEQUENCES: 224

CORRESPONDENCE ADDRESS:

ADDRESSEE: SEED and BERRY LLP

STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle

CITY: Seattle

CONTRY: USA

ZIP: 98104
                                                                1724 AGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783
                                                                                                                                                                                                                                                                                                                                                           521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540
421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro
                                                                                                                                                                                                    481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                       Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 210121.428C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IDA PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, 'Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,606
FILING DATE: 25-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 3410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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US-09-030-606-110
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Alignment Scores:

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r 0 0 0	_	sAlaGlnLev AGCCCAGCT	VIleThrT	CATCACCT	tValLeuGly	TGC	rASPHisTrp 	ACC.	GGGCATCCTGC	ProA	CCCGGATCCCA	sGlyGlnVa]	GCCAG	PHISCYSAR 	rLeu	GGCTACCTCC	GlnGluGluCy	- <u>F</u>	ValA	GTGG	ProSerLeuS	GT	AlaLeuLeuP	CTTC	eValAlaG CGTGGCTG	:GlyG	Trestegees	ArgArgHisTyrAsp(
s: vative: ches: :	(1-3410	HisargLysa 	AlaAlaGl	GCCGCAGG	eMetThrMe1	ATGACCAT	ySerAlaSerA	AGC	TCCTI	LeuCy	CTCTC	euAspPheCysG	٠ ق	neArgAspProAsj 		CCTG	Thr	ACC	AlaThrLeuLeu	GCCACACT	erAla	rceeccc	LeuGlyAl		gArgLeuPh 	ThraspPh	ACACGGATT	AlaArgAr
Matches Conserv Mismatc Indels: Gaps:	-606-110	LLEUArg scrGCGG	lCysLeu	STGTTG	uLysPh	AAGTT	Leugl	CIAGG	TGGGCACTG	Leu	- SC-	GlyLeuLeu	ည်	euPheArg TCTTCCGG	[5	TGGGGGCT	roTyrLeuGly	CTAC	/sValAlaAla7	SCGTAGCA	luGlyLeuSe	AGGGCTG	heArgAsnLeuGlyA	rccggaac	hrLeuArg	Phe		YThrGluAla
	060-60-s	SerargLe 	LeuGluVa	CTGGAG	ValGluGl	GTAGAGG	ValProLeu 		ATC	TrpLeuA	TGGCTAGCAGGG	Lyval	SCGTG	erAspL 	leSer	GATCAGICI	LeuAlaPro	TGGCC	ullePheLeuThrCysVa	CTCACCTC	3luProAlaGluGlyL	CAGCAG	euAlaP	TGGCTT	tProArgT) GCCCCGCAC	heThrI	TTCACGCTC	GluProGl
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imilar 1 Simi ch:	-793A-	MetVal(ValAS	GTCAA	ProLe		Prova	UCAG	CGCTAT	PheLe	TTTCT	GluLe	GAGC	ThrP	Tyrse	TACTCT(IleAspl	ATTGA(GlyLe	- Č		9		PGCTG.	HisGlnI CACCAGO	SerTri	AGCTGG	TyrGlnGly
e: ent S Loca y Mat	09-593	1 284	21	344	4	404	10	òò		101	584	121		141	161	764	181	824	201	884	~ .	44	4 (1004	261	281	1124	301
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ValargmetGlySerLeuGlyLeuPheLeuGlnCysAla1leSerLeuValPheSerLeu	GCTACCAGGCCCTGATGACCAGGCTCCTGCCAGGCCCTAAGCCTGAAGCTCCCCCAGGCCCTAAGCCTGAAGCTCCCCCAGGCCCTAAGCCTGAAGCTCCCCCAGGCCCTGAAGCCTGAAGCTCCCCCCCC	TCGCATTTACTTTGCTACACAG TG 553 GG 1942 FOR THE THERAPY AND ANCER	3410 553 tive: 0 es: 0
LeuPheLeuGlnCysA	ArgaccageTrecrocage AlaglyGlySerGlyL GTGGAGGCAGGCAGGCAGCAGCAGCAGCCAGCCAGCCAGC	CTATATGGTGTCTCGCCGCGCTGGTGTGTGTGTGTGTGTG	Length: Matches: Conserva Mismatch Indels:
ValArgMetGlySerLeuGly	CTACCAGGAGGACAGCCTG heproasnGlyHisValGly	CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	gnment Scores: d. No.: 553.00 re: 553.00 t Local Similarity: 100.00% r Local Similarity: 100.00%
321 341 364 364 424 424 421	1544 G 441 P 1604 T 1664 T 1724 A 1724 A 1784 C	1844 A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	ment Sons: No.: nt Sim Local Ratch
		0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Alignment Pred. No. Score: Percent S Best Loca

DB:		10 Gaps: 0		
us-0	9-593	-793A-113 (1-553) x US-09-822-827-110 (1-3410)	a a	1304
δ	П	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20 	QY	361 <i>p</i>
go ,	284	ATGGTCCAGAGGCTGTGGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG	δλ	381
g g	344	ValashueuleulnirPheciyLeuGiuValCysLeuAiaAlaGiylleThrTyrValPro 40 	qa	1424
3 8		, ,	Qy	401
r q	404		qa	1484 7
δy	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspH1sTrpArgGly 80	δ	421 7
qq	464		q _Q	1544 0
οy	81	ArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlylleLeuLeuSerLeu 100	δ	441
qq	524	CCCTATGGCCGCCGCCCCTTCATCTGGGCACTGTCCTTGGGCATCCTGAGCCTC 583	අධ	1604 1
οy	101	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProArgProArgProLeu 120	ογ Oγ	461 0
qq	584	TTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGCTGCTGTGCTGTGCCCGGATCCCAGGCCCCTG 643	<u>a</u> :	1004
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140	Š 7	104
qq	644	GAGCTGGCACTGCTCATCCTGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTC 703	ar :	1724 6
٥y	141	ThrProLeuGlualaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160	δ đ	100
g	704	ACTCCACTGGAGGCCCTGCTCTGTGTTTCCGGGACCCGGACCACTGTCGCCAGGCC 763	an e	1/84 (
οy	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180	Qy E	521 1
Dp	764	TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG	3 8	1 1 1 1 1
οy	181	IleAspTrpaspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCySLeuPhe 200	à á	1904
QQ	824	ATTGACTGGGACACCACTGGCCCCCTACCTGGGCACCCAGGAGGGGGGCTCTTT 883	gr	,
οу.	201	GlyLeuThrLeuilePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220	NESOLT US-09-	KESULT 11 US-09-115-4 ; Sequence
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දු පු	241	CysCysProCysArgAlaArgLeuAllaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260 	 E O O	FILE REF CURRENT
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<u>8</u>	301 1184	TYTGLIGLYVALVOATGALBGLUPTOGLYTTRCHUALAARGARGHISTYTASPGLUGLY 320 	Score Pred	. NO.: e: ent Sim
δy	321	valArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340	Best 1 Query	West Local
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٥y	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360	60-80	- 593

0y 361 AlaPheProvalAlaAlaGlyAla 0y 361 AlaPheProvalAlaAlaGlyAla 0b 1364 GCTTCCCTGTGGCTGCGTGCC 0y 381 SerAlaAlaLeuThrGlyPheThr 0b 1364 GCTTCCCTGTGGCTGCCGGTCCC 0y 381 SerAlaAlaLeuThrGlyPheThr 0b 1424 TCAGCCGCCCTCACCGGGTTCACC 0y 401 SerLeuTyrHisArgGluLySGln 1484 TCCCTTACCACGGGTTCATG 0y 441 PheProAsnGlyHisValGlyAla 1544 GCTAGCAGCTGAGGAGCAG 0y 421 AlaSerSerGluAspSerLeuMet 1611111111111111111111111111111111111

1364 GCTTTCCCTGTGGCTGCCGGTGCCTGTCCCACAGTGTGGCGTGGTACAGTTTTTTTT	0y 41 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAslace 460	Qy 521 ThralaTyrMetValSerAlaalaGlyLeuGlyLeuvalAalaIleTyrPheAlaThrGln 540	APPLICANT Jiangy Yugin L. APPLICANT Raios, Michael D. APPLICANT Stolk, John A. APPLICANT Stolk, John A. APPLICANT Stolk, John A. APPLICANT Carter, Darrick APPLICANT Carter, Darrick APPLICANT Skeiky, Yasir A.W. APPLICANT Hepler, William T. APPLICANT Hepler, William T. APPLICANT Hepler, William T. APPLICANT Hepler, Milliam T. APPLICANT Hepler, Milliam T. APPLICANT Hepler, Milliam T. APPLICANT Hepler, William T. APPLICANT Houghton, Raymond L. APPLICANT HOUGHTON COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: LOMBOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: LOMBOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: LOMBOSITIONS AND METHODS FOR THE THERAPY AND CURRENT RAPLICATION NUMBER: US/10/012,896
Oy 1 MetValGinargLeuTrpValSerargLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20	81 ArgTyrGlyArgArgArgAroPhelleTrpAlaLeuSerLeuGlylleLeuLeuSerLeu	09 161 TyrSerValTyralaPheMetileSerleuGlyGlyCysLeuGlyTyrLeuLeuProAla 180 161 TyrSerValTyralaPheMetileSerleuGlyGlyCysLeuGlyTyrLeuLeuProAla 180 161 TyrSerValTyralaPheMetileSerleuGlyGlyCysLeuGlyTyrLeuLeuProAla 180 161 TyrSerValTyralaPheMetileSerleuGlyGlyCysLeuGlyTyrLeuLeuProAla 180 164 TACTCTGTCTATGCCTTCATGGTCTTGGGGGCTGCCTGGCCTGCC 823 09 181 IlleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200 161 IlleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200 161 IlleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200 161 IlleAspTrpAspThrLeuIllePheLeuThrCysValalaAlaThrLeuLeuValAlaGluGlu 220 161 IlleAspTrpAspThrCetTcCTCCTGGCCCCTGGTGCTGGGCTGGGGGGGGGGGGGG	Qy 241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260 Db 1004 TGCTGCCATGCCGGCCCCTGGGCCCCCTGCTTCCCCGGCTG 1063 Db 1004 TGCTGCCATGCCGGCCCCTGGGCCCCCTGCTTCCCCGGCTG 1063 Db 261 HisGInLeuCysicysArgMetProArgThrLeuArgArgLeuPheValAaGluLeuCys 280 Db 1064 CACCAGCTGCTGCCTGCCTCCCCCCCCCCCCTTCGTCCTTGTGCTTGTGTGTGTGTTGT

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Mismatches:
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NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FastSEQ for Windows Version 3.0
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                               ) ORGANISM: Homo sapiens
US-10-012-896-704
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                                                        TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.53462
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SOFWHARE: FastSEQ for Windows Version 3.0
SEQ ID NO 704
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                                                                                            Sequence 704, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
                                                                                                                                                                                        APPLICANT: Xu, Jiangchun
PPPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
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Hepler, William T.
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Kalos, Michel D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
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461 CCAGTGCTGGGCCTGGTCTCTGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGA 520	81 A 521 C	101 PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCySProAspProArgProLeu 120 	121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140 	141 ThrProLeuGlualaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnala 160 	<pre>161 TyrServalTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180</pre>	181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluGluCysLeuPhe 200 	201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220 	221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240 	241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260 	261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280 	281 SerTrpMetalaLeuMetThrPheThrLeuPheTyrThraspPheValGlyGluGlyLeu 300 	301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320 	RESULT 14 US-09-895-814-704 US-09-895-814-704 S. Sequence 704, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION:	APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitchan, Jennifer L.	Harlocker, Susan Jiang, Yuqiu Kalos, Michael D		APPLICANT: Day, Craig H. APPLICANT: Vedvick, Thomas S. ADBITANT: Carton Darvice		Skeiky, Yasir A.W. Hepler, William T.	
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       APPLICANT: Vinals de Bassols, Carlota
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
FILE REFERENCE: 20121.427026
CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
SOFWARE: FastSEQ for Windows Version 3.0
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Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
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261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280	Qy Dp	81 521	ArgT) CGCT/
281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyGlyLeu 300 	Qy	101	PheLe -
301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320 	QYDb	121	GluLe
US-09-759-143-704	δ ā	141	ThrP
Sequence /u4, Application US/09759143 Patent No. US2002002248A1 GENERAL INFORMATION APPLICANT: Xu. Jiangchun	o oy	701	ACTC(TyrSe
APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan I.	qa d	761	E
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APPLICANT: Rails, Millager D. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A.	ov du	201	61yte
APPLICANT: Day, Craig H. APPLICANT: Vedvick, Thomas S.	Qy Oy	221	
APPLICANI: Calcet, Daffick APPLICANT: Li, Samuel APDLICANT: Wanc aiin	qa	941	GCAG
APPLICANT: Skelky, Yasir A.W. APPLICANT: Hebler, William	QY	241	Cysc
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	QQ	1001	TGCT
CURRENT APPLICATION NUMBER: US/09/759,143 CURRENT FILING DATE: 2001-01-12 MINDED OF SEC IN MOS.	<i>&</i> 점	261 1061	261 HisGJ 061 CACCA
NOTIFIED OF SEC 1D NOS: 934 SEC 1D NO 704	Qy	281	SerT
TYPE: 4034 TYPE: DAGANISM: Homo sapiens S-09-759-143-704	oy oy	301 Tyrg]	AGCTC TyrG]
Alignment Scores: 1.18e-294 Length: 4034 Score: 320.00 Matches: 320 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 57.87% Indels: 0 Caps: 0	RESC	RESULT 16 US-09-780-669-7 Sequence 704, Patent No. US GENERAL INFOR	1ACC -669- 8 704 10. U INFC
US-09-593-793A-113 (1-553) x US-09-759-143-704 (1-4034)		APPLICANT APPLICANT	: LN
1 MetValGinargLeuTrpValSerArgLeuLeuArgHisArgLysAlaGinLeuLeu 20 		APPLICANT APPLICANT APPLICANT APPLICANT	
21 ValAsnLeuteuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40		APPLICANT APPLICANT APPLICANT APPLICANT	
41 ProLeuLeuLeuGluValGlyValGluGluLySPheMetThrMetValLeuGlyIleGly 60		APPLICANT APPLICANT APPLICANT	TNT:
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                                             SerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla
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US20020051977A1
ORMATION:
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Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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Dillon, Davin C.
Mitcham, Jennifer L.
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Pred. No.:
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                                                THERAPY AND
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                                                 THE
APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Helpler, William
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Houghton, Reymond L.
TITLE OF INVENTION: COMPOSITIONS ND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 704
LENGTH: 4034
                                                                                                                                                                                                              US-09-593-793A-113 (1-553) x US-09-780-669-704 (1-4034)
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Mismatches:
Indels:
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Matches:
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100.00%
57.87%
                                                                                                                 TYPE: DNA
GORGANISM: Homo sapiens
US-09-780-669-704
                                                                                                                                                                        Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                       SerTrpMetalaLeuWetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu
AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis
              HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys
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Patent No. US20020081680A1
GENERAL INFORMATION:
APPLICAT: Xu, Jiangchun
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.534C1
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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Mismatches:
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Matches:
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Best Local Similarity:
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; ORGANISM: HOMO
US-09-822-827-704
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 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe
             ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla
                                                           GGCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG
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CURRENT APPLICATION NUMBER: US/10/012,896
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Alang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Wardy H.
APPLICANT: Wardy Aljun
APPLICANT: Wang, Aljun
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Hondolton, Raymond L.
APPLICANT: Hondolton, Raymond L.
APPLICANT: Hondolton, Raymond L.
APPLICANT: Wanlander, Yoshiron
APPLICANT: Wanlander, Yoshihiro
APPLICANT: Wandeleine Joy
TITLE OF INVENTION: COMPOSITIONS?
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                                                                      Length:
Matches:
Conservative:
Mismatches:
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2001-12-10
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Windows Version
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      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 851
LENGTH: 1203
CURRENT FILING DATE:
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                                                                                    Percent Similarity:
Best Local Similarity:
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                                  TYPE: DNA
CRGANISM: HOMO
US-10-012-896-851
                                                                Scores:
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Pred. No.:
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176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195
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112 GGCCAGGTGTGCTTCACTCCACTGAGGCCCTGCTCTGACCTCTTCCGGGACCCGGAC
                                                 APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C26
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CURRENT FILING DATE: 2001-06-29
NUMBER FILING DATE: 990
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 851, Application US/09895814
Publication No. US20020193296A1
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Dennifer L.
APPLICANT: Mitcham, Dennifer L.
APPLICANT: Application Nugiu
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Langel M.
APPLICANT: Carter, Darrick
APPLICANT: Li Samuel X.
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Hepler, William T.
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LENGTH: 1203
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
NUMBER OF SED ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-593-793A-113 (1-553) x US-09-895-793-851 (1-1203)
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Conservative:
Mismatches:
Indels:
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
                                                                 Sequence 851, Application US/09895793 Publication No. US20020192763A1 GENERAL INFORMATION:
                                                                                                                    APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
                                                                                                                                                                                                                                                                                                                                                                                        Henderson, Robert A.
                                                                                                                                                                                         Jiang, Yuqiu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S.
Carter, Darrick
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Hepler, William T.
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US-09-895-793-851
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1192 GTGGGCGAG 1200
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Best Local Similarity:
                                               US-09-895-793-851
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LENGTH: 1203
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APPLICANT:
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                                                                                                                                   892 GAGGAGTGCCTCTTTGGCCTGCTCACCTCTTCCTCACCTGCGTAGCAGCCACACTG
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                                                                                                                           76 AspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGly
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                               Conservative:
Mismatches:
                   Length:
Matches:
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Patent No. US20020022248A1
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Best Local Similarity:
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            Alignment Scores:
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US-09-759-143-851
US-09-895-814-851
                                            Query Match:
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196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEQ ID NOS: 934
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Mismatches:
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Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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                                                   Jiang, Yuqui
Henderson, Robert A
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
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Vedvick, Thomas S
Carter, Darrick
Li, Samuel
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IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro

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952 CTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGAGAAAGGCTGTCGGCCCCC 1011
                                                                                                                                                                                  216 LeuValalaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaPro 235
                                                                                                                                                                    256 LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Moughton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION UNBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 851, Application US/09780669 Patent No. US20020051977A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Dillon, Davin C.
Mitcham, Jennifer L.
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Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
Li, Samuel
Wang, Aijun
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US-09-780-669-851
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SOFTWARE: FastSEQ for
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Best Local Similarity:
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APPLICANT: Xu, Jia
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US-09-780-669-851
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LENGTH: 1203
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891

176 TyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195

196 GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 215

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FOR THE THERAPY AND

; Sequence 851, Application US/09822827; Patent No. US20020081680A1; GENERAL INFORMATION:

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RESULT 23 US-09-822-827-851

276 ValalaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPhe 295

APPLICANT: Xu. Jiangchun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSITE CANCER
FILE REFERENCE: 210121.53401
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT FILING DATE: 2001-03-28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 851 ; ORGANISM: Homo sapiens US-09-822-827-851 LENGTH: 1203 36 IleThrTyrValProProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMet 55

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		st 55 471	r 75 531	.y 95 - c 591	o 115 G 651	s 135 711	ip 155 C 771	y 175 - ic 831	n 195 - .G 891	.u 215 G 951	o 235 C 1011	a 255 C 1071	e 275 C 1131	e 295 C 1191				
1203 263 0 0 0	203)	uGluLysPheMetThrMe 	oLeuLeuGlyserAlase 	eTrpAlaLeuSerLeuGl 	uAlaGlyLeuLeuCysPr 	1GlyLeuLeuAspPheCy 	pLeuPheArgAspProAs CTCTTCCGGGACCCGGA	rLeuGlyGlyCysLeuGl 	aProTyrLeuGlyThrGl 	rCysValAlaAlaThrLe 	aGluGlyLeuSerAlaPr 	aPheArgAsnLeuGlyAl TTCCGGAACCTGGGCGC	gThrLeuArgArgLeuPh 	rLeuPheTyrThrAspPh 				
Length: Matches: Conservative Mismatches: Indels:	9-822-827-851 (1-13	uLeuGluValGlyValGl 	uGlyLeuValCysValPr 	yargargargProPhe11 	eProArgAlaGlyTrpLe CCAAGGGCCGGCTGGCT	aLeuLeuIleLeuGlyVa 	JGluAlaLeuLeuSerAs 	TyralaPheMetileSe 	AspThrSerAlaLeuAl 	1ThrLeuIlePheLeuTh 	JGlyProThrGluProAl GGCCCACCGAGCCAGC	OcysargalaargLeuAl \TGCCGGGCCGCTTGGC	JCysCysArgMetProAr 	AlaLeuMetThrPheTh			12896	
res: 6.29e-241 263.00 arity: 100.00% milarity: 100.00% 47.56%	93A-113 (1-553) x US-09	IleThrTyrValProProLeuLeuGluValGlyValGluGluLySPheMetThrMe 	ValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaser 	AspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGly 	IleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysPro 	AspProArgProLeuGluLeuAlaLeuLleuIleLeuGlyValGlyLeuLeuAspPheCys 	GlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAsp 	HisCysArgGinAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCySeuGly 	yrLeuLeuProAlaileAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 	GluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu 	LeuValalagluglualaalaLeuglyProThrGluProAlagluglyLeuSerAlaPro 	SerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 	LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 	ValalaGluLeuCysSerTrpMetalaLeuMetThrPheThrLeuPheTyrThrAspPhe 	ValGlyGlu 298 	-702	; Sequence 702, Application US/100128 ; Publication No. US20020183251A1 ; GENERAL INFORMATION:	Xu, Jiangchun Dillon, Davin C.
Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similari Query Match:	us-09-593-793	Oy 36 Ile7 Db 412 ATC/	Oy 56 Vall Db 472 GTG	Qy 76 Aspl 	Qy 96 Ilel Db 592 ATC	Qy 116 Aspi Db 652 GATC	Oy 136 G1y6 111 Db 712 GGC	Qy 156 Hisc 	Qy 176 Tyri Db 832 TACC	Oy 196 Glud Db 892 GAGG	Oy 216 LeuV Db 952 CTGC	Qy 236 Seri Db 1012 TCC1	Oy 256 LeuI Db 1072 CTGC	Oy 276 Vale Db 1132 GTGC	Oy 296 Valg	RESULT 24 US-10-012-896-	<pre>; Sequence 702 ; Publication ; GENERAL INFO</pre>	APPLICANT:

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118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137
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                                                                                                                                                                                                                                                               APPLICANT: Fanger, Gary R.

APPLICANT: Wantanabe, Yoshihiro

APPLICANT: Meagher, Madeleine Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER

FILE REFERENCE: 210121.427C27
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Matches:
Conservative:
Mismatches:
Indels:
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CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
           Harlocker, Susan L.
Jiang, Yughu
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel X.
Mitcham, Jennifer L.
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Hepler, William T.
Henderson, Robert A.
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ORGANISM: Homo sapiens
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0y 198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 217 1	Oy 318 AspGluGly 320	APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. APPLICANT: Hural, John APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Foy, Teresa APPLICANT: Foy, Teresa APPLICANT: Foy, Teresa TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER TITLE OF INVENTION: UNMBER: US/09/895,793 CURRENT FILING DATE: 2001-06-29 NUMBER OF SEQ ID NOS: 982 SOFTWARE: FastSEQ for Windows Version 3.0 SOFTWARE: FastSEQ for Windows Version 3.0 SOFTWARE: DNA ORGANISM: Homo sapiens US-09-895-793-702 Alignment Scores: 2.39e-240 Length: 4894 Score: 263.00 Best Local Similarity: 100.00% Mismatches: 0

us-09-593-793a-113.olig.rnpb

Oy 238 SerProHisc.	Db 2031 GAGGGGCTGTP, Qy 318 ASPG1UG1y Qy 318 ASPG1UG1y Db 2091 GATGAAGGT RESULT 27 GS-09-759-143-702 ; Sequence 702, Appl. ; Sequence 702, Appl. ; GENERAL INFORMATION ; GENERAL INFORMATION ; APPLICANNT: XM, J.	APPLICANT: DILLON APPLICANT: MITCh APPLICANT: HATLON APPLICANT: Handen APPLICANT: Henden APPLICANT: Relos, APPLICANT: Relos, APPLICANT: Retes, APPLICANT: Retes, APPLICANT: Stange, APPL	APPLICANT: DAY, CAPLICANT: Vedvict, APPLICANT: Carter, APPLICANT: Li, St. APPLICANT: Hi, St. APPLICANT: Wang, CAPLICANT: Wang, CAPLICANT: Wang, CAPLICANT: Wang, CAPLICANT: Wang, CAPLICANT: Wang, CAPLICANT: Wang, CAPLICANT	APPLICANT: SKEIK, APPLICANT: Heplen; TITLE OF INVENTION; TITLE OF INVENTION; FILE REFERNE: SELICATION: CURRENT APPLICATION; CURRENT APPLICATION: NUMBER OF SEC. IN	SOFTWARE: FastSEG 15 15 15 15 15 15 15 15 15 15 15 15 15	y. ORGANISM: Homo se U. 09-759-143-702 Alignment Scores: Pred. No.: Score: Percent Similarity: Percent Similarity: Best Local Similarity:	Query Match: DB: US-09-593-793A-113 (1	Qy 58 GlylleGlyPl 	Qy 78 TrpArgGlyAr
APPLICANT: Stolk, John A. APPLICANT: Day, Craig H. APPLICANT: Vedvick, Thomas S. APPLICANT: Carter, Darrick APPLICANT: Li, Samuel X. APPLICANT: Wang, Aljun APPLICANT: Hepler, William T. APPLICANT: Hepler, William T. APPLICANT: Hepler, William T. APPLICANT: Hepler, William T. APPLICANT: Houghton, Robert A. APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Foy, Teresa APPLICANT: Foy, Teresa	APPLICANT: Fanger, Gary TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY, AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILLE REFRENCE: 210121.477C26 CURRENT APPLICATION NUMBER: US/09/895,814 CURRENT APPLICATION NUMBER: US/09/895,814 CURRENT FILING DATE: 2001-06-29 NUMBER OF SEQ ID NOS: 990 SEQ ID NO 702 LENGTH: 4894 TYPE: DA TYPE: DA TYPE: DA ORGANISM: Homo sapiens US-09-895-814-702	Alignment Scores: 2.39e-240 Length: 4894 Score: 263.00 Matches: 263 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 47.56% Index: 0 DB: 9 Gaps: 0		Oy 78 TrpArgGlyArgTyrGlyArgArgArgArgProPhelleTrpAlaLeuSerLeuGlylleLeu 97	118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln	Oy 138 ValcyspherhrproLeuGlualaLeuLeuSerAspLeuPheArgAspProAspHisCys 157	178 LeuproalaileaspirpaspihrSeralaLeualaprofyrLeuGlyThrGlnGluGlu 1671 CIGCCTGCCATTGACTGGGACACCAGGCCCCTGGCCCTTGGGCACCCAGGAGGAG	Oy 198 CysLeuPheClyLeuLeuThrLeuIlePheLeuThrCysValAlaalaThrLeuLeuVal 217 	<pre>Qy 218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237 </pre>

	APPLICANT: TITLE OF I TITLE OF I FILE REFER	CURRENT AP CURRENT FI NUMBER OF SOFTWARE:	SEQ ID NO 7 LENGTH: 4 TYPE: DNA ORGANISM:	US-09-780-669 Alignment Sco Pred. No.:	Score: Percent Simil Best Local Si Query Match:	-60-2	58 GLY 11 1311 GGC	78 Trp 1371 TGG	98 Leu 1 1431 CTG	118 Arg 1491 AGG	138 Val 151 GTG	158 Arg 1611 CGC	178 Leu 1671 CTG		218 Ala	1791 GCT	238 Ser		1911 CCC	278 Glu	1971 GAG 298 Glu
99 LeuSerLeuPheieulieProArgaladlyTrpLeuAladlyLeuleuCysProAspPro 110 TrpAddCCTCTTTTCATCCCAACGGGGTGCTGGGCGATCCTTGGGGGGTGGTGGGGGGTGGTGGGGGGGTGGGGGGG				US A1 Pr	S B B B	SO O	da aa	oy dg	da Db	q α .	QQ Dp	Qy Db	~ <u> </u>	a a	QY	qa ::	oy d	AG VO	qa	οy	oy Oy
99 LeuSerLeuPheieulieProArgaladlyTrpLeuAladlyLeuleuCysProAspPro 110 TrpAddCCTCTTTTCATCCCAACGGGGTGCTGGGCGATCCTTGGGGGGTGGTGGGGGGTGGTGGGGGGGTGGGGGGG																					
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	98	118	138	158	178	198	218	238	258	278	298	318	RESULT 28 US-09-780-669-7 ; Sequence 702, : Patent No IIS								

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           AND METHODS FOR THE THERAPY PROSTATE CANCER
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Mismatches:
NT: Houghton, Raymond L.

FINVENTION: COMPOSITIONS AND METHODS

FINVENTION: DIAGNOSIS OF PROSTATE CA

FERRENCE: 210121.427C24

APPLICATION NUMBER: US/09/780,669

FILING DATE: 2001-02-09

OF SEQ ID NOS: 943

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Matches:
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9-702
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Thu Feb 20 11:11:49 2003

Db 1851 TCGCCCCACTGCTGCCGGCCCGCTTGGCTTTCCGGAACCTGGGCCCTTGTTTTTTCCGGAACCTGCCTTGGTTTGCAACCTGGGCCCTGCTTTGTTTTCCGGAACCTGGGCCCTGCTTTGTTTTCGGAACCTGGGCCCTGCTTTGCAACCTGGGCTTTGCAACCTGGGCTGTGGGTTTGCGGAACCTGGGCGCCTGCTTTGCAACCTGGGCTGTGGGTTTGCGGAACCTGGGCTGTGGAACCTGGCTTTGCAACCTGGGCTGTGGAACCTGGGAACCTGGGTTGAACGTTTGAACGTGTGAACCTGGGCTGTGAACGTGTGAACGTGTGAACGTGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACGTGAACAGAACAGAACAGAACAGAACAGAACAGAACAGAACAGAACAGAACAAAAAA	Qy 258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla		Db 2031 GAGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGACACT. Qy 318 AspGluGly 320	RESULT 30 US-10-012-896-705 ; Sequence 705, Application US/10012896 ; Publication No. US20020183251A1 ; GENERAL INFORMATION:	.00 C D		APPLICANT: L1, Samuel X. ; APPLICANT: Wang, Aijun ; APPLICANT: Skeiky, Yasir A.W. ; APPLICANT: Hepler, William T.	Henderson, Robert R Hural, John McNeill, Patricia E Houghton, Raymond I	APPLICANT: Vinals de Bassols, Carlota ; APPLICANT: FOY, Teresa ; APPLICANT: Fanger, Gary R. ; APPLICANT: Wantanabe, Yoshihiro	HILLS OF INVENTION: Madeleine Joy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND FITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427027	RRENT ARRENT IN MEER OF	; SEQ ID NO 705 ; LENGTH: 6976 ; TYPE: DNA ; ORGANISM: Homo sapiens	out Scores: 3.35e-240 Length:	re: Cent Similarity: 100.00% t Local Similarity: 100.00% ry Match: 47.56%	US-09-593-793A-113 (1-553) x US-10-012-896-705 (1-6976) Qy 58 GlylleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspH:	
Db 2031 GAGGGGTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGGCACCGAGGCCCGGAGACACTAT 2090	Oy 318 AspGluGly 320 Db . 2091 GATGAAGT 2099	ESULT 29 S-09-822-827-702 Sequence 702, Application US/09822827 Patent No. US20020081680A1 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER: FILE REFERENCE: 210121.534C1 CURRENT APPLICATION NUMBER: US/09/822,827 CURRENT FILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 982	; SOFTWARE: FastSEQ for Windows Version 3.0 ; SEQ ID NO 702 : LENGTH: 4894 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-822-827-702	Alignment Scores: 2.39e-240 Length: 4894 Score: 263.00 Matches: 263 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 10 Gaps: 0 Gaps: 0	US-09-593-793A-113 (1-553) x US-09-822-827-702 (1-4894)	<pre>Qy 58 GlylleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77 </pre>	Oy 78 TrpArgGlyArgTyrGlyArgArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeu 97	Qy 98 LeuSerLeuPheLeuIleProArgalaGlyTrpLeuAlaGlyLeuLeuCysProhaspPro 117 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 118 ArgProLeuGluLeuAlaLeuLeuIleEuGlyValGlyLeuLeuAspPheCyśGlyGln 137 D 1491 AGGCCCTGGAGCTGGCACTGCTGGGCGTGGGGCTGGGCT	Oy 138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157	<pre>Qy 158 ArgGlnalaTyrSerValTyrAlaPheMetileSerLeuGlyGlyCysLeuGlyTyrLeu 177 </pre>	Oy 178 LeuProAlaileAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197	OY 198 CysLeuPheGlyLeuLeuThrLeuTlePheLeuThrCysValAlaAlaThrLeuLeuVal 217	18 91	Oy 238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257

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11 GAGCTGTGCAGCTGGATGGCACCTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGC 2030
                                                                                                                  78 GluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297
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LICANT: Ranger, Gary R.
LICANT: Mantanabbe, Yoshihiro
LICANT: Meagher, Madeleine Joy
LE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
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BER OF SEQ ID NOS: 1011
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Wang, Aijun
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Hepler, William T.
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Houghton, Raymond L.
Vinals de Bassols, Carlota
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Juneation No. US20020183251A1
WERAL INFORMATION:
PPLICANT: Xu, Jiangchun
PPLICANT: Dillon, Davin C.
PPLICANT: Harlocker, Susan L.
PPLICANT: Harlocker, Susan L.
PPLICANT: Jiang, Yudiu
PPLICANT: Stolk, John A.
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PPLICANT: Retter, Marc W.
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                                                                                                                ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Dennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Michael D.
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                                                                                                               THE THERAPY
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263
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APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Hural, John
APPLICANT: Moreill, Patricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa
APPLICANT: Proper Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: LIAGUAGE
CURRENT APPLICATION NUMBER: US/09/895,793
CURRENT FILING DATE: 2001-06-29
                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
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                                                                                                                                                          NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 705
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Best Local Similarity:
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             1322 CTGAGCCTCTTTCTCATCCCAAGGCCGGCTGGCTAGCAGGGCTGCTGCTGTGCCCGGATCCC 1381
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DISGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210.21.4.77.223 CURRENT APPLICATION NUMBER: US/09/759,143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 705, Application US/09759143
Patent No. US2002002248A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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US-09-759-143-705
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                                                                                                                     US-09-593-793A-113 (1-553) x US-09-759-143-705 (1-6976)
                                                                                   Conservative:
Mismatches:
Indels:
                                                                      Length:
Matches:
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     NUMBER OF SEQ ID NOS: 934
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 705
LENGTH: 6976
2001-01-12
                                                                   3.35e-240
263.00
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                                          sapiens
CURRENT FILING DATE:
                                                                                Percent Similarity:
Best Local Similarity:
Query Match:
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                                 ; TYPE: DNA
; ORGANISM: HOMO
US-09-759-143-705
                                                              Alignment Scores:
Pred. No.:
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APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Mang, Ajun
APPLICANT: Here, Yasir A.W.
APPLICANT: Heral, John
APPLICANT: Horal, John
APPLICANT: Horal, John
APPLICANT: Horal, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-593-793A-113 (1-553) x US-09-780-669-705 (1-6976)
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
                               Sequence 705, Application US/09780669 Patent No. US20020051977A1
                                                                                                                                                                  Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
                                                                              Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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US-09-780-669-705
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                                                                GENERAL INFORMATION:
APPLICANT: Xu, Jia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
RESULT 34
US-09-780-669-705
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IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197
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al, John
teill, Patricia D.
ghton, Raymond L.
nals de Bassols, Carlota
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US20020183251A1
ON:
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Ccham, Dennifer L.
Locker, Susan L.
ng, Yuqiu
ng, Michael D.
ter, Marc W.
lk, John A.
' Craig H.
yick, Thomas S.
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anabe, Yoshihiro
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iky, Yasir A.W.
ler, William T.
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APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: LOADSOITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427627
CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SSOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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LeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418
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APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Dav, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.
APPLICANT: Handerson, Robert A.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Houghton, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Wowelll, John
APPLICANT: Wowelll, Patricia D.
APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.534C2
CURRENT APLICATION NUMBER: US/09/895,793
CURRENT APPLICATION HUMBER: US/09/895,793
CURRENT APPLICATION HUMBER: 2001.06-29
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Sequence 703, Application US/09895793
Publication No. US20020192763A1
GENERAL INFORMATION:
APPLICANT: W. Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jonnifer L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Ketter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Marc W.
APPLICANT: Carter, Darrick
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APPLICANT: Mitcham, Dannifer L.
APPLICANT: Jang, Yuqiu
APPLICANT: Jang, Yuqiu
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Wang, Aljun
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Wang, Aljun
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Foy, Teresa
APPLICANT: Compositions on PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427026
                                                                                                                                                                                                                                                                                   Conservative:
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CURRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 990
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APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla
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Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
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Matches:
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Indels:
FILE REFERENCE: 210121.427C23
CURRENT APPLICATION NUMBER: US/09/759,143
CURRENT FILING DATE: 2001-01-12
NUMBER OF SEO ID NOS: 934
SOFTWARE: FastSEQ for Windows Version 3.0
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; Sequence 703, Application US/09780669
; Patent No. US20020051977A1
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CORGANISM: Homo sapiens
US-09-759-143-703
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LENGTH: 2904
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459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478
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                                                                                                                                                                                                                 APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: MCNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TILLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT APPLICATION NUMBER: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 3.0
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Matches:
Conservative:
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Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                                                            Henderson, Robert A. Kalos, Michael D. Fanger, Gary R. Retter, Marc W. Stolk, John A. Day, Craig H. Vedvick, Thomas S. Carter, Darrick
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42.50%
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Skeiky, Yasir A.W.
Hepler, William
                                                  Jiang, Yuqui
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Best Local Similarity:
Query Match:
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                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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Thu Feb 20 11:11:49 2003

Db 1170 GCTCCCTTCCCTAATGGAC	Qy 459 AlaLeuCysGlyAlaSerA	Oy 479 GlualaargValValProG	Qy 499 PheLeuLeuSerGlnValA	Qy 519 SerValThrAlaTyrMetV	Qy 539 ThrGlnValValPheAspL 	RESULT 42 US-10-012-896-1010 ; Sequence 1010, Application ; Publication No. US200201832 ; GENERAL INFORMATION	; APPLICANT: Xu, Jiangchun ; APPLICANT: Dillon, Davin ; APPLICANT: Mitcham, Jenni ; APPLICANT: Harlocker, Sus	; APPLICANT: Jiang, Yuqiu ; APPLICANT: Kalos, Michael ; APPLICANT: Retter, Marc W ; APPLICANT: Stolk, John A. ; APPLICANT: Day, Craig H.	; APPLICANT: VGOVICK, Thoma ; APPLICANT: Carter, Darric ; APPLICANT: L1, Samuel X. ; APPLICANT: Wang, Aljun ; APPLICANT: Skeikv, Yasir	; APPLICANT: Hepler, Willia ; APPLICANT: Henderson, Rob ; APPLICANT: Hural, John	; APPLICANT: McNeill, Patri ; APPLICANT: Houghton, Raym . ADDITCANT: Vinals de Base	APPLICANT: Foy, Teresa ; APPLICANT: Foy, Teresa ; APPLICANT: Fanger, Gary R ; APPLICANT: Wantanabe, Yos	APPLICANT: Medging, Maddel ; TITLE OF INVENTION: COMPOS ; TITLE OF INVENTION: DIACH ; FILE REFERENCE: 210121.427	CURRENT APPLICATION NUMBER ; CURRENT FILING DATE: 2001 ; NUMBER OF SEQ ID NOS: 1011 ; SOFTWARE: FastSEQ for Wind	; SEQ ID NO 1010 ; LENGTH: 1065 ; TYPE: DNA ; ORGANISM: Homo sapiens	012-896-1010 ent Scores: No.:	Score: Percent Similarity: 100.0 Best Local Similarity: 100.0 Query Match:	DB: 9
	479 GlualaargvalvalProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla 498 	499 PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518 	519 SerValThralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538 	539 ThrGlnValValPheAspLySSerAspLeuAlaLysTyrSerAla 553 	RESULT 41 US-09-822-827-703 ; Sequence 703, Application US/09822827	GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Xu, Jiangchun TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.534C1	CURRENT APPLICATION NOMBER: US/09/822,827 CURRENT FILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 982 SOFTWARE: PastSEQ for Windows Version 3.0	; SEQ ID NO 703 ; LENGTH: 2904 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-822-827-703	6.32e-214 Length: 235.00 Matches: 100.00% Conservative:	Best Local Similarity: 100.00% Mismatches: 0 Query Match: 42.50% Indels: 0 DB: 0	US-09-593-793A-113 (1-553) x US-09-822-827-703 (1-2904)	319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338 	339 SerLeuValMetAspargLeuValGlnargPheGlyThrargalaValTyrLeuAlaSer 358 	359 ValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValVal 378 	379 ThralaSeralaalaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThr 398 	399 LeualaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418 	419 GlyGlyAlaserSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438	439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProPro 458
qq	Oy Bb	Qy Db	O.Y D.b	Q D	RE US				Al Sc Pe	Bes Que DB:	ns	0y Db	QQ Dp	OY Db	oy Dp	oy Db	Q Dp	ογ

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AlaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518
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Yoshihiro
Modeleine Joy
MacSITIONS AND METHODS FOR THE THERAPY AND
IACNOSIS OF PROSTATE CANCER
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12 GCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCC
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                                                         357 AlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAla
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Meagher, Madeleine Joy
TITLE OF INVENTION: COMPOSITIONS AND METHODS
FILE REFERENCE: 210121.427C27
                               US-09-593-793A-113 (1-553) x US-09-232-880-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/012,896
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFTWARE: FASELSEQ FOR WINDOWS VERSION 3.0
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McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
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Publication No. US20020183251A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Stans, Michael D.
APPLICANT: Stolk, John A.
APPLICANT: Bay, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Cay, Thomas S.
APPLICANT: Vedvick, Thomas S.
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Skeiky, Yasir A.W.
Hepler, William T.
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ORGANISM: Homo sapiens
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APPLICANT: Xu, Jiangchun C.
APPLICANT: Mitchan, Jennifer Lynn
APPLICANT: Mitchan, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOSIS FOR THEIR USE
TITLE OF INVENTION NUMBER: 02/09/232,880
CURRENT FILING DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 10
LENGTH: 789
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US-09-593-793A-113 (1-553) x US-10-012-896-1010 (1-1065)
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Conservative:
Mismatches:
Indels:
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LOCATION: (1)...(789)
OTHER INFORMATION: n =
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ORGANISM: Homo sapien
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Best Local Similarity:
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APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Malos, Widiau
APPLICANT: Kalos, Widiau
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Odvick, Thomas S.
APPLICANT: Odvick, Thomas S.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Hepler, William T.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Parricia D.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Foy, Teresa
APPLICANT: Franger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
                    771,
                                                                                                                                                                                                                                                                                                                                                                                                        397 TyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGly
                    768,
                   718, 758, 762, 765,
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122
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Mismatches:
Indels:
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                                                                                                                    Length:
Matches:
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; NAME/KEY: misc_feature
; LOCATION: 9, 380, 451, 565, 582, 716, 7
; LOCATION: 779, 783
; OTHER INFEMATION: n = A,T,C or G
US-10-012-896-10
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Publication No. US20020192763A1
GENERAL INFORMATION:
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US-09-895-793-10
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Mismatches:
Indels:
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Matches:
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FILE REFERENCE: 210121.534C2
CURRENT APPLICATION NUMBER: US/09/895,793
UNRENT FILING DATE: 2001-06-29
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                 NAME/KEY: misc_feature
                                                                               ORGANISM: Homo sapien
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CTHER INFORMATION: DUS-09-895-793-10
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Best Local Similarity:
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LENGTH: 789
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February 19, 2003, 04:50:30 ; Search time 2882 Seconds
 (without alignments)
 5584.265 Million cell updates/sec

553 1 MVQRLMVSRLLRHRKAQLLL......AIYFATQVVFDKSDLAKYSA US-09-593-793A-113 Perfect score: Sequence:

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Searched:

3872064 noval number of hims satisfy in gathosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Ω ling the state h Score | Match Length DB

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ACCESSION AX106329 VERSION AX106329 VERSION AX106329.1 GI:13922014 KEYWORDS SOURCE human. ORGANISM Homo sapiens Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota: Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Xu.J., Skeiky.Y.A., Reed, S.G. and Cheever,M.A. TITLE Compositions and methods for therapy and diagnosis of prostate cancer JOURNAL Patent: WO 012527-A 110 12-APR-2001; CORIXA CORPORATION (US) FEATURES 1. 3410 //Ab xref="#">Authors xref="#">Au	BASE COUNT 667 a 1014 c 945 g 783 t 1 others ORIGIN Alignment Scores: Pred. No.: Score: Score: Percent Similarity: '100.00% Matches: Cuery Match: DB: 6 US-09-593-793A-113 (1-553) x AX106329 (1-3410)	Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20 1	81 ArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlylleLeuLeuSerLeu	Qy 141 ThrProlecol LublaineusersapleubheArgAspProAspHisCysArgGinAla 160 LillIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
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ACCESSION AX140620 VERSION AX140620 KEYWORDS KEYWORDS NUMBER		JOURNAL Patent: WC CORIXA COF	Source BASE COUNT 667 a	OKIGIN Alignment Scores: Pred. No.:	Score Similarity: Percent Similarity: Best Local Similarity Query Match:	UB: US-09-593-793A-113 (1	284	21 344	Qy 41 ProLeuLeuLeu 	Qy 61 ProValLeuGly Db 464 CCAGTGCTGGG		101	Oy 121 GluLeuAlaLeu 	141		Qy 181 1leAspTrpAsp
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                                                        illon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y., , Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H., A. and Wang, A.
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RESULT 4 AX200480

PAT 29-AUG-2001 (bases 1 to 3410)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Steed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,W.J. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 343 463 523 100 583 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140 9 80 703 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200 20 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu others linear 3410 553 0 0 0 _ Conservative: Mismatches: DNA Patent: WO 0151633-A 110 19-JUL-2001 CORIXA CORPORATION (US) Location/Qualifiers 3410 bp Sequence 110 from Patent WO0151633. Matches: 783 Length: Indels: US-09-593-793A-113 (1-553) x AX200480 (1-3410) 1. 3410 /organism="Homo sapiens" /db_xref="taxon:9606" a 1014 c 945 g 783 Gaps: AX200480.1 GI:15390293 553.00 100.00% 100.00% Percent Similarity: Best Local Similarity: Query Match: 667 cancer human. Alignment Scores: source ACCESSION VERSION ORGANISM BASE COUNT DEFINITION REFERENCE AUTHORS Pred. No.: 464 81 121 181 JOURNAL 61 KEYWORDS SOURCE FEATURES TITLE δy g Qγ g δy Q Ω qq δ Dp QΥ qq Ωÿ q οy ōλ Ω g ò q

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PAT 26-OCT-2001
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PAT 21-JUN-2002
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                            Reed, S.G., Xu, J., Dillon, D.C., Retter, M.W. and Harlocker, S.L. Compositions and methods for the therapy and diagnosis of breast cancer
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                                                                                                                                                      Patent: WO 0198339-A 100 27-DEC-2001
                                     3410 bp
Sequence 100 from Patent WO0198339.
AX429961
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/db_xref="taxon:9606"
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                                                                                                                                                                      Location/Qualifiers
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/ product="prostein" |
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                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 3410)
Xu,J., Kalos,M., Stolk,J.A., Zasloff,E.J., Zhang,X., Houghton,R.L.,
Filho,A.M., Nolasco,M., Badaro,R. and Reed,S.G.
Direct Submission
Submitted (27-APR-2001) Antigen Discovery, Corixa Corporation, 1124
Columbia Street, Seattle, WA 98104, USA
Location/Qualifiers
                                                                                              PRI 23-MAY-2001
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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oy ob	Oy Dp	Oy Dp	Qy Dp	Qy	Qy Dp	QY	Qy Db	Qy Dp	Oy Op	Oy Dp	Qy Db	Qy	Qy	Oy Db	Oy Dp	Qy	Qy

1 LeuCysProAspProArgProLeuGluLeuAlateuLeuTlefeuGlyAalGlyLeuche CTGTGCCCGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	.32 143	.52 103	.72 163	.92	112 083	:32 143	.52 .203	72 263	92 323	12 383	32 443	52 503	72 563	92 623	12 683	32 743	52 803	72
13 LeuCysproAsppp 14 GTGGCCGGATCG 14 A SpPheCysGlyGl 15 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLe 	nValCysPheThrProteuGluAlaLeuLeuSerAspLeuPheAr 	ArgGinalatyrSerValtyralaPheMetIleSerLeuGlyGl 	<pre>iLeuProAlaileAspTrpAspThrSerAlaLeuAlaProT </pre>		AlaGluGluAlaAlaLeuGlyProThrGluProAlaGlúGlyLe 	uSerProHisCysCysProCysArgAlaArgLeuAlaPhèArgAs 	UProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuAr 	SluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTy 	yGluGlyLeuTyrGlnGlyValProArgAlaGluProGl ^y ThrGl 	AspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCy. 	PheSerLeuValmetAspArgLeuValGlnArgPheGlyrhrAr 	ervalalaalapheprovalalaalaGlyAlarhrcys 	/althralaSeralaalaLeuThrGlyPheThrPheSeralaLe 	rThrLeualaSerLeuTyrHisArgGluLysGlnValPheLeuPr 	pThrGlyGlyAlaSerSerGluAspSerLeuWetThrSerPheLe 	oGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGl 	oProAlaLeuCysGlyAlaSerAlaCysAspValSerValArqVal
1	euCysProAspPr GTGCCGGATCC	pPheCysGlyGl 	spProaspHisCy acccgaccacTG	ysLeuGlyfyrLe 	lyThrGlnGlu 	laThrLeuLeuVa 	erAlaProserLe 	JGlyAlaLeuLe 	gLeuPheValA 	hrAspPheValGl 	aargarghisT CGGAGACACT	TeSerLeuVa 	aValTyrLeuA AGTCTATTTGG	ServalAla AGTGTGGCC	lnIleLeuProTy 	rargglyas ccgaggga	roGlyProLysPr 	LeuLeuProProPro
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cabezon Silva,T.E. and Delisse,A.M.
Triple fusion proteins comprising ubiquitin fused between thioredoxin and a polypeptide of interest Patent: WO 0200892-A 6 03-JAN-2002; SmithKline Beecham Biologics SA (BE)
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Oy 181	1 IleAspTrpAspThrSetAlaLeuAlaProTyrLeuGlyThrGlnGluGluGluCysLeuPhe 200	Db 401 ccrc
-	A119AC1666ACACCAG16CCC16GCCCCC1ACC1666CACCCAGGAGGAGGAGGACTTTT	Qy 61 ProVa
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net an	4 TACCAGGCCCCAGAGCTGAGCCGGGCACCGGGGCCCCGGAGACACTATGATGAAGGC 1563	Qy 181 IleAs
AX200995		 Db 821 ATTGA
DEFINITION	AXZUD995 ON Sequence 625 from Patent WO0151633.	Qy 201 GlyLe
VERSION		Db 881 GGCCI
SOURCE	;	Qy 221 AlaAl
ORGANI	SM HOMO Saplens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata	 Db 941 GCAGC
REFERENCE	Mammalla; Eutherla; Primates; Catarrhin; Hominidae; Hom 1 (bases 1 to 4034)	Qy 241 CysCy
AUTHOR		 Db
TITLE	Stolk, J.A., Skelky, Y.A., Wang, A. and Meagher, M.J. Compositions and methods for the therapy and diagnosis of prostate	Qy 261 HisGl
JOURNAL		 Db 1061 CACCA
FEATURES	CORIXA	Qy 281 SerTr
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BASE COUNT	/db_xrei="taxon:9000 721 a 1226 c 1141 g	Qy 301 TyrGl
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4034 bp DNA linear PAY 16402 ; Chordata; Craniata; Vertebrata; Eui ; Primates; Catarrhini; Hominidae; H ; Mitcham,J.L., Harlocker,S.L., Jiane ,G.R., Retter,M.W., Stolk,J.A., Day, er,D., Li,S.X., Wang,A., Skeiky,Y.A., ethods for the therapy and diagnosis -A 704 04-OCT-2001; (US) Qualifiers -Homo sapiens" -taxon:9606"	Length: 320 Conservative: 320 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0 (1-4034) euLeuargHisArgLysAlaGlnL
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ata: Euteleostomi; idae; Homo. . Jiang, Y., etter, M.W., J. agnosis of prostate		aSerasphis 77 	uGlylleLeu 97 	SPróAspPro 117 	eCyśclygln 137 	OASPHISCYS 157 	uGlyffyrLeu 177 GGGCTACCTC 1670	rgihgluglu 197 CCAGGAGGAG 1730	rLeuleuVal 217 ACTGCTGGTG 1790	aProserLeu 237 	yAlaLeuLeu 257 	 UPheValAla 277
a; Craniata; Vertebr. s; Catarrhini; Homin J.L., Harlocker,S.L. er,G.R., Day,C.H., R. ng,A. and Meagher,M r the therapy and diJUL-2001; s piens" 06"	DEOEHO -	/93A-113 (1-553) X A&200993 (1-4894) GlyIleGlyProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis HIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	TrpargGlyargTyrGlyargArgArgProPheIleTrpalaLeuSerLeuGlyIleLeu 	LeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspPro 	ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCyśGlyGln 	ValCysPheThrProLeuGlualaLeuLeuSeraspLeuPheArgaspFroAspH1SCys 	ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGl [†] TyrLeu 	LeuProAla11eAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlhGluGlu 	CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuVal 	AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 	SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu	ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla
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SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES SOUFC	Alignment S Pred. No.: Score: Percent Sim Best Local Query Match DB:	-09-393 58 1311	137	98	118	138	158	178	198	218	238	258
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                                                                                                                                                                                                   Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 6976)

Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,
Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J.

Compositions and methods for the therapy and diagnosis of prostate
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
KaloS,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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/organism="Homo sapiens" /db_xref="taxon:9606" COUNT 1312 a 1996 c 1961 g 1706 t 1 others	nment Scores: 9.05e-271 Length: 6976 e: 263.00 Matches: 263 ent Similarity: 100.00% Conservative: 0 i. Local Similarity: 100.00% Indels: 0 i. Match: 6 Gaps: 0	-593-793A-113 (1-553) x AX267731 (1-6976)	58 GlylleGlyproValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis 77 	78 TrpargGlyargTyrGlyargArgArgProPhelleTrpalaLeuSerLeuGlylleLeu 97 	98 LeuserLeupheLeulleProArgalaGlyTrpLeualaGlyLeuLeuCysProAspPro 117 	118 ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137 	138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157 	158 ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177 	178 LeubroalaileaspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu 197 	198 CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeùLeuVal 217 	218 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237 	238 SerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257 	258 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277	278 GluLeuCysSerTrpMetalaLeuMetThrPheThrLeuPheTyrThrAspPheValGly 297 	298 GluglyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArg ⁱ HisTyr 317 	318 AspGluGly 320 	
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iaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.
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aul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
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ubmitted (18-SEP-2001) Genome Center, University of Washington,
ox 352145, Seattle, WA 98195, USA
n Sep 18, 2001 this sequence version replaced gi:9931838.
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Center project name: chr.1
Center clone name: RP11-6B6 (sc0601)
Center clone name: RP11-6B6 (sc0601)
Center clone name: RP11-6B6 (sc0601)
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator ET; 57% of reads
Chemistry: Dye-terminator Big Dye; 43% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 156488 bases at least Q40
Consensus quality: 156447 bases at least Q20
Consensus quality: 15658; bases at least Q20
Insert size: 157388; sum-of-contigs
Quality coverage: 7.3x in Q20 bases; sum-of-contigs
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6364: gap of unknown length
15785: contig of 9421 bp in length
15885: gap of unknown length
27947: contig of 12062 bp in length
27947: contig of 12062 bp in length
28047: gap of unknown length
52092: gap of unknown length
81154: contig of 23945 bp in length
81254: gap of unknown length
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Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
Drafting Center: SC
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CGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGGCTGCCTGGGCTACCTC 138639
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                                                                                                                        ArgGlnAlaTyrSerValTyrAlaDheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu 177
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138340 IGGCGTGGACGTATGCCCGCCGCCGCCCTTCATCTGGGCACTGTCTTGGGCATCTG
                                                                                                    ArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln
                                                                                           TrpArgGlyArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlyIleLeu
others
                                                                    157988
Matches:
Conservative:
Mismatches:
US-09-593-793A-113 (1-553) x AC096533 (1-157988)
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                       /note="gi|154843|gb|J01829|TRN10IS13 excised from sc0601
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TGATGAATCCCCTAATGATTTTGGTAAAAATCATTAAGTTAAGGTGGATACACATCTT
                                                      CAGCTCAGAGCGTTTTGATATCATGCTGTAATCGCCCTGATGCTTCAACTAACATGT
GGCTTGCGGGGGTTCAAGCTCAGAAACAAGTTGGAACAAGCACTTCCAGGCTAACA
CAGTCAGAAATCGAAACGTACTCTCAACAGTTGGGAAGGTTTGGGAAGTTTTGGGGA
TTCTGGCTACACAATAACAAGGGAAGACTTAACTCGTGGCTGCAACCCTAATAACAAGGGCTCAA
                                                     CCTTCCGAGACTTGAAAAGTCCTGCCTACGGACTAGGCCTACGCCATAGCCGAACGAG
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         61255. .118813
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118914. .157988
              /note="assembly_name:Contig28"
129829. .129830
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182 GTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTG
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                                                                                                    GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly
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Sequence 15 from patent US 6130043.
AR112294.1 GI:14092194
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Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Billing-Medel, P.A., Cohen, M., Hodges, S.C., Klass, M.R., Kratochvil, J.D.
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate
Patent: US 6130043-A 16 10-OCT-2000;
       138760 GCTGAGGAGGCAGCGCTGGGCCCCACCGAGCAGCAGAAGGCCTGTCGGCCCCTTCC 138819
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622 c 569 g
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1 (bases 1 to 2143)
Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N.,
Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D.
Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H.
Reagents and methods useful for detecting diseases of the prostate patent: US 6130043-A 15 10-OCT-2000;
Location/Qualifiers
1. 2143
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Berlin-Charlo information a	FEATURES at itety.//misp Source 1	/ (20) / (11) / (12)		e G	Pred. No.: 3 Score: 2 Percent Similarity: 1 Best Local Similarity: 1	Query Match: 4 DB: 9 US-09-593-793A-113 (1-553	Oy 319 GluGlyvalargMet 	Qy 339 SerLeuValMetAsp 	Qy 359 ValAlaAlaPhePro 	Qy 379 ThralaSeralaala 	Qy 399 LeualaSerLeuTyr 	Qy 419 GlyGlyAlaSerSer 	439 718 459 778	479 838	Db 898 TTCCTGCTGTCCAG	Oy 519 SerValThralaTyr 	
	322 ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuVal 341 	342 MetAspargLeuvalGlnargPheGlyThrargalaValTyrLeualaSerValAlaala 361 	362 PheprovalAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSer 381 	382 AlaalaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 401 	402 LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 421 	422 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441	442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCys 461 	462 GIyAlaSerAlaCysAspValSerValArgValValGIyGluProThrGluAlaArg 481 	482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 501 	502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521 	522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541 	542 ValPheasplysSeraspLeualaLysTyrSerala 553 	21 344 HSM804244 BARNA: cDNA DKFZp666D0110 (from clone DKFZp666D0110). CON AL832933.1 GI:21733520 S human.	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (CE 1 (bases 1 to 2477)	Anisotype, with the control of the c	Research Center (DKFZ): Email S.wiemanne Analysis, German Cancer Research Center (DKFZ): Email S.wiemanne@kfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Labbratories, Heidelberg/Germany) within the CDNA sequencing consortium of the	German Genome Project. This clone (DKFZp66600110) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
අු	Oy Db	Oy 3	Oy 3	oy du	Oy 4	Oy 4	Oy 4 Db 4	Oy 4	Oy 4	Oy 5	Qy 5 Db 6	Oy 5 Db 7	RESULT 21 HSM804244 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	REFERENCE	TITLE	COMMEN	

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Email: clone@rzpd.de Further
the sequencing project is available
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Conservative:
Mismatches:
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Patent: WO 0151633-A 624 19-JUL-2001;
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AX200994
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/db_xref="taxon:9606"
875 c 773 g 714
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Location/Qualifiers
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Best Local Similarity:
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
                                                                                                                                                                                             PAT 26-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                            Compositions and methods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                   1410 TCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGCCATTACTTTGCT 1469
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Indels:
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CORIXA CORPORATION (US)
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Matches:
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/db_xref="taxon:9606"
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AX267729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRI 13-JUN-2001
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Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submitssion
Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Lab. host:
TOP10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                            (Sugano et al., , Institute of Medical Science, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AB060851 3514 bp mRNA linear PRI 13-JU Macaca fascicularis brain cDNA clone:QtrA-11310, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (sites)
Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M.,
Tarao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.
Isolation of full-length cDNA clones from macaque brain cDNA
                       1170 GCTCCCTTCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCCCACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      oligo capping; fis (full insert sequence).
Macaca fascicularis adult male temporal lobe right cDNA to
clone_linacaque brain cDNA library QtrA clone:QtrA-11310.
Macaca fascicularis
 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProPro
                                                                        AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThr
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DraIII (CACTGTGTG)
DraIII (CACCATGTG)
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nd primer [CTTCTGCTCTAAAAGCTGCG]
primer [CGACCTGCAGCTCGAGCACA] )
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5' end primer [Cymrane" '
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AB060851.1
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KEYWORDS
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 /organism="Macaca fascicularis"

source

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/product="hypothetical protein"
/product="hypothetical protein"
/protein_id="maB4681.1"
/daxxef="fg1:1387497"
/translation="WVORLMYSRLLBHRKAQLLLINLLFFGLEVCLAAGITVVPPLLL
EVGVEEKFMTMVLGIGPVLGLVSVPLIGSASDHWRGRYGRRRPFIWALSLGILLSLFL
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Macaca fascicularis brain cDNA clone:QmoA-10594, full insert
                          1116 AGCACTGGGCCCCGCC-GAGCCGGAAGGGCTGTCTGCCCCCTCCCTGCC-GT-CCCA
                                                                                                                                               AlaSerLeuTyrHisArgGluLys-GlnValPheLeuProLysTyrArgGlyA\u00e9prhr-G
                                                                                                                                                                                                                                                                                                                                                aAlaLeuGly-ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerPro--Hi
                                                                                                                                         GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSer
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HVGAGGSGILPPPPPALCGASACDVSVRVVGEPTEARVVFGRGICLDLAILDSAFLLS
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Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
Submitted (IJ-JUN-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail:khashi@nih.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5285-1111(ex.2120), Fax:81-3-5285-1181)
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                                                                                                                                                                                                                                                Macacā fascicularis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca
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Db 1082 GGAGA	Oy 424 uAsps Db 1139 GGACA	1199	Oy 464 rAlac Db 1259 TGCCT	1319	504	524	Oy 544 pLyss Db 1499 CAAGA	RESULT 26 AX106229 LOCUS DEFINITION Seq	SSION ION ORDS	ORGANISM HOM EUK MAM REFERENCE 1	AUTHORS XU, TITLE COM JOURNAL Pat	COR FEATURES Source	misc_featu BASE COUNT	ORIGIN Alignment Score Pred. No.:	Score: Percent Similar Best Local Simi	DB: US-09-593-793A-	Oy 357 AlaSe Db 12 GCCAG Oy 377 ValVa	
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2 5	Oy Dp	oy Op	Qy Db	çy D	O P	Oy Dp	Oy Db	QQ Dp	Q P	94 D	OY DP	Qy Db	OY Db	Q P	0 y	oy g	O.y D.b	οy

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 Qy Db	504		524
Qy Db	524	tValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAs	544
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RESULT 2 AX106229 LOCUS DEFINITI ACCESSION VERSION KEVMORDS	RESULT 26 AX106229 LOCUS DEFINITION ACCESSION VERSION	AX106229 789 bp DNA linear PAT 30 Sequence 10 from Patent WO0125272. AX106229 AX106229.1 GI:13921915	-APR-2001
SOURCE	THORE ORGANISM		ostomi;
 REFERENC AUTHOR TITLE	FERENCE AUTHORS TITLE	1 (bases 1 to 789) Xu,J., Skeiky,Y.A., Reed,S.G. Compositions and methods for t	tate
JOURNA FEATURES SOU	JOURNAL ATURES SOURC	CORING TO 0125272-A 10 12-APR-20 CORIXA CORPORATION (US) Location/Qualifiers e 1. 789	
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 δλ	377	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro	396

72 GTGGTGACA	13	Qy 437 ProGlyAlaProPheProAsnG
UY 39/ TYTINTLEUALASE 	AlasertentyrhisargGlutysGlnValbhetenbroLysfyrargGly 416 	252
Oy 417 AspThrGlyGlyAl 	GlyAlaserSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436 	ProProAla
Oy 437 ProGlyAlaProPl 	ProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuPeroPro 456 	Oy 477 Profits 478 11111 Db 372 CCCACC 377
Qy 457 ProProAlaLeuC)		RESULT 28 AX200380 LOCUS DEFINITION Sequence 10 from Pat.
Qy 477 ProThr 478 Db 372 CCCACC 377		ACCESSION AX200380 VERSION AX200380.1 GI:15390 KEYWORDS SOURCE human.
AX14052 ON Sequenc N AX14052 AX14052	0 789 bp DNA linear PAT 31-MAY-2001 0 GT:14280638	NISM NCE ORS
_	fetazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Itheria; Primates; Catarrhini; Hominidae; Homo.	TITLE Compositions and metical concer JOURNAL Patent: WO 0151633-A CORIXA CORPORATION (CRIXA CORPORATION (CRIXA CORPORATION (CRIXA CORPORATION (CRIXA CORPORATION (CRIXA CORPORATION (CRIXA CRIXA
REFERENCE 1 (bases 1 AUTHORS XU,J., DILLC Reed,S.G., K SKeiky,Y.A. TITLE Compositions	1 (bases 1 to 789) Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Red,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skeiky,Y.A. and Wang,A. Compositions and methods for the therapy and diagnosis of prostate	urce UNT 122 a
cancer JOURNAL PAtent: WO (CREATURES CORIXA LOC SOUTCE 1.	WO 0134802-A 10 17-MAY-2001; CORPORATION (US) Location/Qualifiers / 7789 / Organism="Homo sapiens"	Alignment Scores: 1.64e-120 Pred. No.: 122.00 Score: 100.008 Percent Similarity: 100.008 Best Local Similarity: 100.008
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Alignment Scores: Pred. No.: Score: Percent Similarity: Best Local Similarity: Query Match:	1.64e-120 Length: 789 1122.00 Matches: 122 100.00\$ Conservative: 0 100.00\$ Mismetches: 0 22.06\$ Indels: 0	OS-09-593-1934-113 (1-553) x AXZI QY 357 AlaSerValAlaAlaPheProVē Db 12 GCCAGTGTGGCAGCTTTCCCTGT QY 377 ValValThrAlaSerAlaAlaLe
UB: US-09-593-793A-113 (1-55	Gaps: 520 (1-789)	72
Qy 357 AlaSerValAlaAl 	AlaServalAlaAlaPheProvalAlaAlaGlyAlaThrCySLeuSerHisServalAla 376 	132
Qy 377 ValValThralaSe 	ValValThralaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396 	417
Qy 397 TyrThrLeuAlaSe 	TyrThrLeuAlaSerLeuTyrHiSArgGluLysGlnValPheLeuProLysTyragGly 416 	252
Oy 417 AspThrGlyGlyal 	ASPTHrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436 	Oy 45/ ProProfalaLeurySG1yAlaSe

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PAT 29-AUG-2001
                                                                                                                                                                                                                                                                            Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
D., Fanger,G.R., Day,C.H., Retter,M.W.,
Y.A., Wang,A. and Meagher,M.J.
thods for the therapy and diagnosis of prostate
                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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GIJYHisValGİYAlaGIYGIYSErGİYLENLENProPro 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ValAlaAlaClyAlaThrCysLeuSerHisSerValAla 376
                                            LeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPro 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HisargGlulysGlnValPheLeuProLysTyrArgGly 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyHisValGlyAlaGlyGlySerGlyLeuLeuProPro 456
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Mismatches:
Indels:
Gaps:
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taxon:9606"
221 g | 182 t
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(US)
                                                                                                                                                            789 bp
tent WO0151633.
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us-09-593-793a-113.olig.rge

itts,T.L., Friedman,P.N., C., Klass,M.R., Kratochvil,J.D., oupe,S.D. and Yu,H. tecting diseases of the prostate 258 ative: 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	247
No. No.	Alignment Scores: 4.24e-78 Length: Score: 82.00 Matches:
December Apple A	RESULT 30 AR112280 LOCUS AR112280 258 bp DNA linear PAT 16-MAY-2001 DEFINITION Sequence 1 from patent US 6130043.

RESULT 33 AR112282 LOCUS AR112282 LOCUS AR112282 LOCUS BEFINITION Sequence 3 from patent US 6130043. ACCESSION AR112282 VERSION AR112282 VERSION AR112282.1 GI:14092182 VERSION AR112282.1 GI:14092182 VERSION AR112282.1 GI:14092182 VERSION AR112282.1 GI:14092182 OCGANISM INGOWN. Unclassified. I (bases 1 to 255) AUTHORS BILLIAP Medel.P.P.A., Cohen,M., Colpitts,T.L., Friedman,P.N., Gordon,J., Granalos,E.N., Hodges, S.C., Klass,M.R., Kratochvil,J.D., Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H. Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H. Roberts-Rapp,L., Russell,J.C., Stroupe,S.D. and Yu,H. Acception/Qualifiers Source Aorganism="unknown" 46 to 1 others" ORIGIN	Alignment Scores: 2.69e-66	RESULT 34 HSPE54C06/ LOCUS HSPE54C06 HSPE54C06 HSPE54C06 HSPE54C06 ACCESION H. Sapiens flow-sorted chromosome 1 HindIII fragment, SC1pE54C06, sequence tagged site. ACCESION VERSION AL033941.1 GI:3893713 VERSION KEYWORS SOURCE ORGANISM Homo sapiens. ORGANISM Homo sapiens. Homo sapiens. AUMMANIALIS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE AUTHORS TITLE AUTHORS SUMMANIALTEd (18-NOV-1998) The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: hunquery@sanger.ac.us Vector: pBSIISK+ Marker SEG344CFS (Primer A: TGTAGGGCAGGATCTGCAG; Primer B: CTCGAGCAGTCTATTTGCC; ampliner size: 141 bp) was mapped to chromosome I using Rediation Hybrid
Percent Similarity: 100.00% Mismatches: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 14.83% Indels: 0 US-09-593-793A-113 (1-553) x AR112283 (1-247) Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProProProProProProProProProProP		Prior Scores: Score: Score: Score: 71.00 Matches: 71.00 Matches: 71.00 Matches: 71.00 Matches: 71.00 Matches: 71.00 Mismatches: 0 Ouery Match: 12.84\$ Indea: 0 Gaps: 0 30.0163 30

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TITLE
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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsocks, S.L., Amaratunge, H.C., Are, J.R., Agele, M., Banks, T., Barbaria, J., Benton, J., Bange, K., Blankenburg, K., Bonnin, D., Bunder, J., Borde, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Bunde, C., Burchl, K.L., Byrd, N.C., Carch, R., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Cox., Coyle, M.P., David, N.C., Coyle, M.P., David, R., David, R., David, R., David, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., David, R., David, M.L., Davis, C., Davy, Carroll, L., Dederich, D.A., David, K.J., Draper, H., Dugar-Rochas, S. Durbin, K.J., Earnhart, C., Edgardo, O., Denn, A.L., Enlay, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugar-Rochas, S., Durbin, K.J., Earnhart, C., Edgardo, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Edwards, C.C., Elhaj, C., Escotto, M., Garcia, A., Garner, T., Garza, N., Gill, R., Garcia, A., Garner, T., Garza, N., Gill, R., Garcia, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Huber, J., Havlak, P., Hawes, J., Jackson, L.E., Jacobson, B., Jia, Y., Johloway, C., Voudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus clone CH230-65Fl4, *** SEQUENCING IN PROGRESS
***, 65 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="EBV lymphoblastoid cell line"
/clone_lib="SClpE"
/dev_stage="adult"
128 c 115 q 66 t
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69
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Mismatches:
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                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps:
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                                                                                                    /clone="SC1pE54C06"
/sex="Female"
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HTG; HTGS_PHASE1.
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100.00%
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                       source
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Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., May, J., Maheshwari, M., Mapua, P., Martin, R., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, E., Martinez, Mitchell, T., Mohabbar, K., Morgan, M., Mortis, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, A., Nguyen, N., Oragunye, N., Oviedo, R., Pacce, M., Payton, B., Perez, L., Peters, L., Pickers, F., Prims, E., Oguh, M., Okwuoni, G., Oragunye, N., Oviedo, R., Prims, E., Oguh, M., Okwuoni, G., Peters, L., Pickers, R., Prims, E., Nooster, M., Ron, Y., Royson, N., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Scherer, S., Scott, G., Shen, H., Stoshtari, N., Sisson, I., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, S., Warlen, M., Wang, S., Warren, R., Washington, C., Watlington, S., Weinstock, G. and Gibbs, R., Zorrilla, S., Nelson, D., Vinson, D., Weinstock, G. and Gibbs, R.
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NOTE: This is a 'working draft' sequence. It currently
consists of 65 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N. but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence
as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (06-JUD-2002) Human Genome Sequencing Center, Department Submitted (06-JUD-2002) Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA
3 (bases 1 to 198037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (14-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center clone name: CH300-65F14
Squencing vector: Plasmid;
Schemistry: Dye-terminator Bly Dye: 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 14984 bases at least Q40
Consensus quality: 165599 bases at least Q20
Consensus quality: 165549 bases at least Q20
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gap of unknown length
contig of 1348 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 198037)
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3526:
3556:
3656:
4752:
5972:
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7918:
9266:
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Unpublished
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9267 9367 9367 100155 110155 1	11642 11642 124142 125133 125133 125133 125133 12513 12513 12513 12513 12513 12513 12510 1251	4 5 7 2 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2611)
                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (02-JUL-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
                                                                                                                                                                                                                                                                                                                                                                                                             157
                                                                                                                                                                                                                                                                                                                                                                                                          138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys
                                                                                                                                                                                                                                                                                                                                                                                                                       Db 161817 GTGTGTTTACTCCACTGAGGCTTACTCTCCGACCTTCCGGGACCCAGGCCACTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2611 bp mRNA linear F Mus musculus, clone IMAGE:4457452, mRNA, partial cds. BC034084.
                                          bp in length
length
bp in length
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Contact: MGC help desk
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contig of 440 b
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DEFINITION
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FSVYARMISLGGCLGYLLPAIDWDTSYLAPYTGTQEBCLFGLLTLIFLICMAATLFVY
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AELCSWMALMTFTLFYTDFVGEGLYQCVPRAEPGTEARRHYDEGIRMGSLGLFLQCAI
SLVFSLVMDRLVQKFGTRSVYLASVWȚFPVAAAATCLSHSVVVVTASAALTGFTFSAL
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SGLAAPPALCGASACDVSMRVVGEPPEARVYTGRGICLDLAILDSAFLLSQVAPSL
FMGSIVQLSHSVTAYMVSAAGLGLVAİYFATQVVFDKNDLAKYSV"
92 c 934 g 836 t
                                                                          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurògnathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                     Submitted (06-UUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 45 Row: 1 Column: 2 Feries: IRAK Plate: 45 Row: 1 Column: This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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S., Martin, R.G., Muzny, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Liver, normal. 5 month old male mouse."
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                                                                                                                                                                                                                                                                                                                       NIH-MGC Project URL: http://mgc.nci.nih.gov
contact: MGC help desk
Email: cgapbs-refemail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDM Library Preparation: Life Technologies, Inc.
CDMA Library Arrayed by: The I.M.A.G.E. Consortium (LiNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
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/db_xref="G1:21594809"
/db_xref="LocusID:212980"
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Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk
YCoon, V.S., Kowis, C.R., Lawrence, S., Marti
Richards, S., Gibbs, R.A.
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/db_xref="taxon:10090"
/map="FVB/N"
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  BC031381.1 GI:21594808
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Strausberg, R.
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BASALLGFTFSALGILPYTLASLYHREKQVPLPKYRGDAGGSSGEDSQTTSFLPGPKP GALFPNGHVGSGSSGILDALAIL
BASALLGFTFSALGILPATLASLYHREKQVPLPKYRGDPBRRAVYTGRGICLDLAIL
BASALLGFTFSALGILSQVARSKNDLAKYSV
  Tissue Procurement: Gibert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.
                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 43 ROW: p Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
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Mus musculus, clone MGC:32471 IMAGE:5050610, mRNA, complete cds.
BC031381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="IMAGE:4457452"
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/clonellib="MCL_GGAP_Mam1"
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/note="Uption"
/note-voctor: pcMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       282 TrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyr 301
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/db_xref="taxon:10090"
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                                                                                                                                                           COMMENT
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, Y., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Candrach, Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Gord, S., Gord, S., Gord, S., Gord, M., Lilev, I., Johnson, R., Jones, C., Hagos, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C.,
                                                                                                                                                                                                                                                                                                                     HTG 14-APR-2002
                                                                                                                                                                                                                                                                                                                                          Mus musculus clone RP23-272H13, WORKING DRAFT SEQUENCE, 13 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meheus, L.,
Midrova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C. H., O'Connor, T., O'Connell, P., O'Neil, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Saymond, C., Retter, R., Riebek, M., Riley, K., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.
                                                                                                               8 SerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPheGly 27
                                                                                        28 LeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGly 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R.,
Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G.,
MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus, clone RP23-272H13
                                                                                                                                                                                                                                                                                                                                                                                                                             HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                178567 bp
                                                                                                                                                                                                                                                                                                                                                                                                      AC107837.2 GI:20148020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 178567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                                  AC107837
                                                                                                                                                                                                                                                                    RESULT 38
AC107837/c
                                                                                                                                                                                                                                                                                                                                       DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
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Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Zambek, L., Zimmer, A. and Zody, M. Direct Submission

Submission

Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On Apr 14, 2002 this sequence version replaced gi:18308540.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or the gaps corrections as a submittor. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

I 58509: contig of 58509 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 182000; agarose-fp
Insert size: 177367; sum-of-contigs
Quality coverage: 7.7 in Q20 bases; agarose-fp
Quality coverage: 7.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: L20597

Center clone name: 272.H_13

Center clone name: 272.H_13

Sequencing vector: Plasmid; n/a; 100% of reads
Sequencing vector: Plasmid; n/a; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 175041 bases at least Q40

Consensus quality: 1770485 bases at least Q20

Consensus quality: 177028 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91239 91338: gap of 100 bp
91339 127752: contig of 36414 bp in length
127753 127852: gap of 100 bp
127853 177486: contig of 49634 bp in length
17787 177886: gap of 100 bp
177587 178567: contig of 981 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60624 60723: gap of 100 bp 60724 62950: contig of 2227 bp in length 62951 63050: gap of 100 bp 63051 65309: contig of 2259 bp in length 65310 65409: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58510 58609; gap of 100 bp 58609; gap of 100 bp 58610 59459; contig of 850 bp in length 59460 5559; gap of 100 bp 59560 60623; contig of 1064 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39: gap of | 100 bp | 69956: contig of 2017 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56: gap of 100 bp 73550: contig of 3494 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73551 73650: gap of 100 bp 73651 81298: contig of 7648 bp in length
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91238: contig of 9840 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="RPCI-23 Female Mouse BAC"
1. .58509
/note="assembly_fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-272H13"
                                                                                                                                                                                                                                                                                                                                                        Genome Center
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81399 9123
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67940
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231 57 ttive: 0 les: 1 1	Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus. al Institutes of Health, Mammalian Genomics Office, National Cancer om 11A03, Bethesda, MD 20892-2590, [C.nci.nih.gov Green, M.D. Green, M.D. Green, M.D. Group at the Stanford Human Genome And Genome at the Stanford Human Genome ic. Stanfordedu hool of Nedicine, Stanford, CA 94305 ic. Stanfordedu wood, J., Rodriquez, A., and Myers,	bution information can be found NL at: http://image.llnl.gov :15 :15 ria: Hexamer frequency ORF .5 month old male mouse."
1.11e-26 Length: 34.00 Matches: 34.00 Matches: 98.28\$ Mismatch 6.15\$ Matches: 5.15\$ Matches: 1.15\$ Matches 1.15\$ Matches 1.231) 1.15\$ Matl2284 (1-231) 1.11\$ Matches 1.231 1.331 1.34.00 1.35\$ Matl2284 (1-231) 1.34.00 1.353	house mouse. Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, 1 (bases 1 to 1593) Strausberg, R. Direct Submission Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Cortect: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CONTEXT: Maray Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, Canter: Meb site: http://www-shqc.stanford.edu Dickson, Mark) mackpaxil; Stanford.edu Dickson, Mark) mackpaxil; Stanford.edu Dickson, Mark) mackpaxil; Stanford.edu	Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov Series: IRAK Plate: 59 Row: p Column: 15 Series: IRAK Plate: 59 Row: p Column: 15 Series: IRAK Plate: 60 February 16 Series: IRAK Plate: 60 February 17 Series: 18 Selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis. 1. 1593 2. 1593 3. 1593 4. 1593 4. 1593 7. 1593 7. 1593 7. 1593 7. 1594 7. 1500="IMAGE:4984191" 7. 1500="IMAGE:4984191" 7. 1500="ILAFACI.CGAP_CO24" 7. 1500="Lib="NCI.CGAP_CO24" 7. 1500="Ib="NCI.CGAP_CO24" 7. 1500="NCI.CGAP_CO24" 7. 1500="NCI.CCAP_CO24" 7. 1500="NCI
Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar Query Match: DB: US-09-593-7934-113 QY 496 AspSerAli QY 496 AspSerAli OP 3 GATAGTGG QY 516 LeuSerGl DD 63 CTCAGCCAC QY 536 TYPPHeAll DD 122 TACTTTGG RESULT 40 BCO24519 LOCUS BCO24519 LOCUS BCO24519 LOCUS BCO24519 LOCUS BCO24519 LOCUS BCO24519 BCO2451 VERSION BCO2455	SOUNCE SOUNCE ORGANISM AUTHORS TITLE JOURNAL JOURNAL 301 TO512 COMMENT 170452	MAY-2001 FEATURES SOURCE 11,J.D., rostate
clone_end:SP6 vector_side:left" S8610. :59459 //note="assembly_fragment" 59560. 60623 //note="assembly_fragment" 60724. 65290 //note="assembly_fragment" 60740. 657839 //note="assembly_fragment" 67410. 67839 //note="assembly_fragment" 67410. 67839 //note="assembly_fragment" 67410. 67839 //note="assembly_fragment" 6740. 69956 //note="assembly_fragment" 70651. 31298 //note="assembly_fragment" 73651. 31299 //note="assembly_fragment" 81399. 91238 //note="assembly_fragment" 81399. 91238 //note="assembly_fragment" 127853. 177486 //note="assembly_fragment" 177857. 177486 //note="assembly_fragment" 177857. 177886 //note="assembly_fragment" 177857. 177886 //note="assembly_fragment" 177857. 177886 //note="assembly_fragment" 177857. 177886 //note="assembly_fragment" 177857. 177886 //note="assembly_fragment" 177857. 177886 //note="assembly_fragment" 177857. 177886 //note="assembly_fragment"	7.69e-51 Length: 178567 59.00 Matches: 59 100.00% Mismatches: 0 10.67% Mismatches: 0 10.67% Mismatches: 0 10.67% Gaps: 0 (1-553) x AC107837 (1-178567) 5CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSer[from patent US 6130043. GI:14092184 GI:14092184 GI:4092184 GI:409318 d. to 231) Bel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Grandos, E.N., Hodges, S.C., Klass, M.R., Kratochv Pp.L., Russell, J.C., Stroupe, S.D. and Yu, H. Gd methods useful for detecting diseases of the pocation/Qualifiers 1231 rganism="unknown" 61 g 61 t
misc_feature misc_feature	Alignment Scores: Pred. No.: Scores: Percent Similarity: Best Local Similarity: DB: US-09-593-793A-113 (1) QY 262 GlnLeuCysCy.	ON NY SM I C C C C C C C C C C C C C C C C C C

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Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T.,

Barbaria, J. Benton, J., Bimage, K., Blankenburg, K., Bonnin, D.,

Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,

Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,

Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,

Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R.,

Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A.,

Douthwaite, K.J. Draper, H., Dugan-Rocha, S.R., Durbin, K.J.,

Earnhart, C., Edgar, D., Edwards, C.C., Elhdj, C., Escotto, M.,

Falls, T., Ferraguto, D., Flagon, N., Foster, P.I., Frantz, P.,

Gorrell, J.H., Gacvar, W., Gunrarne, P., Hales, S., Hamilton, K.,

Harris, C., Harris, K., Hart, M., Hallak, P., Hawes, A., Hernandez, J.,

Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B.,

Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,

Kratovic, J., Kureshi, A., Ludier, R., Martin, R., Martinez, E.,

Li, J., Lu, X., Ludier, A., Lucier, R., Luna, R., Martinez, E.,

Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratius norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS AC126523
/product="Unknown (protein for IMAGE:4984191)"
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RGICLDLAILDSAFLLSQVAPSLFMGSIVQLSHSVTAYMVSAAGLGLVAIYFATQVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                           191 GCTCCGTCCCTGTTCATGGGCTCCATTGTCCAGCTGAGCCA-CTCTGTCACTGCCTATAT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      505 AlabroSerLeuPheMetGlySerIleValGlnLeuSerGln-SerValThrAlaTyrMe
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60
0
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2
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Mismatches:
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Matches:
                                                                                                                                      436
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                                                                                                                                  398 g
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401 c
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96.77%
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AC126523/c
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Massey, E., Mawhiney, E., McLeod, M. P., Meador, M., Mei, G., Metzker, M., Miner, G., Miner, Z., Mitchell, T., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Newison, M., Nauyen, A., Nauyen, N., Nauyen, N., Nauyen, N., Nauyen, N., Nauyen, N., Nauyen, N., Okudon, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Oulles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savery, G., Schercer, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Stone, H., Stone, H., Stone, M., Svaterk, A., Tamerisa, A., Tamerisa, R., Tamerisa, N., Tamerisa, N., Tanerisa, N., Tamerisa, N., Wang, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, O., Williams, G., Williamson, A., Warten, R., Washington, C., Watlington, S., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a working draft' sequence. It currently consists of 65 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission | Submission | Submitted (06-JUL-2002) Human|Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 198037)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chemistry: Dye-terminator, Big Dye: 100% of reads Assembly program: Phrap: version 0.990329 consensus quality: 149884 bases at least Q40 Consensus quality: 159599 bases at least Q20 consensus quality: 166549 bases at least Q20
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Contact: hgsc-help@bcm.tmc.edu
------- Project Information
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source 157	Alignment Scores: 0.00118 Length: 57 Pred. No.: 12.00 Matches: 12 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 DB: 6	US-09-593-793A-113 (1-553) x AX201091 (1-57) QY 45 GluValGlyValGluGluLySPheMetThrMetVal 56	RESULT 45 AX267890 LOCUS AX267890 S7 bp DNA linear P DETINITION Sequence 864 from Patent WO01/33032. ACCESSION AX267890.1 GI:16516520 KEYWORDS COURCE human. CORGANISM Homo sapiens	REFERENCE 1 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jia XuTHORS Xu,J., Earler,D.C., Mitcham,J.L., Harlocker,S.L., Jia Yedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A and Henderson,R.A. TITLE Compositions and methods for the therapy and diagnosic	JOURNAL Patent: WO 0173032-A 864 04-0cT-2001; CORIXA CORPORATION (US) FEATURES Location/Qualifiers 157 /Organism="Homo sapiens" /db_xref="taxon:9606" BASE COUNT 8 a 5 c 11 g 12 t 21 others ORIGIN	Alignment Scores: 0.00118	09-593-793A-113 (1-553) x AX267890 (45 GluValGlyValGluGluLysPheMetTh 	Search completed: February 19, 2003, 06:11:58 Job time : 3202 secs
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-UNITS=blts -START=1 -ENN=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=100
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            GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                       OM protein - nucleic search, using frame_plus_p2n model
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Listing first 100 summaries
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51 346.5 12.1 1661 8 AF021808 AF021808 Vitis vin AB036758 Daucus ca A8306541 213 1796 8 AB036758 AR306541 AR306541 Sequence 54 346 12.1 2130 8 AF021809 AR306541 Sequence 55 340 11.9 123280 2 AC117076 AC117076 Dictyoste A716741 AF16741 AP16741 7.5 11.4 2133 8 AB071809 324.5 11.4 2137 8 AF166498 324.5 11.3 1695 8 AF191025 324.5 11.3 1969 6 A36574 324.5 11.3 1969 6 A7084456 324.5 11.3 1969 6 A7084456 324.5 11.3 1969 8 SOS31 323.5 11.3 1570 8 AY113946 323.5 11.3 1570 8 AY113946 323.5 11.3 1800 8 AY088566 323.5 11.3 1867 8 AY080866 323.5 11.3 1867 8 AY080986 323.5 11.3 1867 8 AY080986 323.5 11.3 1867 8 AY080986 323.1 11.3 1867 8 AY080986 323.5 11.3 1985 8 AF242307 317.5 11.1 1985 8 AF242307 317.5 11.1 1844 8 MYSUTIA	316.5 11.1 1824 8 AF176950 313.5 11.0 188 6 AZ59902 310.9 1956 8 RCSCRIR 307.5 10.8 2386 8 AY098894 307.5 10.7 1466 8 AZ59900 307.5 10.7 1503 6 AX259900 306.5 10.7 1556 8 AX098891 306.5 10.7 1568 8 AY098891 306.5 10.7 1906 8 AY098891 305.5 10.7 2044 8 HVUZ72309 305.5 10.7 2132 8 DCSUTIA 307.5 10.6 2106 8 AF408844 302.5 10.6 1764 8 AF191024	RESULT 1 AX327336 LOCUS DEFINITION Sequence 1 from Patent W00181577. ACCESSION AX327336 1 G1:18097882 KEYWORDS Numan. ORGANISM Homen. ORGANISM Home sapiens Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	arkes,D., F n Heuit,P.T ost 03 poly A 1 01-NOV- LLSCHAFT (L	

ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOUTC	BASE COUNT ORIGIN	Alignment Pred. No.: Score: Percent Si	Query Matc	US-09-593- QY 1			Db 404 Qy 61						Db 764 Qy 181	Db 824 Qy 201	Db 884
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oy og	Db 10 Qy 2 Db 10	Oy 2 Db 11	Oy 3	Oy 3	Oy 3	Oy 3	Oy 3	Qy 4 Db 14	Qy 4 Db 15	Oy 4 Db 16	Oy 4 Db 16	Qy 4 Db 17	Oy 5 Db 17	Oy 5 Db 18	Qy 541 Db 1902	RESULT 2 AX106329	LOCUS

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 3410)
Xu,J., Skeiky,Y.A., Reed,S.G. and Cheever,M.A.
Compositions and methods for therapy and diagnosis of prostate
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Conservative:
Mismatches:
Indels:
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CORIXA CORPORATION (US)
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Karyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 3410)
J., Dillon, D.C., Mitcham, J.L., Harlocker, S.L., Jiang, Y.,
ed, S.G., Kalos, M.D., Retter, M.W., Stolk, J.A., Day, C.H.,
pasky, Y.A. and Wang, A.

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prositions and methods for the therapy and diagnosis of prostate 463 523 200 883 uLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220 CCTGCTAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCG 403 40 9 80 nLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro uLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly others 3410 553 0 0 0 Length:
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Conservative:
Mismatches:
Indels: ent: WO 0134802-A 110 17-MAY-2001; IXA CORPORATION (US) Location/Qualifiers : 783 t 113 (1-553) x AX140620 (1-3410) /...oriin /db_xref="taxon:9606" 1014 c 945 g | 783 Gaps: GI:14280737 5.66e-178 2861.00 100.00% 100.00% . .3410 40620 ity: larity: ø :: ::

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QQ	1064	ACCAGCTGTGCTGCCCCCTGCCTCCTGCGCCCGGCTCTTCGTGGCTGAGCTGTGTGTG
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3 (GCIGGATGGCACICATGACCTICACGCIGITITACACGGATTICGTGGGCGGGGGCTG II
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යි	1184	ACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGG
ΟŸ	321	erLeuValPheSerLe
qq	1244	TTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTC
Oy	341	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360
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qa	1364	GCTTTCCCTGTGGCCGCTGCCGGTGCCTGTCCCCACAGTGTGGCCGTGGCGGTGACAGT 1423
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ογ	401	rArgGlyAspThrGl
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Qy	421	SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPr
QQ	1544	GCTAGCAGTGAGGACAGCTGATGACTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC 1603
Qy	441	3lyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLe
Op	1604	TCCCTAATGGACACGTGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCACCGCG
οy	461	ysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAl
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δy	481	yvalvalProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLe
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Οy	501	SlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerV
QQ	1784	STCCCAGGTGGCCCCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGT
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Óγ	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
QQ	1904	AGTATTTGACAAGAGCGACTTGGCCAAATACTCAGC
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RESULT 4 AX200480

PAT 29-AUG-2001 prostate Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 343 463 523 583 120 643 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180 344 GICAACCIGCIAACCITIGGCCIGGAGGIGIGITIGGCCGCAGGCAICACCIAIGIGCCG 403 81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100 823 200 883 09 20 40 80 1 (bases 1 to 3410)
Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W., Stolk,J.A., Skelky,Y.A., Wang,A. and Meagher,M.J.
Compositions and methods for the therapy and diagnosis of picancer ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly others linear 3410 553 0 0 0 Matches: Conservative: Mismatches: DNA Patent: WO 0151633-A 110 19-JUL-2001; CORIXA CORPORATION (US) Location/Qualifiers 1. 3410 Sequence 110 from Patent WO0151633 AX200480 783 Indels: Length: US-09-593-793A-113 (1-553) x AX200480 (1-3410) /organism="Homo sapiens" /db_xref="taxon:9606" 1014 c 945 g 78 AX200480.1 GI:15390293 5,66e-178 2861.00 100.00% 100.00% Percent Similarity: Best Local Similarity: ď 299 human. Alignment Scores: Pred. No.: Query Match: DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM source BASE COUNT ORIGIN REFERENCE AUTHORS 21 41 19 464 161 JOURNAL FEATURES TITLE g ŏ g δλ qq QY Db QY Db ò δy Db Qγ Ω οy Db Ωý D οχ Op

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ThrLeuilePheLeuThrCysvalAlaAlaThrLeuLeuValAlaGluGlu 22	SGInLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGlpLeu IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	GTTCGGATGGCAGCCTGTTTTTTTTTTTTTTTTTTTTTT	CAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTTCTTTTTTTT	"GCCTGTGATGTCTCCGTACGTGGTGGTGGGTGAGCCCACCGAGG TGCTGTGATGTTGTGTTG
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Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A. PAT 26-0CT-2001 Compositions and methods for the therapy and diagnosis of prostate Euteleostomi; 463 523 160 9 80 40 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Mammalia; Eutheria; Primates; Catarrhin; Hominidae; 1 others linear 3410 553 0 0 0 Length:
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Conservative:
Mismatches:
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oy Ob	221	AlaAlaLeuGlyproThrGluproAlaGluGlyLeuSerAlaProSerLeuSerProHis 24	· · · · ACCE VERS KEYW SOUR	ACCESSION AXA VERSION AXA KEYWORDS .
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Oy Dp	281	SerTrpMetAlaLeumetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300	FEAT	G
٥. رو د	301	TyrGlnGlyValProkrgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320	BASE	SE COUNT
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oy Db	341	ValmetaspargleuvalginargphegiymhrargalavalTyrLeualaservalala 3 	Best Quer DB:	Best Local Simi Query Match: DB:
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oy Db	401	SerLeutyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 	Ob Qy	
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Oy Dp	441	PheProAsnGlyHisValGlyAlaGlyGerGlyLeuLeuProProProProAlaLeu 4 	op Oy	464 CCAG
oy B	461	CysGlyalaSeralaCysAspValSerValArgValValValGlyGluProThrGluala 480 	Oy Oy	
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Qy Dp	521	ThralaTyrMetValSeralaalaGlyLeuGlyLeuValalaIIeTyrPheAlaThrGln 540 	oy Oy	704 ACTCC 161 TyrSe
0y	541	ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553	<u>අ</u>	764 TACTO

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ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                              eed,S.G., Xu,J., Dillon,D.C., Retter,M.W. and Harlocker,S.L. ompositions and methods for the therapy and diagnosis of breast
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% Study, Kalos, M., Stolk, J.A., Zasloff, E.J., Zhang, X., Houghton, R.L., Filho, A.M., Nolasco, M., Badaro, R. and Reed, S.G.
Filho, A.M., Nolasco, M., Badaro, R. and Reed, S.G.
Direct Submission

L. Submitted (27-APR-2001) Antigen Discovery, Corixa Corporation, 1124

Columbia Street, Seattle, WA 98104, USA

Location/Qualifiers

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YSVYAFMISLGGCLGYLLPAIDWDTSALAPYLGTQECLFGLLT.FLTCVAATLLVA
EEAAACGPTEARAGAGLSASLSAPRCCPGRARATARRHVDEGVRWGSLGFFRRVA
AELCSWMALMTFTLEYTPYCGECLYOGVPRAEPGTEARRHVDEGVRWGSLGFFLOGA
SLUFSLVMDRLVQRFGTRAYYLASVAAFPVAAGATCLSHSVAVVTASAALTGFTFSAL
QILPYTAASLYHFRKQVFLPKTRGDTGGASSBDSLMTSFLPGPRPGAPFPNGHVGAGG
SGLLPPPPALCGASAGDVSWVVGBPFTEARRVPGRGICLDLAILDSAFLLSQVAPSL
FMGSIVQLSQSVTAYMVSAÁGLGVAIYFATQVVFDKSDLAKYSA"

FMGSIVQLSQSVTAYMVSAÁGLGVAIYFATQVVFDKSDLAKYSA"

1 others
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Xu,J., Kalos,M., Stolk,J.A., Zasloff,E.J., Zhang,X., Houghton,R.L., Filho,A.M., Nolasco,M., Badaro,R. and Reed,S.G.
Identification and characterization of prostein, a novel
prostate-specific protein
Cancer Res. 61 (4), 1563-1568 (2001)
                                                                                                                 PRI 23-MAY-2001
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Length:
Matches:
Conservative:
Mismatches:
                                                                                                               Homo sapiens prostein mRNA, complete cds. AY033593
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, da v da	61	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80
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j	81	ArgfyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
O.Y	101	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Qy Db	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Qy Dp	141	ThrProLeuGlualaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnala 160
Qy Dp	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Qy Db	181	IleaspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluGluCysLeuPhe 200
Oy Db	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaalaThrLeuLeuValAlaGluGlu 220
Oy Dp	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Oy Dp	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
Qy Dp	261 1064	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Qy Dp	281	SerTrpMetalaLeuWetThrPheThrLeuPheTyrThraspPheValGlyGluGlyLeu 300
Oy Dp	301	TyrGlnGlyValProargalaGluProGlyThrGlualaargargHisTyrAspGluGly 320
Qy Db	321	ValargMetGlySerLeuGlyLeuPheLeuGlnCysAlalleSerLeuValPheSerLeu 340
Qy Db	341	Alava
Qy Db	361 1364	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380
Oy Op	381 1424	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400
Oy Dp	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420

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AB060851 3514 bp mRNA linear PRI 13-JUN-2001 Macaca fascicularis brain cDNA clone:QtrA-11310, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 3514)
Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
Direct Submission
Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama I-chome, Shinjuku Ku, Tokyo 162-8640, Japan (E-mail:khashi@nh.go.jp, URL:http://www.nih.go.jp/yoken/genebank/, Tel:81-3-5288-1111(ex.2120), Fax:81/3-5285-1181)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Description: Its strand CDNA was primed with an oligo(dT) primer [ArGTGGCCTTTTTTTTTTTTT]; double-stranded CDNA was synthesized using specific 5 and 3' primers and amplified by PCR. The PCR product was digested with Sfil and size selection was performed to exclude fragments <1.5kb.The Sfil-digested PCR product was cloned tinto distinct Draili sites of pMEIBSFE13. XhoI sites just outside the Draili sites can be used to isolate the CDNA insert. Libraries were constructed by oligo-capping method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligo capping; fis (full insert sequence).
Macaca fascicularis adult male temporal lobe right cDNA to mRNA, clone_lib:macaque brain cDNA library QtrA clone:QtrA-11310.
Macaca fascicularis
                                                                                                                                                                                                1844 ACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAG 1903
                       1604 TTCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCTGCTCCCACCTCCACCCGCGCTC 1663
                                                                                                                                                                           480
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Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M.,
Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.
Isolation of full-length cDNA clones from macaque brain cDNA libraries
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                                                                                                                                                                           CysGlyAlaSerAlaCysAspValSerValArgValValValValGlyGluProThrGluAla
                                                                                                                                                                                                                                                                                                                                                       LeuSerGlnValAlaProSerLeuPheMetGlySerlleValGlnLeuSerGlnSerVal
  AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro
                                                                                        PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu
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SOURCE
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542
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                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
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/db_xref="taxon:9541"
/clone="QtrA-11310"
                                                                                                                                                            Indels:
                                                                                                                                                                          US-09-593-793A-113 (1-553) x AB060851 (1-3514)
Location/Qualifiers
                                                                                                                                        7.67e-174
2798.00
98.55%
98.19%
97.80%
                         /sex="male"
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Best Local Similarity:
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	Db 761 TACTCTGTCTATGCCTTCATGATCAGTCTTGGGGGGCTGCCTGC
T 9955	Oy 181 11eAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluGluCysLeuPhe 200
LOCUS AXZUOYSS 4034 bp DNA 11near PAT 29-AUG-2001 DDEFINITION Sequence 625 from Patent WO0151633. ACCESSION AXZ00995 VERSION AXZ00995.1 GI:15390822	Oy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
NETWOUSS human. ORGANISM Homo sapiens ORGANISM Homo sapiens Lekaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Qy 221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
Manmalla: butherla; Primates; Cararrhin; Hominidae; Homo. AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Fanger,G.R., Day,C.H., Retter,M.W.,	Qy 241 CysCysProCysargAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
SLOIK, J.A., SKERKY, T.A., Wang, A. and Meagner, M.J. TITLE Compositions and methods for the therapy and diagnosis of prostate cancer JOURNAL PATENT: 00 0151633.A 625 19-JUL-2001;	Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgAtgleuPheValAlaGluLeuCys 280
CURIAR CURPORATION (US) FEATURES Location/Qualifiers 1. 4034 /Organism="Homo sapiens"	Qy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
/db_xref="taxon:9606" BASE COUNT 721 a 1226 c 1141 g 946 t ORIGIN	301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu
ent Scores: 1.89e-168 Length:	Db 1181 TACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCAGGGCCCGGAACACTATGATGATGAAGGT 1240 Qy 319
Score: 2716.50 Matches: 553 Percent Similarity: 70.09% Conservative: 0 Asset Local Similarity: 70.09% Mismatches: 0	Db 1241 AAGGCCTTGGCAGCCAGGAGGCTGGTGTGGGAGCCGCCACCAGAGACGACACTCGGG 1300
94.95% Indels: 6 Gaps:	319
US-09-593-793A-113 (1-553) x AX200995 (1-4034)	1301 GCTGTGTCTGGGCTGGTGCCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGG 13
1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20 	Db 1361 ATGGACCCCATCTGCATACACGCCTTCTCATGGGTGTGGAACATCTCTGCTTGCGTTTC 1420
	0y 319 319 Db 1421 AGGAAGGCCTCTGGCTGTCTAGGAGTCTGATCAGAGTTGCCCCCAGTTTGACAGAAG 1480
ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly	QY 319 319 Db 1481 GAAAGCCGCAGCTTATTCAAAGTCTAGAGGAAGTGGAGTTAAGGCTGGATTTCAGAT 1540
ProvalLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 8	DD 1541 CTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCA 1600
ArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlylleLeuLeuSerLeu 10 	Oy 319 319 Db 1601 CCAGCGCCTTCCAGCTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTTT 1660
PheceulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspFroArgProLeu 12	GTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCCAGGAAACCTTCAGACTACC 17
121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140 	Qy 319 319 Db 1721 TTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGGTCAGTGGAAGAACCTA 1780
141 ThrProLeuGluhlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGluhla 160 	Qy 319 319 Db 1781 GACTCCCATTGCTAGAGAGAGAGAGAGGTGCTGGGGAGCAGGGTGCTGCCACAGC 1840
1	OY 319 319 Db 1841 AGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCTGAGACTGCTCCGAC 1900

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FEATURES SOUTCE	BASE COUNT 721 a	Alignment Scores: Pred. No.: Score:	Percent Similarity: Best Local Similarity Ouery Match:		Oy 1 MetvalGlnar 	Oy 21 ValAsnLeuLe 	Oy 41 ProLeuLeuLe 	0y 61 ProvalLeuGl 	Oy 81 ArgTyrGlyAr 	Oy 101 PheLeullePr 	Oy 121 GluLeuAlaLe 	Oy 141 ThrProLeuGl 	Oy 161 TyrSerValTy 	Oy 181 IleAspTrpAs 	Qy 201 GlyLeuLeuTh	Oy 221 AlaAlaLeuGl	Qy 241 CysCysProCy Db 1001 TGCTGTCCATG	Qy 261 HisGlnLeuCy	Db 1061 CACCAGCTGTG
320GlyValArgMetGlySe	DD 1501 CCTTCCCTCCCA65CTCTGTCTGATGGCCCTCTCCCTCTGCGGGCGTTCGGGTGGGCAG 1950 Qy 325 rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspargLe 345	Db 1961 CCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTTTTTTTT	2021 GGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGTTTCCCTGTGGC	Oy 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuTh 385	Oy 385 rGlyPheThrPheSeralaLeuGlnIleLeuProTyrThrLeualaSerLeuTyrHisar 405	Oy 405 gGluLysGlnValPheLeuProLysTyrargGlyAspThrGlyGlyAlaSerSerGluAs 425 	Oy 425 pSerLeumetThrSerPheLeuProGlyProLysProGlyAlaProPheProAnGlyHi 445	Oy 445 svalGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCySGlyAlaSerAl 465 	Oy 465 aCysAspValSerValArgValValUqlQlyGluProThrGluAlaArgValValProGl 485 	Oy 485 yArgGlylleCysLeuAspLeuAlalleLeuAspSerAlaPheLeuLeuSerGlnValAl 505	Oy 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525	Oy 525 ISerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545 	Oy 545 sSerAspLeuAlaLysTyrSerAla 553 	RESULT 10 AX267730 LOCUS AX267730	AX267730 AX267730.1 GI:16516402	Σ.	AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.	and Henderson, R.A. TITLE Compositions and methods for the therapy and diagnosis of prostate	JOURNAL PATENT: WO 0173032-A 704 04-OCT-2001; CORIXA CORPORATION (US)

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281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlyLeu 300	301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 319	TRICKNOOD COTOCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	1241 AAGGCCITGGCAGCCAGCAGAGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGG 1300	319 319	1301 GCTGTGTCTGGGGCTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGG 1360	319 319	1361 ATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGGAACATCTCTGCGCTTGCGGTTTC 1420	319 319	1421 AGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCCAGTTTGACAGAAG 1480	319 319	1481 GAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGGATTTCAGAT 1540	319 319	1541 CTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCA 1600	319 319	1601 CCAGGGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTT 1660	319	1661 GTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACC 1720	319 319	1721 TTCCTCTGCCTTCAGCAAGGGGGGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTA 1780	319 319	1781 GACTCCCATTGCTAGAGGTAGAAAGGGGAAGGTGCTGGGGAGCAGGGCTGGTCCACAGC 1840	319	1841 AGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGACTGCTCCGAC 1900	320GlyvalArgMetGlySe 325	1901 CCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCGTTCGGATGGGCAG 1960	325 rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 345	uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAl	11111111111111111111111111111111111111	365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuTh 385	2081 TGCCGGTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCGCCCCTCAC 2140	385 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405	405 gGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 425
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distribution: MGC clone distribution information can be found h the I M.A.G.E. Consortium/LiNL at: http://image.llnl.gov : IRAR Plate: 45 Row: 1 Column: 2 lone was selected for full length sequencing because it the following selection criteria: Hexamer frequency ORF
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ia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ses 1 to 3354)
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cgapbs-r@mail.nih.gov

Procurement: Jeffrey E. Green, M.D.

ibrary Preparation: Life Technologies, Inc.

ibrary Arrayed by: The I.M.A.G.E. Consortium (LLNL)

quencing by: Baylor College of Medicine Human Genome
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te: http://www.hgsc.bcm.tmc.edu/cdna/
tre. pre-mc.edu
tre. P.H., Garcia, A.M., Lu, X., Hulyk
V.S., Kowis, C.R., Lawrence, S., Martids, S., Gibbs, R.A.
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p mRNA linear PRI 13-JUN-2001
clone:QmoA-10594, full insert
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                                                        ArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyr
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Triple fusion proteins comprising ubiquitin fused
Thioredoxin and a polypeptide of interest
Patent: WO 0200892-A 3 03-JAN-2002;
SmithKline Beecham Biologics SA (BE)
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Sequence 3 from Patent WO0200892.
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/translation="wimwicigpucicysvplicsasDHWRGRYGRRRPFIWALSLGI
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HVGAGGSGLLPPPPALCGASACDVSVRVVVGEPTEARVVPGRGICLDLAILDSAFLLS
QVAABLEMGSTYQLQSQYTATMVSAAGLGLVAIYFATQVVFDKSDLAKYSV"

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Lab host: 7-0P10
                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 2917)
Hida,M., Kusuda,J. and Sugano,S.
Direct Submission
Submitted (11-JUN-2001) Katsuyuki Hashimoto, National Institute of
                                                                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                               Osada,N., Hida,M., Kusuda,J., Tanuma,R., Iseki,K., Hirai,M., Terao,K., Suzuki,Y., Sugano,S. and Hashimoto,K.
Isolation of full-length cDNA clones from macaque brain cDNA
AB062977.1 GI:14388390 digo capting and analysis of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of
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Mammalia; Eutheria; Primates; Catarrhini; Cercopithécidae;
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/clone_lib="macaque brain cDNA library QmoA"
/dev_stage="adult"
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/clone="QmoA-10594"
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end primer [CGACCTGCAGCTCGAGCACA] ).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                            Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
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                                                                                                                  Macaca fascicularis
                                                                                                                                                                                                                                                                                                                                                         libraries
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Query Match:
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ORIGIN
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AUTHORS
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                                                                                                                                                                                                                                                                                                                           TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
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125
266 ArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeu
                                                                                                                                                                                                                                                                                                                                                                                                        66 ValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArg
                                                                       86 ArgProPhelleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArg
                                                                                                                           183 GCTGGCTGGCTGGCAGGGCTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTC
                                                                                                                                                                                                                                                                       423 AGTGCCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTC
                                                                                                                                                                                                                                                                                                                                                               246 AlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         366 AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArg
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325 842 345

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406 GluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAsp 425 :::	426 SerLeumetThrSerPheLeuProGlyProGlysProGlyAlaProPheProAsnGlyHis 445 	446 ValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAla 465 	466 CysaspvalSerValargValValValGlyGluProThrGluAlaargValValProGly 485 	486 ArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAla 505 	506 ProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVal 525 	526 SeralaalaglyLeuGlyLeuvalalaIleTyrPhealaThrGlnValValPheAspLys 545 	546 SerAspLeuAlaLysTyrSer 552 	AX200993 4894 bp DNA linear PAT 29-AUG-2001 TION Sequence 623 from Patent W00151633. N AX200993 GI:15390820 S human. NISM Homo sapiens Eukaryota i Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.	E 1 (bases 1 to 4894) S Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jia Reed,S.G., Alos,M.D., Fanger,G.R., Day,C.H., Retter, Stolk,J.A., Skeiky,Y.A., Wang,A. and Meagher,M.J. Compositions and methods for the therapy and diagnosi	cancer CABLE Patent: WO 0151633-A 623 19-JUL-2001; CORIXA CORPORATION (US) ES Location/Qualifiers Ource / Organism="Homo sapiens"	/db_xref="taxnoi906"")UNT 928 a 1448 c 1354 g 1163 t 1 others	ment Scores: 9.98e-157 Length: 4894 No.: 2538.50 Matches: 551 int Similarity: 51.11% Conservative: 0 Local Similarity: 51.11% Mismatches: 2 Match: 68.73% Index: 2 Gaps: 2	593-793A-113 (1-553) x AX200993 (1-4894) 1 MetValGlnArdlenTrbValSerArdlenJenArdHisArdIxsAlaGlpLenLenLen 20	MECVALGINATGLEUTTPVALSETATGLEULEUATGHISATGLYSALAGINLEULEULEU
Qy 4	Oy 4 Db 13	Oy 4 Db 13	Oy 4	Oy 4	Oy to	Oy :	Qy 5	RESULT 14 AX200993 LOCUS DEFINITION DEFINITION VERSION KEYWORDS SOURCE ORGANISM	REFERENC AUTHOR TITLE	JOURNAL FEATURES SOUR	BASE COUNT ORIGIN	Alignment S Pred. No.: Score: Percent Sim Best Local Query Match	-60-sn	

Oy Db	21	ValasnLeuLeuThrPheGlyLeuGluValCysLeuA aAlaGlyIleThrTyrValPro 40
δy	41	roLeuLeuCluValGlyValGluGluLysPheMetThrMetVa
QQ	394	CCTCTGCTGGTAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCT-GGGTGAGTC 452
Οy	57	25
Dp	453	ACTACATCCTCCTTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 512
Qγ	57	25
qq	513	CCTCTGCCCTGGGAGCTGCTTGGAGGGAGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 572
οy	57	57
qq	573	GGAGGGTGACCCTGGGGTGAGGGGGCACACCAAGAGAAGAAGAAGAATACCAAGGACATA 632
Qy	57	57
qq	633	CCCCAGTCACCTCTGGATCCCTGGTCCTGCACAGAGCCTGGCTCATAGGAGACACTGGAG 692
٥y	57	25 57
qa	693	AAATGCTCCTAAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC 752
Οy	57	25
qq	753	TTACAACCACCATTTGAGGTGATCCATTTTACAGAGGAAGGA
δλ	57	25
qq	813	TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAAGAGTAGAGCTGGGACTCCATCAA 872
Qγ	57	25
qa	873	GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 932
Qy	57	57
qq	933	GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCTCACC 992
Qy	57	25
qq	993	CCCAGGAAGAGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 1052
Qy	57	25
qq	1053	GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTCTTAGTTGCTCC 1112
Oy	57	57
ΟD	1113	ATGCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1172
QY	57	25 57
qq	1173	AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC 1232
Qy	57	57
qq	1233	TTCTCACGGAGCTTGGTTCCCCTTCCCCTTTACTTGTCCCAGCCATTGACTCAT 1292
. Qγ	58	GlylleGlyProValLeuGlyLeuValCysValProLeuLeu 71
qq	1293	GGTCCAGTGCTGGCTGTCTGTCTCCCGCT
οy	7	
QQ		GCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCA 14
ΟŊ	92	LeuSerLeuGlylleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111

QQ	2493 TCT	TGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTG	2552
Qy	319		319
qq	2553 AGAC	CTCCCAGGAAACCTTCAGACTACCTTCCTCTTCAGCAAGGGGCGTTGCCCACA	2612
ογ	319		319
QQ	2613 TTCT	CTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGG	2672
0y	319		319
QQ	2673 TGCT	3GGGAGCAGGGCTGGTCCACAGCAGGTGCTGCAGCAGGTACCTGTGGTTCCGCC	2732
Qy	319		319
qq	2733 TICIC	ATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG	2792
Qy	320	GlyvalArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe	336
qo	2793 TCCCT	TGCAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCTT	2852
oy d	336 uVa]	uValPheSerLeuValMetAspArgLeuValĠlnArgPheGlyThrArgAlaValTyrLe 3 CHRINIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	356
?	356		92
- qa	13		2972
Οy	376 aVa]		396
QQ	2973 CGT	CGTGGTGACAGCTTCAGCCGCCCTCACCGGTTCACCTTCTCTCAGCCCTGCAGATCCTGCC	3032
Qy	96		16
qq	3033 CTAC		3092
δy	416	yaspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 4	36
ΩD	m		3152
Oy Dp	436 sPro 3153 GCC1	sProGlyalaProPheProAsnGlyHisValĠlyalaGlyGlySerGlyLeuLeuProPr 4 	456 3212
Οy	456 oPro	-	476
QQ	3213 TCCA		3272
Qy	476 uPro	uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 4	496
q	3273 GCC	CCTGGA	3332
Qy	496 pSer	pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 5	516
qa	3333 TAG	rccretriareserrccarrerccascr	3392
Qy	516 uSer(31nSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy	536
QQ	3393 CAG	SAGTCTGTCACTGCCTATATGGTGTCTGCCGCAGGCCTGGGTCTGGTCGCCCATTA	3452
Qy	536	5	
Dp	3453 CTT	rgctacacaggtagtatttgacaagagcgacttggccaaatactcagcg 3504	
RESC AX26 LOCU DEFI ACCE	RESULT 15 AX267728 LOCUS DEFINITION SE ACCESSION AVERSION	AX267728 4894 bp DNA linear PAT 26-C Sequence 702 from Patent WOOL/73032. AX567728.1 GI:16516400	OCT-2001
KEYW		*01001:10 T:07//0	

S	SOURCE ORGANISM	human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
R	REFERENCE AUTHORS	Primates; Catarrhini; Hominidae; Mitcham, J.L., Harlocker, S.L., Ji.R., Retter, M.W., Stolk, J.A., D., Li.S.X., Wang, A., Skeiky, Y.
ĮT.	TITLE JOURNAL FEATURES sourc	the therapy and diagnosis of prostator.
78 O	BASE COUNT ORIGIN	/dysalism- nome sapiens /db_xref="taxon:9606" 928 a 1448 c 1354 g 11
Property Pro	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	Alignment Scores: 9.98e-157
ñ	us-09-593	-793A-113 (1-553) x AX267728 (1-4894)
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oy Op	7 21 5 334	ValAsnieuleuthrPheGlyLeuGluValCysLeuAlaAlaGlyIlethrTyrValPro 40
ογ		7
å å	394	CCTCTGCTGCTGGGGGGTAGGGGGAAGTTCATGACCATGGTGCT-GGGTGAGTC 452
g q	4	<
δý	1 57	25
g	513	CCTCTGCCCTGGGAGCTGCTTGGAGGGAGGTGTCTGCTGGGAAGGCATTGCTGGGGCA 572
δ	1 57	57
qq	573	GGAGGGTGACCCTGGGCTGAGGGGGCACACCAAGAGAAAGAGAGAATACCAAGGACATA 632
οy	1 57	25 57
a	5 633	CCCCAGTCACCTCTGGATCCCTGGTCCTGCACAGAGCCTGGTCATAGGAGACACTGGAG 692
ογ	7 57	25
g	5 693	AAAIGCTCCTAACCTITGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAAIGC 752
δý	7 57	25
a) 753	TTACAACCACCATTTGAGGTGATCCATTTTACAGAAGGAAG
ò	7 57	25 21
QO	813	TTAGGTAAGTCTTAGCCAAAGGCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 872
ογ	1 57	
q	5 873	GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 932

Qy	57
Dp	933 GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCCTCACC 992
ΟY	57
qq	993 CCCAGGAAGAGGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 1052
Qy	57 57
Db	1053 GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTCTTAGTTGCTCC 1112
Qy	57 57
QQ	1113 ATGCCTCAGTTTGTCCATCTGAAAATGGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1172
Qy	57 57
QQ	SAAGACGTAGCACAGTGTCGAGTACGGAAT
Qy	
Dp	CTCACGGAGCTTGGTTCCCCTTCCCCTTGCCCTTTACI
Qy	58GlylleGlyProValLeuGlyLeuValCysValProLeuLeu 71
QQ	SCATTGGTCCAGTGCTGGCCTGGTCTGTGTCCCGCTCCTA 1
Qy	72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPhelleTrpAla 91
QQ	rcasccastsaccactsscstscacsctatssccsccsscccttcatctssca
Οy	92 LeuserLeuGlylleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
οqα	rcciresecarccisascerciticarccanssesses
Qγ	112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLleuLeuGlyValGlyLeu 131
qq	SCIGIECCCGGAICCCAGGCCCCTGGAGCIGCACTGCTCATCCTGGGCGTGCGGCI
Qy	132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
qq	TCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGACCTCTT
Qy	152 ArgaspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
qq	SACCCGGACCACTGTCGCCAGGCCTACTGTCTATGCCTTCATGATCAGTCTTGG
Qy	172 GlyCysLeuGlyTyrLeuLeuProAlalleAspTrpAspThrSerAlaLeuAlaProTyr 191
Dp	SCCTEGECTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTTA
Qy	192 LeuGlyThrGlnGluCgsLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
QQ ::	ACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGT.
Qy	212 AlaalaThrLeuLeuValAlaGluGluAlaAlaLeuGlyproThrGluProAlaGluGly 231
qq	CACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGGAAAG
Qy	232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
qq	redececectectraresecececatereses
Qy	252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
qq	SCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCCGCATGCCCCGCACCCTG 19
ΟŊ	272 ArgargLeuPheValalaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
qq	CGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTT

	QY 516 userClnSerValThralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy 536 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	NISM NCE ORS E E NAL ES OUIT	Alignment Scores: 8.88e-131 Length: 6976
292 TyrThrAspPhevalGlyGluGlyLeuTyrGlnGlyValProArgalaGluProGlyThr	Db 2353 GTGTGGAACATCTGGTTGCGGTTTCAGGAAGGCTCTGGTGCTCTAGGAGTCTGATC 2312 Qy 319	319	Oy 320

QQ	285	CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCT-GGGTGAGTC 343	_
٥y	57	5	
Db	344	ACTACATCCTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 403	
οy	57	25	
Db	404	CCTCTGCCCTGGGAGCTGCTTGGAGGGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 463	
δý	57	75	
Dp	464	GGAGGGTGACCCTGGGCTGAGGGGCCACACCAAGAAAAAAGAAGAATACCAAGGACATA 523	
ογ	57	57	
QQ	524	CCCCAGTCACCTCTGGATCCCTGGTCCTGCACAGAGCCTGGTCATAGGAGACACTGGAG 583	
ΟŊ	57	57	
QQ	584	AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC 643	
οy	57	22	
QQ	644	TTACAACCACCATTTGAGGTGATCCATTTTACAGAGAAGGAAG	
Qy	57	22	
QQ	704	TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763	
ογ	57	22	
QQ	764	GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 823	
οy	57	22	
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οy	57	25	
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οy	57	22	
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Οy	28		
QQ	1184		
QV Db	72	GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91 	-
o S S	92 1304	LeuSerLeuG1yILeLeuLeuSerLeuPheLeuILeProArgAlaG1yTrpLeuAlaG1y 111 	
Oy Dp	112	LeukeucysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131 	

AsphecysciycityalcysPheThrProLeugiuAlaleuleusernspleuph	
AspPheCysGlyGlnValCysPherhrP GACTTCTGTGGCCAGGTGTGCTTCACTC CysLeuGlyTyTcGTGGCCAGGCCTACT CysLeuGlyTyTcGTGGCCAGGCCTACT CysLeuGlyTyTcGTGGCCAGGCCTACT CTGGGCTACTCTCGTGGCCAGGCCTACT CTGGGTACCTCTTGGCCCAGGCCTACT CTGGGTACCTCTTGGCCCAGGCCTACT CTGGGTACCTCTTGGCCCAGGCCAGG	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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~	yy 319 319	δy	409
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ą	2024 ITCICAICICCIGAGACIGCICCGACCCITCCCICCCAGGCICIGICIGACIGCCCCIC 20	0y	409
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ζλ	yy 336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356	7 E	3823 AG
q	2744	- A	
≿ :	356 ualaservalalaalapheprovalalaalaGlyAlaThrCysLeuSerHisSèrvalal	qa ———	3883 GGC
Ω.	2804 GGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGC	δλ	409
≿ 4	376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 	qq	3943 TT
3 3	305	Qy	409
, A	2924 CTACACACTGGCCTCCTTAACCGGGGAGAGGCAGGT-ACTCATTGGCCAGTGGGTGG	qa	4003 CTJ
. >	609	Qy	409
. A	2983 AGTCAGGGAGGGGGGGGTCTGGGTTTTTGGGAGGCCAACTAGCTCAGAACTTGGTAT	QQ	4063 GTP
<u> </u>	409	Qy	409
. A	3043 CTGGCAAGCAATTTGGAGAATGCTTTTGAATCAGAGAAGGTTATCCTAGCCCCA 3	qq	4123 ATG
~	409	Qy	409
. <u>a</u>	3103 GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT	qα	4183 AG
<u>></u>	409	Qy	409
. <u>a</u>	3163 TCAGGACTGTGTAGCACTTGAATGGATGATTGCAGGAAATGCAAAATACGATAGTGGGAA 32	qq	4243 CAC
>	60 h	Qy	409
. <u>a</u>	3223 TCCCGAAAGGTCAGGAGCCAAGCAGCAGCCTTCTAGGCTGGTTGTTCTAGGAGAGAGA	qu	4303 CTC
. ≥	409	Qy	409
. <u>a</u>	3283 CAGGGCGCTGAATCAGATGACCCCTGGGCCATTCAGCCTCAGCAGAGGGAGTGGGAATG	qa	4363 TTC
2	409	Qy	409
<u>.</u> ۾	3343 GTCCAGCCTTAGCAACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3	qq	4423 GCC
2	507	oy	409
۽ ج		qa	4483 CAG
2	10.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.1.	QY	409
5 5	サント 37.6.3 であって、	qu	4543 AGA
2	1001001110000111000111001110011001100111001111	QY	409
5 5	ひびがかか そうかん かいかい かんかい かんかん かんかん かんかん かんかん かんかん か	qa	4603 AGG
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QQ	3583 CACT	retetaagttgtggggacctccttcttggttggccctacactaaccagccctccag	364
ΟŊ	409		409
qq	3643 GGG	GGGCCCCTTTCCTTGGGAAGCCACCTAACCCÀGGTAGTGTGGGTCATCCTTGTCCCCTCCA	370
δy	409		409
qq	3703 CTG	CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCCTTGAGGGGCATGAAGTTGG	376
Qy	409		409
qq	3763 GGTC	GGTGTCCCAAGGGAGGAGGAGATGCAGGACTGCTCTCATAGAGCTCTCAGACTGTAGGGA	382
Qy	409		409
QQ	3823 AGAC	AGACCTGCCCCTGCGTCTCGTAGCACTTGAGGAGGAGTAGGTAAGTTCGTAGCTGAGA	388
Qy	409		409
qq	3883 GGC1	GGCTGGTTAACTGAGTAGGTAGCTGCAGGGGTGAGAGGTATGGAGGGGAGGGGCTAAAGGT	394
Οy	409		409
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ΟŸ	409		409
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Οy	409		409
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Qy	409		409
Dp	4423 GCC#	GCCATCAAGGGCAGGGGTTGGGGGGATGGTGGTCGACCAGTCACTCTGATCTAAGTCAGA	448
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Dp	4483 CAGC	AGCAGGAAGGAAGTGAGAAGCCTTCAACATTAGCACAGCTGGGGCTGGGGAGGTGGGA	454
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Qy	409		409
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REFERENCE 1 AUTHORS Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T. and Henderson,R.A. and methods for the therapy and diagnosis of prostate cancer JOURNAL Patent: WO 0173032-A 705 04-OCT-2001; CORIXA CORPORATION (US) FEATURES Location/Qualifiers Source //Organism="Homo sapiens" //db.xref="Haxon:9606" BASE COUNT 1312 a 1996 c 1961 g 1706 t 1 others	Alignment Scores: Pred. No.: Score: Score: Percent Similarity: Best Local Similarity: Query Match: Guery Match: Guery Match: Guery Match: Guery Matches: Guery Match: Guery Match	9LeurrpValSerArgL 	344 ACTACATCCTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA	Db 524 CCCCAGTCCTGGATCCTGGACCTGGAGCGTGGCTCATAGGAGACACTGGAG 583 Oy 57	Db 824 GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCTCACC 883
Db 4663 TCTCTGCACCGGGCAATGAGGATTTCCAGATGTCGGAGGGAG	Db 4903 AGGGAGACCTAGACTTCTGGGTTCACATTTGTCCCCGCCCTACCCGTTACCCTTCTC 4962 Oy 409	Qy 409 Db 5083 GCTGGGGTGCTGGGTACACCCTGTCCTCTTCCCCTTTTCTTCACCCCTCT 5142 Qy 410 PheLeuProLysTyrArgGlyAspThrGlyGlyAlaserSerGluAspSe 426 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	446 1G1yAlaG1yG1ySerG1yLeuLeuProProProAlaLeuCySG1yAlaSerAlaCy	Db 5443 ATCCCTGTTTATGGGCTCCAGTCGCCGAGTCTGTCACTGTCATATGGTGTC 5502 Oy 526 ralaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysse 546	Primates; Catarrhini; Hominidae; Homo

è	23	0y	312 GluAlaArgArgHisTyr
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3 6	C	qa	2024 AGCCGCCCACCAGAGACGA
3 8	20100110011001100011000110001100011000	Qy	319
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3 8		Qy	319
g a	AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTCCATCC	qq	2144 GTGTGGAACATCTCTGCT
δy		, Qy	319
qq	1124 TICTCACGGAGCTTGGTTCCCCTTCCCCTTACTTGTCCCAGCCATTGACTCAT 1183	qa	2204 AGAGICGIIGCCCCAGII
Οy	58	δλ	
qq	1184 ACTACTTCCCTTCTTGCAGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTA 1243	අධ .	2264 TGGAGGAGTTAAGGCTGG
οy	72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPhelleTrpAla 91	δο O	319
g	1244 GGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCCGC	3 8	
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δλ	112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131	Qy	319
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o, d	132 LeuaspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151 	7. da	2504 TTCTCTGAGGGTCAGTGGA
δý		Qy	
QQ		qa	2564 TGCTGGGGAGCAGGGCTGG
λο d	172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191 	ζ G G	2624 TTCTCATCTCCCTGAGACT
3 8	Sectional sectional and a sectional section of sectional sections and sectional sections and section s	QY	320GlyvalArg
B 5	194 belong 1111 1111	qa	2684 TCCCTCTGCAGGCGTTCGG
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οy	252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271		376 aValValThrAlaSerAla
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oy B	272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291 	qa 7.2	
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319 319	Qy
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319 319	δŏ.
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319 319	QY
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319 319	QY
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Qy	409
qq	4183 AGGGAGGAGAAGTCCTGGGAGGCCCCTTCCTAACAGCAGCTGATGGCAGACTTGGCACTG 4242
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qq	4243 CACGCTGTCTGCCTGTTCCTTTGCCCACTTGTTGAGCTGCATGGTGAGCCGTGGGCTTCC 4302
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Qγ	604 408
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Qy Db	426 rLeumetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446

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Homo sapiens chromosome 1 clone RP11-6B6, WORKING DRAFT SEQUENCE, 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae, Homo.
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Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
Direct Submission
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1 (bases 1 to 157988)
Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.
Direct Submission
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                                                                                               sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality coverage: 7.3x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing vector: plasmid; L08752; 100% of reads Chemistry: Dye-terminator ET: 57% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 154688 bases at least 0.00 consensus quality: 156347 bases at least 0.00 linsert size: 157388; sum-of-contigs
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Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
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Center clone name: RP11-6B6 (sc0601)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        5563 CGACTTGCCCAAATACTCAGCG 5584
                                                                                                                                                                                                                                                                                                                                                                                                                 546 rAspLeuAlaLysTyrSerAla 553
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soon as it is available
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MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu

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Conservative:
Mismatches:
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(1-157988)

US-09-593-793A-113 (1-553) x AC096533

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138081	GCTGCCTCTTACCCTCCCTAGGTCTGCGCCCTTTGAATAAGTATCACTTCTTAGTTGCTCC	138022	Db
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57		57	Οy
137781	TTACAACCACCATTTGAGGTGATCCATTTTACAGAAGGAAG	137722	g
57		57	٥y
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57		57	Qy
137481	ACTACATCCTCCTTCCTTTCCAGATACATGCCACCTGGCATGTGGGGACAGGAGTA	137422	qq
57		57	Qy
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0	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro	7	Óγ
137302		137243	S A

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8382	
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Qy Db	336 139822	uvalPheSerLeuvalMetAspargLeuvalGlnargPheGlyThrargAlavalTyrLe 356
QY	356 139882	uAlaSerValAlaAlaPheProValAlaAlaĠlyAlaThrCysLeuSerHisSerValAl 376
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οg	139942	4
δy	396	ThrLeuAlaSerLeuTyrHisArgGl
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o o	142521	CCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTG	4
QY Dp	526 526 51 5142581	ralaalaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe 	546 142640
ò	546	rAspLeuAlaLvsTvrSerAla	
Z QQ	14264	CGACTTGGCCAAATACTCAGCG 14	
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Thu Feb

BE034084 2611 bp mRNA linear ROD 07-AUG-2002 Mus musculus, clone IMAGE:4457452, mRNA, partial cds. BC034084.1 GI:21707615 house mouse. Mus musculus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. (Dases 1 to 2611) Strausberg, R. Strausberg, R. Strausberg, R. Strausberg, R. Submitsion Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, Mp 20892-2590,	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Contact: MGC help desk Tissue spebs-femail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford Human Genome Web Site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at: http://image.llnl.gov Series: IRAK Plate: 43 Row: p Column: It. http://image.llnl.gov This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF Location/Qualifiers 1. 2611 / Organism="Mus musculus" //db_xref="taxon:10090" //map="FVB/N" //clone="IMAGE:4457452" //tissue_type="Mammary tumor. Metallothionien-TGF alpha model. 10 month old virgin mouse. Taken by blopsy." //lab_bost="DH10B" //lab_bost="DH10B" //lab_bost="DH10B" //note="Vector: pCMV-SPORT6" //lab_boststart= //product="Unknown (protein for IMAGE:4457452)" //db_xref="C1:21707616" //db_xref="C1:21707616" //db_xref="C1:21707616" //db_xref="C1:21707616" //translation="PRRGWLAGILYPDERRELALLILGYGELDECLFGLILL SDLFRDPDHCRQAFSVYAFMISLGGCLGYILLPAIDWDTSVLAPYLGYLGLILL SDLFRDPDHCRQAFSVYAFWISLGGCLGYILLPAIDWDTSVLAPYLGYLGLILL	a a
BC034084 LOCUS BC034084 LOCUS BC034084 VERSION KEYWORDS ONGANISM BC034084 KEYWORDS ONGANISM Mus musc ENKATYOL Mus musc AUTHORS Strausbe TITLE JOURNAL Gene Col	REMARK NIH-MGC COMMENT Email: C Tissue P Tissue P CDNA Lib CDNA Lib DNA Seque Center, Web site Contact: Dickson, R. M.	Clon thro Seri This Pass pass source CDS	BASE COUNT 519 a ORIGIN Alignment Scores: Score: Percent Similarity: Best Local Similarity: Query Match:

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                                                                                                                                                                                                                                              GlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCySGlyAla
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See Streen, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Barren, B., Linton, L., Nusbaum, C., Canglavi, L., Boukingalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Faro, S., Farzenta, P., FitzHugh, M., Galagan, J., Gardyna, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hullme, W., Illev, I., Johnson, R., Jones, C., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Mackernan, K., Mells, C., Lancocque, K., Liu, G., MacLean, C., Mackernan, F., Major, J., Marquis, N., Matthews, C., McCarthy, M., Mador, J., Marquis, N., Matthews, C., McCarthy, M., Mador, J., Marquis, N., Meneus, L., Mihova, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, T., O'Connor, R., Riere, C., Rogov, P., Roman, J., Peterson, K., Phunhang, P., Pierre, N., Pollara, V., Raymond, C., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strawers, M., Travis, N., Travis, N., Travis, N., Yola, R., Vola, M., Travis, N., Wamn, D., Ye, Wuj, Yola, N., Vola, M., Tavis, N., Wamn, D., Ye, Wuj, Young, G., Shainer, M., Santos, M., Santos, M., Santos, M., Santos, M., Santos, M., Santos, M., Santos, M., Santos, M., Santos, M., Wamn, J., Yola, R., Yola, M., Wilson, B., Wu, X., Wamn, D., Ye, Wu, J., Young, G., Shainer, M., Shainer, M., Santos, M., Sandon, J., Yer, Wu, J., Young, G., Shainer, M., Santos, M., Wamn, J., Wann, J., Yola, M., Wilson, B., Wu, X., Wamn, D., Yer, Wu, J., Yong, M., Man, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M., Wann, M.,
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musculus clone RP23-272H13, WORKING DRAFT SEQUENCE, 13 ordered
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 178567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyr 523
       SerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArgValVal
                                                                                                                                                   484 ProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGln
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP
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Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacCarly, W., McEwan, P., McRernan, K., Melorim, J., Mencas, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nouyen, C., Nicol, R., O'Connor, T., O'Connell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Polizara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Shencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Taalamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo. A., Wilson, B., Wu, X., Wyman, D., Yesmick, J., Robert, C., Milson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Direct, Submission

Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, Ma 02141, USA on Apr 14, 2002 this Sequence version replaced gi:18308540.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft,' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 58509: contig of 58509 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 7.7 in Q20 bases; agarose-fp
Quality coverage: 7.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ap of 100 bp , contig of 49634 bp in length
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73550: contig of 3494 bp in length
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60623: contig of 1064 bp in length
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f 850 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Insert size: 182000; agarose-fp
Insert size: 177367; sum-of-contigs
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79610 58609: gap of 850 bp
79610 59459: contig of 850 bp
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139: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39: gap of 100 bp
69956: contig of 2017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91338: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
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Qy 57 Db 171294 AGGTGTTTATAACACCCACTGAGAGGAGTGTTCTTTTTTTT	170 170 170 170 170	Oy 261 OB 170574 OY 281 OY 301 OD 170454 OY 319 OD 170394 OY 319 OD 170374
	/note="" 81399." /note="" 13385." 127853." /note="" 177587." /note="" 177587." /note="" 201313.29 3.29 3.29 3.29 3.29 3.29 3.23 3.16	US-09-593-793A-113 (1-553) x AC107837 (1-178567) OY

Qy	57	25
QQ	171294	AGGTGTTTATAACACCCACACTGAGAGGAGGAGTCTCTGTGAATGCTGTATGGGGGCT 171235
Qy	58	60 (1) (1) (1) (1) (1) (1) (1) (1) (1) (1)
qq	171234	CTGTGCTGTTTGTCCTTGCAGGCATTGG
ογ	61	ProValLeuGlyLeuValCysValProLeuteuGlySerAlaSerAspHisTrpArgGly 80
ò	00	rgTyrGlyArgArgArgProPheIleTrpÅlaLeuSerLeuGlyIleLeuLeuSerLeu 100
qq	171114	
óγ	101	PheLeuIleProArgAlaGlyTrpLeuAla $\frac{d}{d}$ JyLeuLeuCysProAspProArgProLeu 120
qq	171054	TTCTCATCCCGAGGGCTGGCTGGCTGGCAGGACTGTACCCAGACACCAGGGC
δ	12	euLeuAspPheCysGlyGlnValCysPhe 140
QQ	170994	AGTTGGCCCTGCTGATCTTGGGAGTGGGGCTGCTGGACTTTTGTGGCCCAGGTGTGCTTT 17
δ δ	14	0
a	m	ICCATTGGAGGCCTTACTCTCCGACCTCTTCCGGGACCCAGACCACTGCCGCCAAGCC 17
QY	16	80
qq	170874	CTCTGTCTACGCCTTCATGATCAGCCTTGGGGGCTGCCTGGGCTACCTCTTACCTGCC 1
O.y. Db	181 170814	IleaspTrpaspThrSeralaLeualaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
οy		alAlaAlaThrLeuLeuValAlaGluGlu 220
οqα	170754	SCCTCCTCACCCTCATTTTCCTCATCTGCÁTGGCAGCCACTCTGTTTGTGACGGAGGA
δy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
QQ	170694	STACTGGGCCCACCCGACCGGCAGAGGGTTGTTGGTCTCTGCCGTGTC
Οy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
g	170634	CTGCCCATGCCACGTTGGCCTGGCTTTCCGGAATCTGGGTACCCTGTTTCCCCGGCT
δy	261	isGlnLeuCysCysArgMetProArgThribeuArgArgLeuPheValAlaGluLeuCys 2
g	170574	AGCTGTGCTGCCGCATGCCTCGCACCCCACCTCTTGTGGCTGAGCTGTG
Qγ	281	
qq	170514	GATGGCACTTATGACTTTCACACTGTTCTACACGGACTTCGTGGGAGAGGGCT
ΟŊ	301	GlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHi
QQ	170454	CAGGGTGTACCCAGAGCCGGGCCAGGCAGGCCCGGGGAGACACTATGATGA
δλ	319	319
qa	170394	GAGTCTTTAGCACCAGTGGAAGCTGCTATTGGCGGCTGCCTGC
Qy	319	319
QQ	170334	TTGGGAGATGCTCACAGCCTGGGTGACTCTACCCTGGGTGACTCTACCCTGGGTCCCAGC 170275
Qy	319	319
ď	170274	TOOLOGTICAGTAAAAGGAAAAAGGATOTTOTTOTTATATGCAGTAGCTCATGAACATGAACAGTGCTGCTTGCT

TOTTGSTGACTGGTGGGGTTCTAGGTCTATGGGCTCCAGTTGGATTGGGTGCT 17015 TOCCTGCTGCTTGCTGTGGGTTTTGGTGATCCTTCTAGTTCGGCTTCCTGGAAC 17009 TTAGAGCCAGTGGTTTTGGTGTTTGGATCCCTTCTAGTTCGACATTCCTGTAGT 17003 TTAGAGCCAGTGTTTGGTGTTTTGGATCCCCTTACTCCTTCTTTTTTTT	÷			
199 170154 GTGCTCCTGCTTGCTTTCAGTACTCACAGGCCTTCAGGTTCAGCATTCCAGGAC 17009 139 170094 TGTCTTAGAGCCAGTGGTGTTTTTGTGATCCCCCCCCCC	H	0214 GCTGT	TGGGT	015
170154 GTGCTCCTGCTTCCACTAACTCACCATGCCTTCAGTTCTAGTTCACCACTCACACACTCCACAGAAC 17003 1319 170034 TGTCTTAGACCACTGTGGGGGGCTGTTTTGTGATCCCCCCCC		19		319
319	-	0154	rgccttctagttcagcattccacagaac	o.
170094 TGTCTTAGAGCAGTGTGGGGCTGTTTTGTGATCCCCCACCCCTACATACA		19 -		319
199 170034 TCTTCCCTGGAACATCTTCCTGCCCTTTGTCAACAGCCCTGGTCACCTTGATA 16997 189974 CAATCTAGGTGCTCCTTGCAGGCAGGGGGGGGGGGCCCGGGGCCAGTGCCT 16991 189974 CAATCTAGGTCTCTTGCTCCTTGCAGGCGGGGGGGGGGG		0094 T	ATCCCCCCACCCTTACATACCTTGTACT	03
170034 TCTTCCCTGGAACATCTTCCTGCCCTTTGCAACACGCCTGGTCACCTTCATATTA 169973 189974 CAATCTAGGACATCTTCCTGCAGGGGGGGGGGGGGGCCTGCTCCTTCCT		19		319
199974 CAATCTAGATGCTGCTGCTGCGGGGGGGGGGGGGGGGGG		0034 TCTTCCCTGGAACAT	CAACAGCCCTGGTCACCTTCACTAATTA	6997
169914 CAATCTAGATGCTGTGCTGCAGGGAGGGAGGGCGCCCAGGGAGCAGTGCCCA 1699 319		19		319
319	7	9974	သည	6991
169914 TGGCTACTAGCTCCCCTAGATTGTGTAGGGTCCTTACCCCCTTTCCCTA 16985 320		19		319
320	-	9914 T	STAGGGTCCTTACCCCACTTCTTCCCTA	6985
338 PheserLeuvalMetaspargLeuvalGlnArgPheGlyThrargAlavalTyLLeuala 357 169794 TTCCCCTGGTCAGGCAGGCTGCACAGAGCTGCCCCCGCACAGCGTGGTGT 16973 358 SerValalaalaPheProvalAlaAlaGlyAlaThrCysLeuserHisSerValalaVal 377 169734 AGTGCATGCTGTGGCTGCCGCTGCCCCCCCCCCCCCCCC		320 - 9854 C	PheLeuGlnCysAlaIleSerLeuVal 	79
358 ServalalaalaPheProvalalaalaGlyalaThrCysLeuSerHisSerValAlaval 377 169734 AGTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	-	338	PheGlyThrArgalaValTyrLeuAla 	57 6973
378 ValThralaseralaalaceuThrGlyPheThrPheSerAlaceuGlnIleLeuProTyr 169674 GTGACAGCCTCACCCGGGTTCACCTTCTCGGCCTTCCAGATCCTGCCTTAC 16961 398 ThrLeuAlaserLeuTyrHisArgGluLys	7	358 S 9734 A	ThrcysLeuSerHisServalAlaVal	67
### This control is a read of the control of the co	76	378 9674	CPheSerAlaLeuGln1leLeuProTyr 	97 6961
	7	398		07
GGGCGGCCTGAGTATGTGGCGTCTGACAAGTGATGTTGGAAAAGACTTGGATCTCTCTGA	i	407		07
	16	554 GGGCGCCTGAGTATGTGGCGTCT	ATGTTGGAAAAGACTTGGATCTCTGA	6949
94 CCAGAGGGCCAGAGGCTACAGCCGCTGAAGAAGGGTAGATTCTAGGAAT 16943 97		407		407
	16	9494	CCCCTGAAGAAGGGTAGATTCTAGGAAT	6943
34 GACTTCCTGGCTTTAGAACTAGAAACCACTTGAGTGGATGATTGCAGAAGTGCTGAGTC 16937 37		0		407
	16	9434 GACTTCCTGGCTTTAGAACTAGAAAGCACTT	AGTGGATGATTGCAGGAAGTGCTGAGTC	6937
14 CCTCACTAGGAATCTTGAACAATAAGCATACAGCGGAAGTCCTTTATTCTGGGCTGTATT 16931. 17		407		407
ATTATATCCAGAGGTAGAGTGTGGGTCCCTGGCGTGTGGCTGTGGCAGGTGGCAGTGGAA	16	4	GŢ	6931
ATTATATCCAGAGGTAGAGTGTGGGTCCCTGGCGTGTGGCTGTGGCAGGTGGCAGTGGAA		407		407
	16	9314 ATTATATCCAGAGGTAGAGTGT	GTGGCTGTGGCAGGTGGCAGT	6925
4 ATGCCTGGCCTTAGCTAATCTTTGCTAAGAGGCAATGTGATGGATCTGTATCCTGCT 16919 7		407		407
37	16	54 ATG	GTGATGGAT	6919
94 TGCTGCAAGATGGCGGAGGCTTCTTCCTGCCCCTCTTTCTAGTTTACCTTCTAATC 16913		407		407
	16	34 TGCTGCAAGATGGCGGAGGCTTCTTT	SCCCCTCTTCTAGTTTACCTTCTAATC	169135

407		407	٥y
168055	AGGGACCAGTATGGGGTAAAACCTTGTCTTGTTATTCAGTAGGAAGCCCCAGGCCATTGG	168114	Db
407		407	δy
168115	CTTCCAGCTCTCTGTTGCAACCAGCTTCATCAGCCTTCTGTGTTAGACACCGCCTGGCAC	168174	qq
407		407	Qy
168175	CACTTCCTGAGTTATGGGATGAGCTGATGAGTTGTGGGTTTCTCTGGTACTGCCTGGGAG	168234	qq
407		407	Qγ
168235	GGGTCTATAGCAGTAGCTGGGGACAGGCTTGGTCCTGCATACTGTCCAACTGTCCTTTGC	168294	QQ
407		407	QY
168295	GGGGACCTTTCTAGTAGCCAGCCTTAGTGGCCTTTCCTTGGATGGCAGGCA	168354	qq
407		407	QY
168355	AGCACCTGTGGTTATACCAGGAGTAGCCTTCCTCTGTACTGAGGAACATGTCTGTC	168414	ΟQ
407		407	Qy
168415	TTGACTCTTATGGAGCTCTGGGGCTTTAAAAAGCTGCTGTCCAAAGATGAGGCTTG	168474	qq
407		407	ΟY
168475	TCTGGATCTTTGGAAGAGCAGTCGGGTACTCTTACCCATTGAGCCATCTCACCAGCCCTG	168534	qq
407		407	QY
168535	AGGGCATCAGATCTCGTTATGGATGGTTGTGAGCCACCATGTGGTTGCTGGGATTTGAAC	168594	qq
407		407	Qγ
168595	AAAGATTTATTTATTATTATGTAAGTACACTGTAGCTGTCTCAGACACACCAGAAG	168654	QQ
407		407	Οy
168655	GTGGTGGGGGGTGGTAATGGGAACCTGGTCCTTTCTTTTTTTT	168714	qq
407		407	ΟY
168715	TCAGAGTTAGGAAAGACCTGGCCCTGGCCCACAGCTTGTTCAGCAGTAATTTGCAGGGGT	168774	Dp
407		407	Οy
168775	AAGAAGCACAAGTTGGTGTAGCTTAGGGAAGAGCCACCACCCCTCCCCTTCTAGAGTTT	168834	qq
407		407	Qy
168835	ACCCTGTCTCCAGCACTGTCCTCCCTGAGCTTTAAGGACCTGGATTCAGAACTCCATCAG	168894	qq
407		407	Οy
168895	AACCAGTTCCTGCAGAAGGCCCTCTTCCTTGGCAGGCTTCCTGACTTAGACAGCGTGCTC	168954	Dp
407		407	QY
168955	GAGCTTAATAAGCTGGGGAGGGGGAGAGGCCGGGGCGCTGGCACCTTAATCCACACT	169014	QQ
407		407	Óγ
169015	ATCCTTTTCCTCAATCCCTTCAGTGCATATCTGAGCCTGACATACTAACTTCGTTTACCT	169074	qq
407		407	Qy
169075	CTOTGTGTCTCTCTGTCCCCCCCCCCCCCCCCCTCCTCCTCCT	169134	Db

168054 GGCTTAGGGTTGGTGGAGGGGGGTGGTGACCCTACAGGCATGTGTTCTCTAGTCCTGGC	Oy 539 ThrGlnValValPheAspLysSerAspLeuAlaLys1
407	
16/994 AGCCTACAGGAAGAAATTGAAAAATGTCAGGGTCAGGCAGCTGGGCTGTGGAGGTCAACA	RESULT 21
407	AX200994 2904 bp
167934 AGAAAAAAAAAAAGTTCTCCCTGCTGCTCTCTTTTGTAGGCCCAATTACTGGGCTCT	ION Sequence 624 from Patent ON AX200994
Qy 407 407	VERSION AX200994.1 GI:15390821 KEVWORDS
Db 167874 CCCTGGCCAAAGGCAAAGGCCAAGGCAGTGACCTCGTGTTGAACAGTTATCTCTAGCAGG 167815	ž
Qy 407 407	Eukaryota, Metazoa, Chordata,
Db 167814 CCTGGATCCTAGAGGGCCAGGACAGTGAAGACTTCCCTATGGCCCAGTGGAAGGAA	REFERENCE 1 (bases 1 to 2904)
Qy 407 407	Rolling Reed, S.G., Kalos, M.D., Fangeri, G.R.,
Db 167754 GTGCAGGGGGTTGAGGTAGTCCCTGTGGAACTTGGGACCTCGAAAGCACCTCCTTTGTTT 167695	TITLE Compositions and methods for the th
Oy 407 407	JOURNAL Patent: WO 0151633-A 624 19-JUL-200
Db 167694 GTTTGTTTGTTTGTTTTTGTTTTCCCCCTCTGTTCTTCTGTCTCTATTCTGTCTCAG 167635	
Oy 407 407	/organism="Homo sapiens"
Db 167634 TTTCCTATCTTTTCTAGAGGGCTCTGCACTTTTCTCAATCTGTGGATCTGAGTTGACTGA 167575	ASE COUNT 542 a 875 c 773 g 714
Qy 407 407	C
Db 167574 CTCCTTGTGTATTCTAAGAAAAGCTAGAATAGACTTCAGGCTGTTTCCCCAACCATGTTA 167515	ent scores: No.: 1.43e-116
Ογ 407 407	
Db 167514 AGGGGGTGGGGGTGGGGGTGGAGTCTGCTTGGAATCCACACCAAGTAGCACCTCTT 167455	: 77.23% 67.13%
Qy 407 407	٥
Db 167454 AGGITTIGGATTITITCCCCCCCCGGAAAGCCAGITGCCIGGTTICCTAIAGCCCCIGA 167395	-09-593-
Qy 407 407	Τę
Db 167394 TTAGAGGCAGTGAGGGCCTGTTGTCATATACGGGAATCCCCGCACCTGAATACACACCTG 167335	1 0
Qy 408GlovalPheLeuProLysTyrArgGlyAspThr 418 	UY 183 TEPASPINISSETALALEUATARTOLYTLEUGLYTHU
419 GlydlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438	
Db 167274 GGAGGTAGCAGCGGTGAGGACAGCCAGACAACCAGCTTCTTGCCAGGCCCTAAGCCAGGA 167215	121
Qy 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProPro 458	VY ZZS PEGGYFLOTHESTUFIONAGGIGGETARE Db 181 CTGGCCCCACCGAGCCAGAAGGCTGTCGCCC
Oy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478	Qy 243 ProCysArgAlaargLeuAlaPheArgAsnLeuGlyA
479 GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAgbSerAla 498	Qy 263 LeuCysCysArgMetProArgThrLeuArgÅrgLeuP
SAGGCCAGGGTTGTTACGGGACGG	
Db 167034 TTTTGGTGTCCCAGGTGGCTCCGTCCTGTTCATGGGCTCCATTGTCCAGCTGAGCCAC 166975	Db 361 ATGGCACTCATGACCTTCACGCTGTTTTACACGGATT Ov 303 GlyValDroArd&laGluDroGlyRhrGlualaArd
Oy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIIeTyrPheAla 538	

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linear PAT 29-AUG-2001
                                                                                                       Harlocker, S.L., Jiang, Y.,
., Day, C.H., Retter, M.W.,
and Meagher, M.J.
therapy and diagnosis of prostate
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arrhini; Hominidae; Homo.
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LOCUS AX267729 2904 bp DNA DEFINITION Sequence 703 from Patent WO0173032. ACCESSION AX267729 CHIES16401 VERSION AX267729.1 GI:16516401 KEYWORDS human. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vi REPERENCE 1 Mammalia; Eutheria; Primates; Catarihini;	AUTHORS XUJJ., DILLON,D.C., MICCABM,J.L., HAILOCKEY,S.L., JIANG,Y Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., H and Henderson,R.A. TITLE Compositions and methods for the therapy and diagnosis of cancer JOURNAL Patent: WO 0173032-A 703 04-OCT-2001; CORIXA CORPORATION (US)	Source Location/Qualifie. Source 1. 2904 /organism="Homo ss./db_xreff="taxon:9" COUNT 542 a 875 c 773 g IN nment Scores:	Pred. No.: 1.43e-116 Length: Score: 1920.50 Matches: Percent Similarity: 77.23% Conservat Best Local Similarity: 77.23% Mismatche Query Match: 67.13% Indels: DB: 6 Gaps: US-09-593-793A-113 (1-553) x AX267729 (1-2904)	Qy 163 ValTyralaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp	Qy 203 LeuThrLeuIlePheLeuThrCysValAlaalaThrLeuLeuValAlaGluGluAlaAla	Qy 243 ProCysargAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln	Qy 263 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp	Qy 283 MetalaLeuWetThrPheThrLeuPheTyrThraspPheValGlyGluGlyLeuTyrGln	Qy 303 GlyvalProArgAlaGluProGlyThrGluAlaArgAlgHisTyrAspGluGlyVal	Db 480 TCTGGCTGTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAAGGAAAGGGGG	Qy 321
TCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGAAG	TCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCT 719	ე~ ც	PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368	PheSeralaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln 408	ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448	SerValargValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488 	CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508 	PheMetGlySerIleValGlnLeuSerGlnSerValThralaTyrMetValSerAlaAla 528 	GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeu 548 	AlalystyrSerala 553 	

GI:21700488

540	AGCTTATTCAAAGTCTAGAGGGAGTGGAGGTTAAGGCTGGATTTCAGATCTGCCTGGT 599	KEYWOKUS
321	321	SOURCE ORGANISM
009	TCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAATCTCACCAGCGCCT 659	
321	321	REFERENCE
099	TCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGGCTATGGCCAGCTGTCTTTGTGTTCCCT 719	AUTHORS
321	321	
720	CTCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGC 779	
322		
780	CTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGCGTTCGGATGGGCAGCCTGGGGCTG 839	
	PheteuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348	
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349	PheGlyThrargalaValTyrLeualaSerValAlaalaPheProValAlaalaGlyala 368 	
369	ThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThrGlÿPheThr 388	
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409	ValpheLeuproLysTyrargGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet 428 	
429	ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448 	.•
449	G1yG1ySerG1yLeuLeuProProProProAlaLeuCysG1yAlaSerAlaCysAspVa1	
1700	GONGCHOLDCICCACICCACICGCGCICIGCGGGCCICIGCGIGIGAIGIC 1239	
469	SerValargValValValGlyGluProThrGlualaArgValValProGlyArgGlyIle 488 	TITLE JOURNAL
489	CysteuAspteuAlaileLeuAspSerAlaPheLeuLeuSerGinValAlaProSerLeu 508 	AUTHORS TITLE JOURNAL
509	PheMetGlySerileValGInLeuSerGlnSerValThrAlaTyrMetValSeFAllaAla 528 	REFERENCE
		TITLE
	GIYLƏBGIYLƏBVA IALALIÇIYIR MƏALATIR CINVALYALFINAS PLYSSERASPLƏN 548 	JOURNAL
549	AlalystyrSerala 553 	COMMENT
RESULT 23 AC126523 LOCUS DEFINITION	AC126523 Rattus norvegicus clone CH230-65F14, *** SEQUENCING'IN PROGRESS ***, 65 unordered pieces.	
ACCESSION	AC126523	_

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MASS RELEGY DEVENDED.

MINISTRUCTOR METADOLINE |

MARINEYOLD METADOLINE SCHOOLAGE, Vertebrata Enteleostomi;

MANDROORS S. L., Mariatunge H.C., Arai, JR., Aydele, M., Mariatunge;

Ratus:

10088 MAINTY, D.M. Addis.C., Addio-Odula, B., All-osman, P. R., Allen, C.,

Alstrooks, S. L., Mariatunge; H.C., Arai, JR., Aydele, M. Banks, T.,

Bandria, D., Borde, S., Bircean, M. Banks, T.,

Bandria, D., Borde, S., Bircean, M. Banks, T.,

Carron, P. Carron, T. Caraco, S. R., Chen, C., Thinh, B.,

Doulland, R. R., Delgado, D. Carro, C., Cople, M.D. Bandria, J. Characo, D.,

Carron, T. Cartor, M. Caraco, R. B., Delancy, R., Bonnin, D.,

Doulla, M. L., Devis, C., Devy-Carroll, L., Dederlin, D.,

Doulla, M. L., Devis, C., Devy-Carroll, L., Dederlin, D.,

Earnhart, C., Edgar, D., Edgar, D., Bandria, S., Durbin, K. J.,

Earnhart, C., Edgar, D., Edwards, C., Elbaj, C., Escotro, P., Raris, C.,

Ratlason, E., Maris, R., Hart, M., Havidk, P., Hawes, A., Herrandez, J., Hart, R., Harts, C., Hartis, R., Hart, R., Harth, M., Harth, M., Harth, M., Harth, C., Hartis, C., Hartis, R., Harth, M., Harth, M., Harth, M., Harth, M., Harth, M., Harth, M., Harth, M., Harth, C., Hartis, R., Harth, R., Harth, M., Harth, M., Harth, M., Liu, M., Lad, S., Durbin, K., J.,

Mandria, L., La, Licharge, C., Hartis, R., Harth, M., Marias, M., Miner, G., Mandria, M., Martis, S., Mandria, J., Martis, R., Harth, M., Mandria, J., Martis, M., Martis, S., Mandria, J., Martis, M., Martis, S., Mandria, J., Martis, M., Martis, S., Mandria, J., Martis, M., Martis, S., Mandria, J., Martis, M., Martis, S., Mandria, J., Martis, M., Mandria, J., Martis, M., Mandria, J., Martis, M., Mandria, J., Mandria, J., Martis, M., Mandria, J., Martis, M., Mandria, J., Mandria, J., Martis, J., Martis, M., Mandria, J., Martis, J., Martis, M., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Martis, J., Martis, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mandria, J., Mand
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                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
Assembly program: Phrap; version 0.990329 Consensus quality: 149884 bases at least Q40 Consensus quality: 159599 bases at least Q30 Consensus quality: 166549 bases at least Q30
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1084 181 1144	0y 201 GlyLeuLeu 002	Oy 241 CysCysPrc Db 1324 TGCTGCC Qy 261 HisGlnLeu Db 1384 CACAGCTCT	281 1444 301	No. No.	NISM NCE ORS	(BASE COUNT 17.	Alignment Scores: Pred. No.: Score: Dercent similarity	Best Local Similar Query Match: DB: US-09-593-793A-113	Oy 30 VALCYSLEV DD 379 GTGACATTC OY 45 GLUVAIGHY
GATCCTGCCTTACACGCTCGCTCCTCTACCATCGAGAAGCAGGTACTCCCATT 1631 STyrArgGlyAspThrGlyGly 420 111 GGCTAGATTCGGGGGGGTGGGGGGGGC 163194		artificial sequences. In the sequence of the	a)	Alignment Scores: Pred. No.: 1593 Score: 1696.00 Marches: 1000.00\$ Michaervative: Conservative: Query Match: 59.28* Indels: Gaps: US-09-593-793A-113 (1-553) x AX343860 (1-1593)	 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII 4 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGGGGAACCCCAAAGCCTTTGCTG 663 1 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlylleThrTyrValPro 40 		ProvalLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly		THE CONTROL OF A CONTROL OF THE CONT	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgaspProAspHisCysArgGlnAla 160
Db 163104 Oy 413 Db 163161 RESULT 24	AX343860 LOCUS DEFINITION ACCESSION VERSION VERSION SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE BASE COUNT ORIGIN	Alignment Sc Pred. No.: Score: Percent Simi Best Local S Query Match: DB:	0y 1 0b 604 0y 21	Db 664 Qy 41 Db 724	7	Qy 81 Db 844 Ov 101		Oy 141 Db 1024 Ov 161

Db 439 GAAGTGGGGGTAGAGGA	AAATTGGGGGTAACAACAACAACAACAACAACAACAACAAAAAAAA	_		
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Oy 185 ThrSeralaLeualaPr B59 ACCAGTGCCCTGGCCCC	ThrSeralaLeualaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThr 204 	QY	85 A 	Argarg cccccc
Qy 205 LeullePheLeuThrCy 	LeullePheLeuThrCysValAlaalaThrLeuLeuValAlaGluGluAlaAla ^l LeuGly 224 	oy da	105 A 619 A	ArgAla AGGGCC
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Oy 265 CysargMetProArgTh 	ysargMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284 	Qy	165 A 799 G	AlaPhe GCCTTC
Qy 285 LeuMetThrPheThrLe 	LeuMetThrPheThrLeuPheTyrThraspPheValGlyGlu 298 	oy da	185 T 859 A	Thrser ACCAGT
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AUTHORS Xu,J., Dillon,D Kalos,M.D., Fan Vedvick,T.S., C	Xu.J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H., Vedvick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.	QY	265 C 1099 T	CysArg TGCCGC
	nd methods for the therapy and diagnosis of prostate	QY		LeuMet
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/organism="Homo sapiens"

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Sequence 16 from patent US 6130043. AR112295. AR112295.1 GI:14092195 Unknown.	oy oy		ServalTh TCTGTCAC
Unclassified Unclassified Unclassified RS Billing-Medel, P.A., Cohen, M., Colpitts, T.L., Friedman, P.N., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Kratochvil, J.D., Roberts-Rapp, L., Russell, J.C., Stroupe, S.D. and Yu, H. Reagents and methods useful for detecting diseases of the prostate AL Patent: US 6130043-A 16 10-OCT-2000; Location/Qualifiers U. 2152 Urce Organism="unknown" Voganism="unknown" Voganism="unknown" Voganism="unknown"	RESULT AR1122 LOCUS DEFINI DEFINI ACCESS VERSIO KEYWOR SOURCE ORGA	/22 T 28 294 ITION SION ON RDS E	ACACAGGTY AR11229 AR11229 AR11229 Unknowi
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GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318 	Aligr	Alignment Pred. No.:	Scores:
GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe 338 	Score Percel Best Query	Score: Percent Simi Best Local S Query Match:	Score: Percent Similarity Best Local Similar Query Match:
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AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478 	OY Dp		LeuTyrHis
GlualaargValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerala 498 	da D		Sersergin
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Qy Db	519	ServalThralaTyrMetValScralaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538
Qy	E 0	hrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
RESUI AR11: LOCUS DEFIN ACCES VERS	LT 2 2294 S NITI SSIO ION	AR112294 2143 bp DNA linear PAT 16-MAY-2001 Sequence 15 from patent US 6130043. AR112294.1 GI:14092194
SOURCI SOURCI ORGA REFERI	CCE CANISM CRENCE THORS	Unknown. Unknown. Unclassified. 1 (basss 1 to 2143) Billing-Medel,P.A., Cohen,M., Colpitts,T.L., Friedman,P.
TII JOI FEATU	CE SANA SES	Gordon, J., Granados, E.N., Hodges, S.C., Klass, M.R., Krato Roberts Rapp, L., Russell, J.C., Stroppe, S.D. and Yu, H. Reagents and methods useful for detecting diseases of th Patent: US 6130043-A 15 10-0CT-2000; Location, Qualifiers
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Qy	302	GINGIYVAIProArgAlaGluProGlyThrGluAlaA ⁱ gArgHisTyrAspGluGlyVAl 321
ζ D	322	ArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaileSerLeuValPheSerLeuVal 341
Qy F	342	TyrLeuAlaSerValAlaAla 36
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Qy	422	SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
Oy d	442	ProksnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCys 461
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	Qy 268 ProArgThrLeuArgArg-LeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetTh 287 11 1 1 1 1 1 1 1 1	Oy 287 rPheThrLeu	Qy 295 eValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgAr 315	Qy 315 gHisTyraspGluGlyValargMetGlySerLeuGlyLeuDheLeuGlnCysalaIleSe 335 ::	Qy 335 rLeuValPheSerLeuValMetAspargLeuValGlnArgPheGlyThrArgAlaValTy 355	Qy 355 rLeualaserValalaAlaPheProValalaAlaGlyAlaThrCysLeuSerHisserVa 375 	Qy 375 IAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLe 395 	Qy 395 uProfyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrAr 415	Qy 415 gGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyPr 435	Qy 435 oLysProGlyalaProPheProAsnGlyHis [†] valGlyAlaGlyGlySerGlyLeuLeuPr 455 	Qy 455 OProProBroAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValG1 475	Qy 475 yGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLe 495 	Oy 495 uaspseralaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGl 515	Qy 515 nLeuSerGlnSerValThralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIl 535 	Qy 535 eTyrPhealaThrGlnValValPheaspLySerAspLeuAlaLySTyrSerAla 553 	AX106229 N Sequence 10 from Paten AX106229	VERSION AX106229.1 GI:13921915 KEYWORDS SOURCE human. COURCE human. COURCE human. COURCE Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Db 483 GGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGG 542	Oy 482 ValValProGlyArgGlyIleCysLeuAspLeuAspleuAlalleLeuAspSerAlaPheLeuLeu 501 	Qy 502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 521	Oy 522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 541 	Oy 542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553 		TION HOMO SAPLENS MKNA; CUNA DKFZP666UUIIU (IIOM CIONE DKFZP ION AL832933 AL832933.1 GI:21733520 DS	_	CE I (bases 1 to 2477) RS Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann Direct Submission AL Submitted (09-JUL-2002) 1, D-85764 Neuherberg, GERMANY	CUMMENT CLONE Trom S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ): Email S. Wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the CDNA sequencing consortium of the	:11n. 14059 her	Antonmarion about the cione and the sequencing project is available at http://mips.gsf.de/proj/cDNA/. FEATURES Location/Qualifiers source 12477		/Cince_ilb="bbb (synonym: nstoz). Vector psport; nost DH10B; sites Not1 + Sal1" /dev_stage="adult" polyA_signal 24252430	Site 244/ 505 a 713 c 634 g 625 t		St Local Similarity: 76.11% Mismatches: 29 ery Match: 41.23% Indels: 45 ery Match: 5 9 Gaps: 5	OY 228 POALAGIUGIYLOUSERALAPTOSEKLEUSERFPOHISCYSCYSPIOCYSARGAIAAEG 247

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( Dases 1 to 789)

Xu, J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y., Reed,S.G., Kalos,M.D., Retter,M.W., Stolk,J.A., Day,C.H., Skeiky,Y.A. and Wang,A.

Compositions and methods for the therapy and diagnosis of prostate
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Sequence 10 from Patent WO0151633.
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Location/Qualifiers

1. 789
/organism="Homo sapiens"
/db_xref="taxon:9606"

122 a 250 c 221 g 182
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Wertebrata; Buteleostomi; nl; Hominidae; Homo. ocker,S.L., Jiang,Y., y.C.H., Retter,M.W., agher,M.J. py and diagnosis of prostate	6: 192 2 7 7 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	JyalathrCysLeuserHis 373 	1		rrLeuPheMetGlySerIle 513
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ACCESSION VERYWORDS SOURCE ORGANISM AUTHORS TITLE JOURNAL FEATURES SOURCE BASE COUNT ORIGIN	Alignment Scores Pred. No.: Score: Percent Similari Best Local Simil Query Match: DB: US-09-593-793A-1	Qy 354 Db 3 Qy 374 Db 63	Oy 394 Db 123 Oy 414 Db 183 Oy 434	Db 243 Qy 454 Db 303 Qy 474 Db 363	Oy 494 Db 423 Oy 514 Db 482 Oy 534 Oy 534

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26-OCT-2001
                                                                                         Xu,J., Dillon,D.C., Mitcham,J.L., Harlocker,S.L., Jiang,Y.,
Kalos,M.D., Fanger,G.R., Retter,M.W., Stolk,J.A., Day,C.H.,
Vedyick,T.S., Carter,D., Li,S.X., Wang,A., Skeiky,Y.A., Hepler,W.T.
and Henderson,R.A.
                                                                                                                           Compositions and methods for the therapy and diagnosis of prostate
                                                         Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Patent: WO 0173032-A 10 04-OCT-2001;
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AC126523/c DEFINITION

RESULT 34

ORGANISM

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ACCESSION VERSION

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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 65 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                    runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                            Sequencing vector: Plasmid; Chemistry: Dye-terminator Big Dye: 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 149884 bases at least Q40 Consensus quality: 159599 bases at least Q30 Consensus quality: 166549 bases at least Q20
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gap of unknown length
contig of 1162 bp in length
                      Web site: http://www.hgsc.bcm.tmc.edu/
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                                  Contact: hgsc-help@bcm.tmc.edu
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Rattus norvegicus clone CH230-65F14, *** SEQUENCING IN PROGRESS
***, 65 unordered pieces.
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                                                                                                                                                                                                                                                Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
AC126523.1 GI:21700488
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Rattus norvegicus
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198037	208	34	147	113	17	
 Length.	Matches:	Conservative:	Mismatches:	Indels:	Gaps:	(1-198037)
4.336-33	673.00	48.30%	41.52%	23.52%	2	53) x AC126523
Alignment Scores:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:	US-09-593-793A-113 (1-553) x AC126523 (1-198037)

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/note="transporter"
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Strausberg,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-shgc.stanioiu.euu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                             59431 TAGGCCCTAAGCCAGGAGCTCCCTTCCCCAATGGACACGTGGGCCCTGGCGGCAGCAGCA 59372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 59 Row: p Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF
                                                                      493
433 roGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyL 453
                                                        euLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValV 473
                                                                                                                                                                       laIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerI 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       month old male mouse."
                                                                                                                alValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuA
                                                                                                                                                                                                                                                                                                                                                          Mus musculus, clone IMACE:4984191, mRNA, partial cds.
BC024519
BC024519 1 GI:19353990
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<1. .340</pre>
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Fukamachi, S., Shimada, A. and Shima, A. Mutations in the gene encoding B, a novel transporter protein, reduce melanin content in medaka
Nat. Genet. 28 (4), 381-385 (2001)
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Fukamachi, S., Shimada, A. and Shima, A.
Direct Submission
Submitted (13-MAR-2001) Integrated Biosciences, University of Tokyo, Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCys
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Mus musculus B/AIM-1-like protein mRNA, complete cds.
AF360357
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Mismatches:
Indels:
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	AY0343 AY0343	ACCESSION VERSION	ACC
-JAN-200 mRNA,	AY034377 1998 bp mRNA linear ROD 21-N Mus musculus membrane-spanning transport protein 1 (Mstpl)	RESULT 37 AY034377 LOCUS DEFINITION	AYO. LOCI DEF
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382	ProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAla :::	363	о о
1228	AAAGCTATGGTCTCCTACATTGGATTAAAAGGCCTTTATTTCATGGGATATTTGCTCTTTTT	1169	qq
362	AspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPhe	343	Οÿ
342	MetGlySerLeuGlyLeuPheLeuGlnCysAlaileSerLeuValPheSerLeuValMet	323 1109	Qy Dp
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322		303	Οy
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898	: :: Tattgagaagttaaaaatggaggtg	808	qq
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Mus musculus. Mus musculus Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1998) Newton, J. M., Cohen-Barak, O., Hagiwara, N., Gardner, J. M., Davisson, M.T., King, R.A. and Brilliant, M.H. Mutations in the human orthologue of the mouse underwhite gene (uw) and J. Hum. Genet. 69 (5), 981-988 (2001) 11574907 2 (bases 1 to 1998) Newton, J. M., Cohen-Barak, O., Hagiwara, N., Gardner, J. M., Davisson, M.T., King, R.A. and Brilliant, M.H. Submitted (11-MAY-2001) Pediatrics, University of Arizona, 1501 N	Campbell	/map="between D15Mit10 and D15Mit179" 1. 1998 /gene="Mstp1" 18. 1610 /gene="MsTp1" /note="MSTp1" /codon_start=1 /product_="membrane-spanning transport protein 1"	/db_xref="G1:18252806" //translation="MSGSNGPTHTYQSLAEDCPFGSVEQPKRSTGRLVMHSMAMFG //translation="MSGSNGPTHTYQSLAEDCPFGSVEQPKRSTGRLVMHSMAMFG //translation="MSGSNGPTHTYQSLAEDCPFGSASDHCRRWGRR RPYILTLAIMMLLGMALXLNGDAVVSALVANPRQKLIWAISITMVGVVLFDFSADFID GPTRAYLFDVCSHQPRKGHLHYAHALFTGFGSALGALGXILGGADWHLDDFGRLGGFEGQVM FFFSALVLILCFTTHLCSIPEAPLRDAATDPFSQQDPQGSSLSASGHHEYGSIEWKN GGADTEQPVQEWRNKKPSGQSQRTMSMKSLLRALVNMPSHYRCLCVSHLIGWTAFLSN MEFFTDFRAQIYYHGDPYGAHNTYSTEVLISWFGVSYGSTYSFPGKAMV SYIGLKGIYFMGYLLFGLGTGFIGLFPNYYSTLVLCSMFGYMSSTLYTVPFKLIAEYH REEKKKGQEAPGGPDNQGRGKGVDCAANTYSTLVLCGSMFGYMSSTLYTVPFKLIAEYH REEKKKGQEAPGGPDNQGRGKGVDCAANTCMYQLAGILVGGGLGFLVNMAGSVVVVV	misc_feature ITASAVSLIGCCFVALFVRYVD" 126. :212 /gene="Mstp1" /note="transmembrane domain 1; transmembrane-region site" 225. :284 /gene="Mstp1" /gene="Mstp1" /gene="transmembrane domain 2; transmembrane-region site" misc_feature 336. :401	/gene="Mstpl" /note="transmembrane domain 3; transmembrane-region 400. 482. /gene="Mstpl" /note="transmembrane domain 4; transmembrane-region 567. 632. /gene="Mstpl"	### Arches"Kransmembrane domain 5; transmembrane-region site" foote=".rtansmembrane domain 6; transmembrane-region site" foote=".rtansmembrane domain 6; transmembrane-region site" foote=".rtansmembrane domain 7; transmembrane-region site" foote=".rtansmembrane domain 7; transmembrane-region site" foote=".rtansmembrane domain 8; transmembrane domain 8;	/note="transmembrane domain 9; transmembrane-region site" misc_feature 12841340
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TITLE Use of an in vitro immunoselected tumor line to identify shared melanoma antigens recognized by HA-A*0201-restricted T cells JOURNAL Cancer Res. 61 (3), 1089-1094 (2001) EDITOR 11221837 TOURNAL SUBMISSION TITLE 1 Conservation Pike, Bethesda, MD 20892, USA Location/Qualifiers 1 Conservation Pike, Bethesda, MD 20892, USA Location/Qualifiers 1 Conservation Pike, Bethesda, MD 20892, USA FEATURES COGADISMAL SUBMISSION SURGERY BRANCH, National Cancer Institute, 9000 Rockville Pike, Bethesda, MD 20892, USA Location/Qualifiers 1 Conservation Pike, Bethesda, MD 20892, USA Location/Qualifiers 1 Conservation Pike, Bethesda, MD 20892, USA Codanisma Homo sapiens 1 Conservation Pike, Bethesda, MD 20892, USA Alssue_type="molanoma"	BASE COUNT 363 a 429 c 437 g 421 t ORIGIN Alignment Scores: 3.14e-23	48 ValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCys i:::::
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574	184	204	694	224	244	802	246	865	254 925	274	985	294	1045	314	334	1165	354 1225	374	1285	394 1345	₹*	1393	434	454	1420	474	1435	464	1459
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518	165 575	185	635	205	225	752	245	808	247	255	926	275	986	295 1046	315	1106	335 1166	355	1226	375 1286	395	1346	415	435	1412	455	1421	475	1436
QQ	Oy Op	Οy	Q	Oy Dp	ογ	QQ	ογ	QQ	0,y	δý	gg	ογ	Ω	Qy Dp	Οy	qq	oy D	0y	g	Qy Dp	γo	a	S S	οy	Dp	٥y	QQ	ογ	qq

ACU18319 18567 bp pNA linear HTG 09-DEC-1999 Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered pleces. ACO18319
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BTG: HTGS_PHASE2.

Drosophila melanogaster.

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Ephydroidea; Drosophilidae; Drosophila.
Ephydroidea; Drosophilidae; Drosophila.
Endams, M. and Venter, J.C.
Direct Submission
E. Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, 14261 CGGAAGACGCGGTTCGATGTTTCGATTGTCCGCCATGGCCATGGCCATTGAATTTGCC 14320 ||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::|| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::|| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::||| :::|| LeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleVal 514 515 GlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAla 534 submitter ArgHisArgLysAlaGlnLeuLeuValAsnLeuLeuThrPheGlyLeuGluValCys 31 51 71 This sequence was identified as CDM:10214336 by the submitter. For more information on this record e-mail to fly@celera.com.* NOTE: This is a "working draft' sequence.

* This sequence will be replaced 32 LeuAlaAlaGly11eThrTyrValProProLeuLeuGluValGlyValGluGluLys PheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeu by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
1. 18567 18567 166 101 247 200 19 /organism="Drosophila melanogaster" /db_xref="taxon:7227" 3897 c 3763 g 5202 t Length: Matches: Conservative: Mismatches: Indels: LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro US-09-593-793A-113 (1-553) x AC018319 (1-18567) Gaps: 1580 TGTTGCTTTGTCGCTCTTTGTT 1603 542 535 IleTyrPheAlaThrGlnValVal 3.71e-20 458.50 37.39% 23.25% 16.03% Rockville, MD, USA Percent Similarity: Best Local Similarity: ø 5705 Alignment Scores: Pred. No.: Query Match: DB: source LOCUS DEFINITION BASE COUNT ORGANISM REFERENCE AUTHORS TITLE JOURNAL 495 12 52 72 14441 92 ACCESSION RESULT 39 VERSION KEYWORDS SOURCE AC018319 FEATURES COMMENT ORIGIN pp QQ g g ò δ d Dp q δλ ò g δ δy Qγ

;	105		Qy
÷	0	COT DIV.	Db 15
g	14561	CTGCTTGGCGATGCCGGATATACTTATGCAGAGTCAGCCTTGAATTTCACATCTTCGTCG 14620	> 0
දු ද	106	AlaGlyTrpLeuAlaGlyLeuLeuCys	57 Db 15
λά do	120		Oy Db 19
දු ස	138	ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys	Qy Db 15
දු දු	158 14798	ArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeu :::	Oy Db 15
λα Q	178 14858	LeuProalaileaspTrpAspThrSeralaLeualaproTyrLeuGlyThrGlnGluGlu 197 ::: ::: :::	Oy Db 15
oy Ob	198 14918	CysLeuPheGlyLeuLeuTlePheLeuThrCysValAlaAlaThrLeu' 215 ::: :::	Oy Db 15
λo qo	216	TTCCGTGAAATTCCATTGCTTGATCGAGGAGGATGACCTGTGACGAA 15037	Oy Db 16
δà	225		
g	15038	CAGGCCATCAAGAAGAAGTTGAAAAAAAAAAAAAAAAAA	Dp 16
g g	226	ThrGluProAlaGluGly 231	Qy Db 16
λ	232	LeuSerAlaProSerLeuSerPro	
g	15158	AGCTATCAGAATGGCTATTCACCCGCTGTGGAGAAGCAAGGGAAATCCCAGGAȚTTGGAG 15217	ag is
à a	240	HisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAla 255	27 Db 16
à	256	LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArdLeuPhe	Qy Db 16
ą	15278		RESULI
ž g	276 15305	ValalaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThfaspPhe 295 :::	AC0100 LOCUS DEFINI
λζ Q	296 15365	ValGiyGluGiyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArg 315 GTGGGTGAGGCAGTTTTCCACGGTGATCCCACGGCTGCTCCCAACTGGAAGCTGCTCTC 15424	ACCESS VERSIC KEYWOF
5. 2.4	316 15425	HisTyraspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlålleSer 335 ::: :::	SOURCE ORG\$
င် ရ	336 15485	LeuvalpheserLeuvalmetAspargLeuvalGlnArgPheGly 350 ::::: :: :: :::: TCCATTTACTGGCTGTGGTGACCAAGTTAATGAAGTGGTTGGGGTAAGTAGGACACTA 15544	REFERE AUTE
දු ද	351	351	
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oy Op	360	AlaAlaPheProValAla 365 :: AATAGATTATAAAGACAAATTCAGATCTTGGTATTAAACAAATGAGGTTTTTCATTGACT 15664
Qy	366	AlagiyalaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThr 385
QQ	15665	GTTGGCAAACAGTGTACGAACTTGCAAACTGTCAAG
Οy	386	
QQ	15707	TTTACCTTTAAAATTCTTAAAGACAGTAGCTTTGATTAACCACCTGAGCTATAATAT 15763
Qy	393	397
QQ	15764	GTTGACGTCTGCTTCCAAATCGAATATCTAAAAGAAATCCAAATGTATTGAATATATT 15823
QY	398	
q	15824	GTTAACCGTGATTATCTCGCTCTTTTTTAGAACCAAGGCGGTTTACATTAGTGGAATGAT 15883
Qy	414	424
QQ	15884	TIACTATGGTATCGGAATGCTTGTCCTGGGCTTGTGGCCAACTAAGTGGGGAGTCTTGGT 15943
Qy dy	424	uaspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 441
3 6		191
6 6	16004	FIGNSIGLYALEVALGETYALGGETYSEGETY FOR THE THE GEOTTERANDICT 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
οy	461	sGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaAr 481
qq	16064	TITAATCAAAATATGTTAATTTCAGTTCTCTATTAAGAATGGAGAG 16109
Qy G	481	gvalvalproGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAl 498 ::: -ATAGTACCACTGAAACAGGCTCGTGGATTGGGCACTGATGGGCCATTATCAGCAGTAT 16168
ò	498	aPheLeufenSerGlnValAlaProSerLeuPheWetGlvSerIleValGlnLeuSerGl 518
g 20	9	GGTTTTATTGCCCAGTTGATGTATCCCTTCGTGGGTCCTTTGGTATCCTGGATGGA
Οy	518	nSerValThrAlaTyrMetValSerAlaAlaĠlyLeuGlyLeuValAlaIleTyrPheAl 538
QQ	16229	CACAACTIGFGCCGTGCTCTACGCCTCGACGTTTCTGTCCTTTTTGGCGGCCATTGCAGC 16288
Qy	538 16289	aThrGlnValValPheAspLysSerAspLeuAla 549
RESUL ACO10 LOCUS DEFIN	RESULT 40 AC010022/C LOCUS DEFINITION	
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•	AUTHORS	
		Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E.,

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Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Jackson, B., Jácky, Johnson, R., Jalivk, S., Hume, J., Jackson, B., Jácky, Johnson, R., Jackson, B., Jácky, Johnson, R., Jackson, B., Jackson, B., Jackson, B., Jackson, B., Jackson, B., Jackson, B., Jackson, R., Jackson, J., Karlsson, E., Karlsson, E., Karlsson, E., Karlsson, E., Lind, L., Lind, L., Lind, L., Lind, R., Lind, C., Liu, J., Liu, M., Liu, M., Laal, B., Lewis, L. C., Lous, Seged, H., Lozado, R.J., Licter, A., Lucier, R., Luna, R., Martinez, E., Makhiney, E., Mached, M., Marsey, E., Mached, M., P., Meador, M., Marsey, E., Machedo, M., Massey, E., Machedo, M., Massey, E., Machedo, M., Mohabbat, K., Morgan, M., Morris, S., Moser, M., Nedl, D., Newtson, J., Newtson, N., Nayen, M., Nayen, N., Nayen, N., Nayen, N., Nayen, N., Nayen, N., Nayen, N., Nayen, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quilses, M., Ren, Y., Rives, M., Rojas, A., Stanley, H., Shooshtari, N., Stanley, H., Savery, G., Scherer, S., Soqtt, G., Shen, H., Struch, A., Stanley, H., Tansey, J., Taylor, C., Taylor, T., Talfrod, B., Thomas, S., Usmani, K., Vasquez, L., Varae, L., Vallalon, D., Vinson, R., Wall, R., Wang, S., Ward Moore, S., Warren, R., Washington, C., Walliams, S., Wall, R., Wu, Y.

Direct Summission

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Worley, K.C., Addins, C., Are, J.R., Banks, T., Barbaria, J.,

Benton, J., Bingage, K., Bindenburg, K., Bonnih, D., Bouck, J.,

Benton, J., Bingage, K., Bindenburg, K., Bonnih, D., Bouck, J.,

Burch, D., Burtett, C., Burcall, K.L., Brdw. C., Carron, T.F.,

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> 4 (bases 1 to 165852) 3 (bases 1 to 165852) Worley, K.C. Direct Submission Unpublished TITLE JOURNAL JOURNAL AUTHORS REFERENCE TITLE

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% (bases 1 to 100032)
Box 1 to 100032)
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99201 CGGAAGACGCGGTTCGAGATGTTTCGATTGTCCCCCATCGCCATGGCCATTGAATTTGCC 99142 99081 CACATGTCCATGACCTGGGGACTGTCGCCACTGATTGGATTCTTTATGTCCCCGCTGCTG 99022 98961 CTATCATTTGGCATAATGTGGGGTTTGATTCTGGTGCCATATGGCAAGGATCTGGGTCTG 98902 98901 CTGCTTGGCGATGCCGGATATACTTATGCAGAGTCAGCCTTGAATTTCACATCTTCGTCG 98842 98841 GGGGGATCTGTGGTTTGGTTTTCGGGTGAAGCGACGACGACGTTTCTGCATCCGAC 98782 106 AlaGlyTrpLeuAlaGlyLeuLeuCys-------ProAspProArgPro 119 32 LeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGlyValGluGluLys 51 52 PheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71 12 ArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPheGlyLeuGluValCys 31 LeuSerLeuGlyIleLeuLeuSerteuPheLeuIlePro-------Conservative: Mismatches: Indels: Length: Matches: US-09-593-793A-113 (1-553) x AC010022 (1-165852) 3.77e-19 458.50 37.39% 23.25% 16.03% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match 92 105 Score: ò g අ q g g 셤 ò ò ò ò à ò

δy	120		
Оp	98781	GTTCGCCGTGATCCTTACGATTTTGGGCATGGTCCTATTGGATTT	98722
Qy Db	138	ValCyspheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys	157 98665
δy	158	rValTyrAlaPheMetIleSerLeuGlyGlyCysLv	177
qq	98664	CTCTTCGCGGGATTCGGCGGCACGATTGGATA	98605
δy	178	LeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGlu	197
QQ	98604	ATTGGAGGAGTGGATTGGGAGACACACATATTGGCAGCTTCATGGGTGGCAATATACCC	98545
Οy	198	CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu	215
QQ	98544	ACTGTATTCACCCTGGTCACCATCATTTCGCGGTGTGCTATCTTATCACGGTGACCACA	98485
δλ	216		225
qq	98484	TTCCGTGAAATTCCATTGCCCTTGATCGAGCAGGATGAGCTGCTGAGACCGCTGTCCGAA	98425
δλ	225		225
Dp	98424	CAGGCCATCAAGAAGGAGTTGAAAAAGAAGAACAATAACCATTTACTATATCCAGGAGACC	98365
ογ	226	ytania in in in in in in in in in in in in in	231
QQ	98364	ACACAGCTGGAGCTTCAGATGGCCAGTGATGCCCAAGCGATTGGAGGCACTGCAAGGC	98305
δy	232	LeuSerAlaProSerLeuSerPro	239
Dp	98304	AGCTATCAGAATGGCTATTCACCCGCTGTGGAGAAGCAAGGGAAATCCCAGGATTTGGAG	98245
ΟŽ	240	gLeuAlaPheArgAsn	255
qq	98244	ACCCAGTCGGATTACGATGCTCCCGTCTCCCTTAAGGCCTATCTCAAGAGCATCTTCATC	98185
δy	256	LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe	275
QQ	98184		98158
δy	276	AlaGluLeuCysSerTrpMetAlaLeuMet 	295
Dp	98157	CACCTATTGCCTGTACTTCACGGACTT	86086
Qy Db	296	ValGlyGluGlyLeuTyrGlnGlyValProÁrgAlaGluProGlyThrGluAlaArgArg	315 98038
Qγ	316	HisTyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlalleSer	335
QQ	98037		97978
ΟŸ	336	1PheSerLeuValMetAspAr	350
Db	97977	CGCTGTCGGTGACCAA	97918
QY	351	ThrArgAlaValTyrLeuAlaSerVal	359
qq	97917	CTAAAAATGCCATCGGAATTTGTTTAAGTGTAAACATCATTTTTCTTGCTTTGGTCAACA	97858
δλ	360	AlaAlaPheProValAla	365
οg	97857	AATAGATTATAAAGACAAATTCAGATCTTGGTATTAAACAAATGAGGTTTTTCATTGACT	97798
δλ	366	AlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThr	385
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COMMENT

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clones are only CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage. SEQUENCING READ COVERAGE: Sequencing is completed to a minimum

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found

at URL: http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annot 176929 166 101 247 200 melanoqaster Conservative: Mismatches: /function="polymorphic site" a 36803 c 36491 g 50820 t US-09-593-793A-113 (1-553) x AC091203 (1-176929) Matches: Indels: 1. .176929 /organism="Drosophila /db_xref="taxon:7227;" /chromosome="3L" /note="BCM C/CELERA Location/Qualifiers /clone="RP98-48N8" 34056 4.03e-19 458.50 37.39% 23.25% 16.03% Similarity: ation.html 52815 Percent Similarity: misc_feature Alignment Scores: Query Match: BASE COUNT Best Local Pred. No.: FEATURES ORIGIN

Department

21 32 LeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGlyValGluGluLys g Dp

52 PheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeu 71 g δ

72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91 g δý

LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro-92 ŏ

105 g ò

15421 CTGCTTGGCGATGCCGGATATACTTATGCAGAGTCAGCCTTGAATTTCACATCTTCGTCG 15362 106 AlaGlyTrpLeuAlaGlyLeuLeuCys---;-------ProAspProArgPro 119 g

Вb ò

15301 TATAAGTTCGCCGTGATCCTTACGATTTTGGGCATGGTCCTATTGGATTTCGATGCGGAT 15242 LeuGluLeuAla-----LeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGln 137 120 Dρ δ

138 ValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCys 157 15241 ACCTGCCAGACACGGCTCGCACTTATTACTGGATATGTGT----GTGCCAGAGGAGCAG g δ

158 ArgGlnAlaTyrSerValTyrAlaPheMetileSerLeuGlyGlyCysLeuGlyTyrLeu 177 δ

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CysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu----δλ

15064 ACTGTATTCACCCTGGTCACCATCATATTCGCGGTGTGCTATCTTATCACGGTGACCACA 15005 --LeuValAlaGluGluAlaAlaLeuGlyPro----216 Qγ

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δγ	276	ValalaGluLeuCysSerTrpMetalaLeuMetThrPheThrLeuPheTyrThraspPhe ::	295 14618
è	296		315
r qq	14617	TITELY TO THE TENED TO THE TENED TO THE TENED TO THE TENED THE TENED THE TENED THE TENED THE TENED THE TENED TO THE TENED THE	14558
ò	316		335
q	14557	:::	14498
ò	336		350
g q	14497	TCCATTTACTCGCTGTCGGTGACCAAGTTAATGAAGTGGTTCGGGTAAGTCGGCACACTA	14438
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ò	386	$_{ m G1y}$	392
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QQ	14218	GTTGACGTCTGCTTCCAAATCGAATATCTAAAAGAAATCCAAATGTATTGAATATTATAT	14159
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Οy	442	-ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCy	461

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Subsophila melanogaster.

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Bucsophila melanogaster.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           518 nSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAl 538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 54, complete sequence.
AE003552 AE002602
AE003552.2 GI:10728030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
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gene	mRNA	CDS			gene	mRNA	CDS				gene	mRNA	CDS
	: :												
Gibbs, R.A., Myers, E.W., Rubin, G.M. and Venter, J.C. The genome sequence of Drosophila melanogaster Science 287 (5461), 2185-2195 (2000)	10731132 2 (bases 1 to 286784) Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. Direct Submission	Submitted (1-MAY-2000) Cetera Genomics, 45 West Gude Drive, Rockville, MD, USA On Oct 9, 2000 this sequence version replaced gi:7294927. Location/Qualifiers	3		/product="CT14602" /db_xref="FLYBASE:FBan0004484" /db_xref="FLYBASE:FBan0035968" complement(join(1301213233,1329413468,1379415196)) /gene="CG4484"	/codon_state=1 /protein_id="AAF50310.1" /db_xref="GI:7294981" /db_xref="FIYBASE:FBan0004484"	/UD_XTEL="FLYBASE: FBGNUSJS988" /Lranslation="WVGVTADASQANQLSSVRNPMIKYMLKTRENHAREQDRDYSHVF RRKTRFEMFRLSAIAMALEFAYABETLSFVSPTLLQIGVDHKHMSMTWGLSPLIGFFMS PLLGSISDRCKLRWGRRRPIISILSFGIMCGLILVPYGKDLGLLLGDAGYTYAESALN FTSSSGGSVAALVSGEATTGPSASDYKFAVILTILGMVLLDFPADTCQTPARTYLLDM	CYLITYTFREIPLD-LIEGDELLRPLSEGAINGETHIGSENGGAIPTVFTLYTIIFAV CYLITYTFREIPLD-LIEGDELLRPLSEGAINGETHKNNYTIYTOETTQLELQMASD DPRRLEALQGSYQNGYSPAVENGGRSQDLETQSDYDAPVSLKAYLKSIFIMPYSHRML ALTNLFCWMGHVTYCLYFTDFVGEAVFHGDPTAAPNSEAALNYEAGVRFGCWGMAIYA FSCSIYSLSVTKLMKWFGTRAYYISGMIYYGIGMLVLGLWPTKWGVLVFSTSAGILYG TIFTYDFILLVARYHAKNFCTRAYYISGMIYYGIGMLVLGLWPTKWGVLVFSTSAGILYG DINSUMNTTCAUTNAGNFISFILAATAAMWVIYV		/uc.rtel= Fibaba::Fbguru33999 joun(2256822896,2309424 /gene="CG4476" /product="CT14566" /h. voof="ETVBSG: EPG20004476	/db_xret="firbass::Banloud44/0" /db_xref="Firbass::Bandoud44/0" join(2261422896,2309424158,2429024466,2453224788) /gene="CG4476" /note="CG4476 gene product"	/cooicraft_1 /protein_id="AAF50309.1" /db_xref="G1:7294980" /db_xref="FLYBASE:FBan0004476" /db_xref="FLYBASE:FBgn0035969" /dranslat_in="MALESSELSPDRKADNWGSSLEFLMSCIALSVGLGNVWRFPFT /translat_ip="Invitation""MALESSELSPDRKADNWGSSLEFLMSCIALSVGLGNVWRFPFT /Lanslat_ip="Invitation""MALESSELSPDRKADNWGSSLEFLMSCIALSVGLGNVWRFPFT /LENGGGAFLTPYLVVIFPYLYVRMIJGGPSSRGTVOVPFPAPIMRGVGYAGIL.	ALGVLATYTASVMALTLRYFFDSFASELPWSFCREEWGDGCVGASGGQPLQGQLSRNF SSSTQLYLQRTVLNETDSEGTGYPSGSLALMIGISMLTYTLIIRGVKSSGRAAY LALFPYVWRTILLVRALTLPGAYDGSSLALMIGISMLTYTLIIRGVKSSGRAAY LALFPYVWRTILLVRALTLPGAYDGSSCALMIGISMLTHIIRGVKSSGRAAY GVIIMYSSYNRFGHWYRDANIYTTLDYFTSLLGOWKLIFDQWYNAVTQVFFSLAVCF GVIIMYSSYNRFGHWYRDANIYTTLDYFTSLLGOWITGILGMLAHESGTKDLASVV KAGPGLAFISYPDAIARFKMFQVFSLLFFAMLEMLGVGSNVGMYSCIMTVLKDQFVN VKLMIIVVSLSVIGFLUGGLIYTTPGGQHITTLMPHGYTFVSLANFALSGTEJAVGMIYG TKRLCODAEYMLNIFGSNYYRLGWSIYTPLWALVILVSCSLLMRPLSYNGGFPLVYR VVGWCVSGCIIGQLFYWAGYANFKQPKGSLKSRINNSIKPHSJMGPSDPKKLMDYQMF
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ý g	-	ArgHisArgLysAl	laGlnLeuLeuLeuV.	aGlnLeuLeuLeuValAsnLeuLeuThrPheGlyLeuGluValCy	eGlyLeuGluValCys	
2	206	CGGAAGACGCGGT	TCGAGATGTTTCGAT	GGAAGACGCGGTTCGAGATGTTTCGATTGTCCGCCATCGCCATGGCCATTGAATTTGC	GGCCATTGAATTTGCC	15002
oy D	32	LeuAlaAlaGlyIl TATGCGCGGAGAC	leThrTyrValProP :::::: CGAGTTTCGTCTCTC	eThrTyrValProProLeuLeuGluValGlyValGluGl :::::: ::: :: GAGTTTCGTCTCCGATTCTCCTACAGATCGGTGTGGATCA	eualaalaGlyIleThrTyrValProProLeuLeuGluValGlyValGluUsys	51 14942
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Οý	72	GlySerAlaSerA	spHisTrpArgGlyA	rgTyrGlyArgArgAr	gProPheileTrpAla	91
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qq	14821	CTATCATTTGGCA	::: TAATGTGCGGTTTGA		CAAGGATCTGGGTCTG	14762
ò	105	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			Arg	105
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Οy	158	ArgGlnAlaTyrS	erValTyrAlaPheM	etIleSerLeuGlyGl	yCysLeuGlyTyrLeu	177
QQ	14524	::: :	:::::::: ccatgitigcgcici	 TCGCGGGATTCGGCGG	::: :::::::::::::::::::::::::::::::	14465
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QQ	14104	ACCCAGTCGGATTACGATGCTCCCGTCTCCCTTAAGGCCTATCTCAAGAGCATCTTCATC 1	14045
ΟŸ	256	LeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhe 2	275
QQ	14044		14018
Qy	276	ValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPhe 2	295
QQ	14017		13958
Qy	296	ValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArg 3	315
qo	13957		13898
Qy	316	HisTyrAspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSer	335
qq	13897		13838
Qy	336	LeuvalPheSerLeuvalMetAspArgLeuvalGlnArgPheGly3	350
QQ	13837	TAAGTCGGCACACTA	13778
Οy	351	ArgalavalTyrLeuAlaSerVal	359
qa	13777	CTAAAAATGCCATCGGAATTTGTTTAAGTGTAAACATCATTTTTTTT	13718
0y	360	AlaAlapheprovalAla 3	365
qa	13717	AATAGATTATAAAGACAAATTCAGATCTTGGTATTAAACAAATGAGGTTTTTCATTGACT 1	13658
Qy	366	AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThr 3	385
qq	13657		13616
Qy	386	eThrPheSerAlaLeu	392
qa	13615	TTGATTAACCACCTGAGCTATAATAT	13559
, 0y	393	Yr	397
qq	13558	GTTGACGTCTGCTTCCAAATCGAATATCTAAAAGAAAGTCCAAATGTATTGAATATTATAT 1	13499
 Qy	398		413
qq	13498	AGAACCAAGGCGGTTTACATTAGTGGAATGAT	13439
Qy	414	-TyrArgGly	424
qq	13438	TTACTATGGTATCGGAATGCTTGTCCTGGCCTTGTGGCCAACTAAGTGGGGAGTCTTGGT 1	13379
QY	424	rLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro	441
qq	13378	ATTCAGCACGTCAGCTGGTATTCTGTATGGAACCATTTTCACGGTGCCTTTCATATTGGT 1	13319
Qy	442	-ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCy 4	461
qq	13318	GGCTAGATATCATGCCAAAAATTGTGTAAGTATACTGTAAGACCTTTAAAATTCAACTT 1	13259
Qy	461	sGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaAr 4	481
qq	13258		13213
ΟŊ	481	gvalvalproGlyargGlyIleCysLeuaspLeualaIleLeuaspSeral 4 :::	498

DD 13121 -ATMOSTACCACTEGAACACCTGGAATGGGCACTGATGTGCCCATANTCACACTAN 13154 DD 13131 GATTTTATTCACCACTTGATTCATCCCTTTCCTTTTTATCACTCAC	Best Local Similarity: 23.96% Mismatches: 198 Query Match: 15.94% Indels: 164	Gaps:) x AF332510 (1-1980)	Oy 12 ArgHisArgLysAlaGlnLeuLeuValAshLeuLeuThrPheGlyLeuGluValCys 31	Oy 32 LeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluValGlyValGluGluLys 51 :::	52 PheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeu :::::::	Oy 72 GlySeralaSeraspHisTrpargGlyArgTyrGlyArgArgFroPheIleTrpala 91 	92 LeuSerLeuGlylleLeu	Qy 103	115 ProAspProArgProLeuGluLeuAlaLeuLéuIleLeuGlyValGlyLeuLeuAspPhe	DD 083		Oy 153 AspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGly 172	Qy 173 CysLeuGlyTyrLeuLeuProAlaIleAspTphrSerAlaLeuAlaProTyrLeu 192 	Qy 193 GlyThrGlnGluGluCysLeuPhe	898 GGCTCTGAGTACCAAGTGATCTACTTCTCTGCACTCACTTGGGGCGTCTTTCTCATC	QY 206 ILEPHELEUTDrCysVal	Oy 212AlaAlaThrLeuLeuValAlaGluGluAjaAlaLeuGly 224 ::: Db 1018 TCCAGTGCGCTCTTTACTAGGCCCCCACAGCAATGGCTACGAGGAAGGG 1077	Qy 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244	244	Db 1138 CTTGGAGAAGACCCAGATCTTTCTGTGCGTGGGGGAGCCAACTCTGTGACTTCAAGT 1197 Qy 245	Db 11998 GCCAAACGAATTAAGGAGGACCAGAAGAAGATGACGTTCAGGTCT 1245	1246TIGATGAAAGCTATCTTCAACATGCCAAACCACTACGGTTCCTGTGCATC
	AGTAT 131	SerGl		rGlnValValPheAspLysSerAspLeuAla 549 ::::: STTGTGTTATATGTCTAGGATATAAGGTATAGCG 12994	1980 bp mRNA linear VRT s membrane-associated transporter protein	omplete cds. F332510 F332510.1 GI:15004312	ryzias latipes. ryzias latipes kikaryotis, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	contributions and contribution of the contribu		ac. befor. 20 (4), 381-383 (2001) 1372467 1479596	(bases 1 to 1980) ukamachi,S., Shimada,A. and Shima,A.	sity	ganism="Oryzias latipes rain="HNI" xref="taxon:8090"		/rpt_unit=ctt 1841914		/translation="mtlleedogarpopelleepdkhistslooyrpdytkedymdsv ETSVFGTVEPPRRSRGRLILHSWVMFGREFCYAVEAAFVTPVLLSVGLPRSLYSLVWL ISPILGFLLQPIIGSASDYCRSSWGRRRPYILVLGILMLVGLSMFLNGDAVVSELVSD	KSSKSTWALTVVWMEGVVLEDEAADEIDGEIKATLEDVCSYQDKERCLHYHALFTGLGG ACGYLORADWGHSVLGRLLGSZYQVIYFFSATTWGVFLIVHJESIPERFYSES SASSALRLLGPHSNGYGALGKEPVSPVITPTSSPEIRPRSYSAJGERPRSFSALGEANS VTSSAKQPIKEDQKKMTFRSLMKAIFNMPNHYRFLCISHLLGWAAFLCNMLFFTDFMG	QIVYRGNPYAEHNSTAYITYERGVEVGCWGLCINAVSSALYSYVQRFLLPYIGLKGLY FWGYFVFGMGTSLIGLFPEVIATLILCSVFGVMSSTLYTIPFNLIAEYQREEEEQVKL EGGNESPRGTGMDCAALTCMVQLAQIIVGAGLGALVNAAGSVĮVVVLSASSISLIGCI	FIALFIRYVE" 19491954 25 a 519 c 489 g 547	5.07e-21 Tenath:	456.00 Matches: 39.77% Conservative:

2y 1 3b 6	134 PhecysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAsp 153
2y 1	154 ProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlÿGlyCys 173
2y 1 0b 7	174 LeuGlyTyrLeuLeuProAlaileAspTrpAspThrSerAlaLeuAlaProTyrLeuGly 193
	ThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaAla 21
	ThrLeuLeuValAla21
	: : TTCACCCTGGTTAGCATCCCCGAGAGGCCCCTTCGGCCACTGGGAGAGAAGAGAGAG
2y 2	219GludlüAlaAla 222
6 qc	907 ATGAAGAGCCCAAGTCTCCCACTGCCCCCCCCCCCCCTGTCTTGGAGGGGGGGG
2 4c	223 LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerPro 239
	HisCysCysPro243
Т	111 024 ATCTCGCCACCCACCCGCTCACCCCCAAGTACGGCAGCTTCATCAGCAGGACAGTTCC 1083
2y 2	243 243
0p 10	084 CTCACAGGCATCAATGAGTTCGCATCGTCTTTCGGGACCTCCAACATAGACAGGGTGCTC 1143
2 Z	243 243
ob 114	44 ATCGACTGCTTCACGGCGGCCCACGATAATTACTTGGCTCTTCCCAGCAGTGTCCCCAGG 1203
λ 2.	244CysArgAlaArgLeu 248
)b 12	1204 CAGGCCATCAGTGTCAGCTTCCCCCGGGCCCCCGATGGTTTCTACTGCCAGGAGAGGGGA 1263
2 Z	49 AlaPheArgAsnLeuGlyAlaLeuLeu257
3b 12	264 CTGGAGAGAGAGAGAGGCCCCTGACCTTGGGCTTGGATGGA
λy 2:	28
b 13	24 TCTCTGGACACCTCTAAGCCACCGCGCCTCGGGGATTCTGAAGAGGCCCCAGACCTTGGCT 1383
λy 2:	59 259
b 13	384 CTCCCGGACGTGGCGGGGAGAAACGGCCCTGAAACCAGCAGGAGAAGGAACGTGACCTTC 1443
λy 2.	259 259
)b 14	444 AGCCAACAGGGGCAAACATCCTCTTGAATGGTGTGAAGTACGAGAGTGAGCTGACGGGC 1503
λy 2.	260Arg 266
)p 15(504 TCCAGTGAGCAGTCGGAGCAGCCGCTGTCTTGCGGGGGTCTTCTTCCACCATCTACAAC 1563
•	MetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMet 286
et a	4
74	87 ThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArg 306 [11] [11] [11] [11] [11] [11] [11] [11
7	57

AlaGluProGlyThrGluAlaArgArgHisT ^l yrAspGluGlyValArgMetGlySerLeu 326 	GlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuVal 346 ::: :::::::: ::: ::::::::: GGCATGTGCATCTACGCGCGCCTTCTACTCAGCCATCCTGGAGAAACTGGAG 1803	GinargPheGlyThrargAlaValTyrLeuA [†] laSerValAlaAlaAhaProValAlaAla 366 ::: GAGTGCCTGAGCGTCGTACCTGATCGCCTACCTTCTCGGCCTGGGGACT 1863	GlyalaThrCysLeuSerHisSerValalaValValThralaSerAlaAlaLeuThrGly 386 	PheThrPheSeralaLeuGlnIleLeuProTÿrThrLeualaSerLeuTyrHisArgGlu 406 	LysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSer 426 	LeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVal 446	ACACGG2019	llyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAlaCys 466	2019	spValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyArg 486		90	SCATGGGAGTAGACATCTCGCTGCTCGCTGCCAGTACTTTCTGGCTCAGATCCTCGTG 20	<pre>srLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSer 526 </pre>	CTCTGGGGCCCC	AlaalaGlyLeuGlyLeuValalaIleTyrPheAlaThrGlnValValPhe 543 	AR112282 255 bp DNA linear PAT 16-MAY-2001 Sequence 3 from patent US 6130043. AR112282 AR112282.1 GI:14092182	Unclassified. 1 (bases 1 to 255)	Roberts-Rapp.L., Russell,J.C., Stroupe,S.D. and Yu,H. Reagents and methods useful for detecting diseases of the prostate , Patent: US 6130043-A 3 10-OCT-2000; Location/Qualifiers 1255	/organism="unknown": 45 a 94 c 69 g 46 t lothers	
307 Ala 1684 GCG	327 Gly 1744 GGC	347 Gln ::: 1804 GAG	367 Gly 1864 GGA	387 Phe 1924 ATC	407 Lys 1984 AAG	427 Leu	2014 ACA	447 Gly	2019	467 Asp		487		507	2083 TCT	527 Ala 2110 GCT			R LLE R IRNAL P IRES SOUTCE	NOON	Alignment Sco Pred. No.: Score:
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	398 61	418	438	458 241	
0 0 0	InileLeuProTyrThr 	ysTyrArgGlyAspThr 	roGlyProLysProGly 	euleuProProProPro 	
Conservative: Mismatches: Indels: Gaps: 2282 (1-255)	379 ThralaseralaalaLeuThrGlyPheThrPheSeralaLeuGlnIleLeuProTyrThr 	399 LeualaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418 	GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438	439 AlabroPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProProPro 458	
98.818 98.818 15.388 6 53) x AR11:	MaLeuThrGly	YrHisArgGl ACCACCGGGA	erGluAspSei GTGAGGACAG	snGlyHisVa.	462 253
Percent Similarity: 98.81% Conser Best Local Similarity: 98.81% Mismat Query Match: 15.38% Indels DB: 6 Gaps: US-09-593-793A-113 (1-553) x AR112282 (1-255)	Thralaserala? 	LeuAlaSerLeu1 	GlyGlyAlasers 	AlaProPheProA	459 AlaLeuCysGly 462
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SUMMARIES
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Copyright (c) 1993 - 2003 Compugen Ltd.

    nucleic search, using frame_plus_p2n model

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Database :

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Prostate gene PS10 Clone 1711346IH, t

Human prostate-rel

cDNA sequence of a

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The invention relates to isolated nucleic acid (ABNB1319-ABNB1324),

corresponding to genes differentially expressed in mast cells following

cutivation or in patients with allergic hypersensitivity disease, (I)

that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of

that encodes proteins (ABB77569-ABB77575) (II) or a protein fragment of

(II) if at least 6 amino acids (II) is useful for identifying binding

construction or (II) is useful for diagnosing or treating a disease

caticaria or atopic dermatitis or mastocytosis) in a subject which

involves determining the level of expression of (I) or (II). A computer

cystem, comprising a database containing information identifying the

expression level in a tissue or at least one mast cell of (I), is useful

consending information to identify the relative expression level of

control of the protein can also serve as a target that

response in a patient. The protein can also serve as a target that

condulate gene expression or activity and as an antigen to raise

colyclonal or monoclonal antibodies. (II) is useful for identifying

agents that modulate expression of the protein or agents, such as

modulating biological activity and function of (II) and thus are useful

for alleviating disease conditions such as allergic bypersensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
                                                                                  Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240
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(I) is also useful for diagnosing and treating diseases of cell confidention such as prostate cancers. (I) is also useful for generating proliferation such as prostate cancers. (I) is also useful for generating of proliferation such as prostate cancers. (I) is also useful for primary and metastatic tumours. (I) is also useful for stimulating immune caponse to PROST 03 containing cells. (II) is useful in diagnostic assays for detecting the levels of polymorlectides encoding prost or antisense coll in the law of the law of the production of antisense collination and therapeutic purposes. The present sequence represents

C clinical and therapeutic purposes. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                       Novel PROST 03 polypeptides and polynucleotides useful in research, diagnosis and therapeutic applications, particularly for use in cancer
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P-PSDB; AAU10324.
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Db 1662 TGCGGGCCTCTGCCTGTGATGTCTCCGTACGTGGGTGGTGGGTG	DD 1722 AGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG	Qy 501 LeuSerGlnValAlaProSerLeuPheWetGlySerIleValGlnLeuSerGlnSerVal	Qy 521 ThralaTyrMetValSeralaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	Qy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553 	RESULT 4 AAV61201 ID AAV61201 standard; cDNA; 3410 BP.	XX AC AAV61201;	XX DT 06-JAN-1999 (first entry)	L1	Prostate; cancer; tumour; vaccine; immunogen; clone; s	OS Homo sapiens.	AA WO9837093-A2.	XX PD 27-AUG-1998.	AA PF 25-FEB-1998; 98WO-US03492.	AA 09-FEB-1998; 98US-0020956. PR 25-FEB-1997; 97US-0806099. PR 01-AUG-1997; 97US-0904804.	AA PA (CORI-) CORIXA CORP.	AA PI Dillon DC, Xu J;	AA WPI; 1998-609886/51. DR P-PSDB; AAW71869.	Polypeptides comprising immunogenic portions of used in a vaccine for the treatment of prostate	AA PS Claim 3; Page 79-80; 130pp; English. vv	The present sequence is a new DNA of a prostate tumour protein. The can be used as a vaccine for the twas identified by analysis of a subtracting a prostate tumour CDNA tissue CDNA library.	SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

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This sequence represents a human prostate tumour specific gene, and can be used in the method of the invention. The method is for detecting prostate cancer comprises contacting a biological sample with an agent able to bind an immunogenic portion of a prostate protein (such as encoded by this sequence). An antibody which binds to an immunogenic portion of the prostate protein, and the method can be used to detect, monitor progression of, or treat prostate cancers. The antibody may also be conjugated to a therapeutic agent for use in therapy of prostate
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   fragments
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 and
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Matches:
Conservative:
Mismatches:
Indels:
   protein
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                treating prostate cancers
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 specific tumour
                                               Claim 1; Page 84-85; 141pp; English
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el human prostate
detecting and tre
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                                                                      ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu
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                                                                                                     CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla
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                                                                  TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly
                                                                                                                                SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla
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AAC79473 standard; cDNA; 3410

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The present sequence was isolated from a breast tumour cDNA library. It is provided in a specification relating to compounds for immunotherapy and diagnosis of breast cancer. Breast tumour antigens and the polynucleotides that encode them may be used in the production of a pharmaceutical composition to be used in the treatment of breast cancer. Proliferated T cells and incubated antigen presenting cells are also required. The polypeptides and polynucleotides may also be used to
                                                                                                                                                                                                                                                                                                                                                                                        of a
breast
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                                                                                                                                                                                                                                                                                                                                                                                        l isolated polypeptide comprising an immunogenic portion cancer protein useful in the detection and treatment of
                                                             cytostatic; immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           945|G; 783 T; 1 other;
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                              human breast tumour
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3410 BP; 667 A; 1014 C;
                                                           Lumour antigen;
vaccine; ss.
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                                                             breast tu
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07-FEB-2001
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% qc	101	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
λ, q	121	GluLeualaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
λ Q	141	ThrProLeuGlualaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnala 160
ç q	161 764	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
λ g	181	IleaspTrpaspThrSeralaLeualaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200
ž g	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaalaThrLeuLeuValAlaGluGlu 220
S S	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
7 ,	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
λ Q	261 1064	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
2 <u>y</u>	281	SerTrpWetalaLeuWetThrPheThrLeuPheTyrThraspPheValGlyGluGlyLeu 300
2 <u>4</u>	301 1184	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
λ q	321	ValargMetGlySerLeuGlyLeuPheLeuGlnCysalalleSerLeuValPheSerLeu 340
α	341	#ThrargalaValTyrLeualaSerValAla 36
λ Q	361	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValYalThrAla 380
<u>ک</u> ۾	381	SeralaalaLeuThrGlyPheThrPheSeralaLeuGlnIleLeuProTyrThrLeuala 400
<u>ک</u> و	401	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420
λ 2	421	S – Š
≿ q	441	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProPloAlaLeu 460

0y	461		SerAlaCysAspValSerValArgValValV	alGlyGluProThrGluAla 480
qa	1664			
QY	481		ProGlyArgGlyIleCysLeuAspLeuAlaI	leLeuAspSerAlaPheLeu 500
qa	1724		AGGGGGGTGGTTCCGGGGGGGGTGTTCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG	
Qy	501		LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal	520
qα	1784		GTGGCCCCATCCCTGTTATGGGCTCCATTG	rccaccrcaccacrcrcrc 1843
δy	521		ThralaTyrwetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln	laileTyrPheAlaThrGln 540
qq	1844		ATGGTGTCTGCCGCAGGCCTGGGTCTGGTCG	ccarrracrrrgcracacag 1903
QY	541		ValValPheAspLysSerAspLeuAlaLysTyrSerAla	553
qa	1904			1942
RESULT AAA063	SULT 7 A06349			
G X	AAA06	349 st	andard; cDNA; 3410 BP.	
AC H	AAA0634	6349;		
XX DI	13-JUN	-2000	(first entry)	
XX DE	Huma	Human immunogenic	nic prostate tumour protein CDNA	A sequence SEQ ID NO:110.
XX XX XX	Human;	; prosta	te cancer; diagnosis; tumour; ge cytostatic; vaccine; ss.	gene therapy; detection;
××	HOH	noines		
X		suprens.		
Z X	MOZOM	00004149-A2	•	
2	27 - J	-JAN-2000.		
XX PF	14 - JI	-JUL-1999;	99WO-US15838.	
XX	14-1	.1008.	08HS-0115453	
7 Y	14 - J	14 - JUL - 1998; 14 - JUL - 1998;	98US-0115433.	
ም ም ማ	23-S	EP-1998; EP-1998;	98US-0159812. 98US-0159822.	
PR	15-J	AN-1999;	99US-0232149.	
ም ማ	15-J	AN-1999; PR-1999;	99US-0232880. 99US-0288946.	
XX	1900/	AYTOOD (-T		
××				
PI	Dill	on DC, Ha	rlocker SL, Yuqiu J, Xu J,	Mitcham JL;
DR.	WPI;	2000-1712	68/15.	
PT	New	polypeptide usef	ul for treating and dia	state
PT	compri	rises an i	enic portion of prostat	protein -
PS	Clai	im 1; Page	135-136; 263pp; English.	
X S	The	present invention	vention describes isolated poly	peptides, comprising an
ខូខូ	immu and	nogenic po polynucleo	f a prostate tumour neoding them have ev	protein (PTP). The polypeptides tostatic activity and can be
ည (nseq	in vaccin	es and in gene therapy. The pol	ypeptides and
ខ្លួ	poly.	nucleotide polypeptid	s encoding them, antigen presenes, antibodies against the polym	ting cells which express peptides and vaccines
55	СОШР	rising the	m can be used for inhibiting the	
38	canc or a	er in a pa nti-idioty	tient. The polypeptides can be pic antibodies for passive immu	used to generate antibodies no therapy. A portion of
ខ្ល	the to	polynucleo odulate th	tides encoding the polypeptides e expression of the polypeptides	can be used as a probe or s. AAA06241 to AAA06691 and
: :	AAY8	2000 to AA present in	AAY82000 to AAY82020 represent sequences used in the exemplification of the present invention.	in the exemplification of

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                                                                                                                                 SerLeuTyrHisArgGluLysClnValPheLeuProLysTyrArgGlyAspThrGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                    immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                       cancer; ss; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                       sequence #109
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 SQ Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;

 Alignment Scores:
 1.58e-218
 Length:
 3410

 Fred. No.:
 2861.00
 Matches:
 553

 Percent Similarity:
 100.00%
 Conservative:
 0

 Best Local Similarity:
 100.00%
 Mismatches:
 0

 Ouery Match:
 22
 Gaps:
 0

US-09-593-793A-113 (1-553) x AAS63557 (1-3410)

Οy	1	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu	
Ор	284	11111111111111111111111111111111111111	
ΟŊ	21		
qq	344	GTCAACCTGCTAAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCG 403	
δλ	41	ш, -	
qq	404	CCTCTGCTGCTGGAAGTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGGCATTGGT 463	
Qy	61	61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80	
qq	464	CCAGTGCTGGGCCTGGTCTGTGTCCCGGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGA 523	
Οÿ	81	ArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlylleLeuLeuSerLeu 100	
qq	524	CGCTATGGCCGCCGCCCCTTCATCTGGGCATCCTTGGGCATCCTGAGCCTC 583	
ΟŊ	101	101 PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120	
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ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIJeThrTyrValPro

ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlylleGly

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ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla

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LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal
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GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC
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Skeiky
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Retter MW, Stolk JA, S
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Kalos MD, Fanger GR, Day CH,
                                                                                                                                                                                                                                                            AAH93465 standard; cDNA; 3410
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                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 265-266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for use in vaccines -
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prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), anticologies to (II), (Iusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic.
                                                                                                                                                               methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
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343

945 G; 783 T; 1 other;

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3410 553 0 0 0

Matches: Conservative: Mismatches:

1.58e-218 2861.00 100.00% 100.00%

Indels:

Length:

403

40

463

09

523

80

ArgTyrGlyargArgArgProPhelleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100

ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly

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The present invention describes an isolated polypeptide (P1) comprising at least an immunogenic portion of a prostate-specific protein, or its variant. Also described are polynucleotides (N1) encoding (P1). (P1) and (N1) have cytostatic activity and can be used in vaccine production. The polypeptides, nucleic acids and antibodies from the present invention are useful in the diagnosis and therapy of prostate cancer. Prostate specific genes P704P, P712P, P775P and B335D are located in a genomic region on chromosome 22gil. 2 known as the Cat Eye Syndrome region. Prostate specific antigen (P5A) P501S was located on promore and polypeptide sequences used in the exemplification of the present invention.
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                                            Human; prostate cancer; therapy; diagnosis; cat eye syndro
chromosome 22q11.2; prostate-specific protein; chromosome
prostate specific antigen; PSA; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SL, Jiang Y,
Skeiky YAW,
prostate-specific cDNA sequence L1-12/P501S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harlocker;
, Day CH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prostate-specific protein, useful in the prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5; Page 164-165; 325pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cham JL, Ha
Stolk JA,
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99US-0443686
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Kalos MD, Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
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                                                                                                                                                               Homo sapiens
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  Human
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GCTATGGCCGCCCGGCCCTTCATGENER I I I I I I I I I	CTTCATCTGGGCACTGTCCTTGGGCATCCTGCTGAGCCTC	583
101 PheLeulleProArgAlaGlyTrpLe 111111111111111111111111111111111111		
121 GluLeuAlaLeuLeuIleLeuGlyVa	IrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 	120 643
4 GAGCTGGCACTGCTCATCCTGGGCGT	9uG1yVa1G1yLeuLeuAspPheCysG1yG1nVa1CysPhe 	140
141 ThrProLeuGlualaLeuLeuSerAs 	uSerAspLeuPheArgAspProAspHisCysArgGlnAla	99
Oy 161 TyrSerValTyralaPheMetileSer 	1eSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 	2 8
rseralai 	eualabroTyrLeuGlyThrGlnGluGluGluCysLeuPhe 	ŏä
eullePhel 	uThrCysValAlaAlaThrLeuLeuValAlaGluGlu :	6 4
Qy 221 AlaAlaLeuGlyProThrGluProAla 	uProAlaGluGlyLeuSerAlaProSerLeuSerProHis 	240 1003
Qy 241 CysCysProCysArgAlaArgLeuAla	JLEUALAPHEALGASNLEUGLYALGULEUPOARGLEU 	260 1063
Qy 261 HisGlnLeuCysCysArgMetProArg	tProArgThrLeuArgArgLeuPheValAlaGluLeuCys 	280 1123
Oy 281 SerTrpMetAlaLeuMetThrPheThrLeuPh 	=TyrThrAspPheValGlyGluGlyLeu :	300
Qy 301 TyrGlnGlyValProArgAlaGluPro	-aGluProGlyThrGluAlaArgArgHisTyrAspGluGly 	320 1243
euPh 	LeuPheLeuGlnCysAlalleSerLeuValPheSerLeu 	0 0
Qy 341 ValMetAspArgLeuValGlnArgPhe	nargPheGlyThrargalaValTyrLeuAlaSerValAla 	360 1363
Qy 361 AlaPheProValAlaAlaGlyAlaThr 	.yalaThrCysLeuSerHisSerValAlavalValThrAla 	380 1423
Qy 381 SerAlaAlaLeuThrGlyPheThrPhe	#ThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla	400
6 – E	SGInValPheLeuProLysTyrArgGlyAspThrGlyGly 	
uAspSerLeuMetTh 	MetThrSerPheLeuProGlyProLysProGlyAlaPro	40
441 PheProAsnGlyHisValGlyAlac 	11y11yerGlyLeuLeuProProProProAlaLeu	99

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The present invention describes an isolated polypeptide (I) comprising at least an immunogenic portion of a prostate tumour antigen protein or lifs variant. (I) have extostatic activity and can be used in vaccine production. (I), prostate tumour antigen polynuclectides, an antigen presenting cell (APC e.g. a dendritic cell) that expresses (I), and a pharmaceutical composition containing (I) are useful for inhibiting the appearance in a patient. Antibodies specific for prostate specific proteins and oligonuclectides that hybridise to a polynuclectide that encodes a prostate specific protein are useful for detecting the presence or absence of a cancer or monitoring the progression the progression a cancer, especially prostate cancer. Antibodies to AAR20122 to AAR20123, AAB71821 and AAB74821 and AAB74830 are sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                      Prostate tumour antigen determined full length cDNA sequence for L1-12.
                                                        1664 TGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGAGCCCACCGAGGCC 1723
                                                                                                                                  CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480
                                                                                                                   LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prostate specific protein and its encoding polynucleotide, useful for the treatment and diagnosis of prostate cancer ^{\circ}
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; prostate tumour antigen; prostate tumour; therapy; diagnosis;
prostate cancer; immunogenic; cytostatic; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3410 BP; 667 A; 1014 C; 945 G; 783 T; 1 other;
                                                                                                                                                                                                                                    Cheever MA;
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                                                                                                                                                                                                                                                                                                                             AAH02530 standard; cDNA; 3410 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2000; 2000WO-US27464.
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                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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P-PSDB; AAB74800.
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Alignment Scores:

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3410 553 0 0	LysalaginLeuLeuLeu 	lyileThrTyrValPro 	tValLeuGlyileGly GGTGCTGGGCATTGGT	rAsphisTrpArgGly 	VIleLeuLeuSerLeu 	OASPProArgProLeu 	ysGlyGlnvalCysPhe 	oAspHisCysArgGlnAla 	YTYrLeuLeuProAla 	InGluGluCysLeuPhe	uLeuvalAlaGluGlu 	OSerLeuSerProHis 	aLeuLeuProArgLeu 	eValAlaGluLeuCys 	eValGlyGluGlyLeu 	gHisTyrAspGluGly
Length: Matches: Conservative: Mismatches: Indels: Gaps: 0 (1-3410)	gLeuLeuArgHisArg 	uValCysLeuAlaAlaG 	GluGluLysPheMetThrMetV 	roLeuLeuGlySerAlaSe 	eTrpAlaLeuSerLeuGl 	JAlaGlyLeuLeuCysPr 	lGlyLeuLeuAspPheC 	JeuPheArgAspPr 	reuGlyGlyCysLeuGl 	ProTyrLeuGlyThrG 	rCysValAlaAlaThrLe 	aGluGlyLeuSerAlaPr 	aPheArgAsnLeuGlyAl 	coArgThrLeuArgArgLeuPheV 	rLeuPheTyrThrAspPh 	uProGlyThrGluAlaArgArgHiSTyr.
1.58e-218 2861.00 100.00% : 100.00% 100.00% 22	.euTrpValSerAr	uLeuThrPheGlyLeuGlu 	uGluValGlyVa] 	LeuvalCysvalF 	rgArgArgProPhell(.eProArgAlaGlyTrpLeu 	laLeulleulleLeuGlyVa.	.uAlaLeuLeuSerAspl 	rralaphemetileseri 	PASPThrSerAlaLeuAlal 	uThrLeuIlePheLeuThrC 	yProThrGluProAl 	SArgAlaArgLeuAl 	SCYSArgMetPi 	laLeuMetThrPheThrLeuPheT 	Glyvalproargalaglupre
Similarity: al Similarity tch: 3-793A-113 (1	1 MetValGlnA 	1 ValAsnLe	1 ProLeuLeuLe 	1 ProvalLeuGly: 	1 ArgTyrGlyA 	1 PheLeuIl 4 TTTCTCAI	1 GluLeuA 	1 ThrProLeuGluAla 	1 TyrServalTy 	1 IleaspTr 4 ATTGACTG	1 GlyLeule 	1 AlaAlaLeuGl 	1 CysCysProCy 	1 HisGlnLeuCy 	1 SerTrpMetA	1 TyrGln 4 TACCAG
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1544 GCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCC
                                                                                                                                                                                                     AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro
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                                                                                                                                                                                     1664 TGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGGTGAGCCCACCGACGAGCC
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                                                                                                                                                                                                                               LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal
                                                                                                                                                                                                                                                                                Human L1-12 cDNA sequence SEQ ID NO 110
                                                                                                                                                                                                                                                                                                                      BP
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97US-0904804.
98US-0020956.
98US-0030607.
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09-FEB-1998;
25-FEB-1998;
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their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
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Retter MW, Stolk JA, Day CH, Vedvick TS,
A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    other;
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                                                                                                                                                                                                                                                                                                                                                                     New prostate-specific polynucleotides for diseases, in particular prostate cancer, progression of cancer
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 110; 87pp;
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98US-0115453.
98US-0159812.
99US-0288146.
99US-0288946.
99US-0439313.
99US-0433313.
99US-043686.
2000US-0483672.
2000US-0503793.
2000US-0503793.
2000US-0503793.
2000US-0503783.
2000US-0503783.
2000US-0503783.
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DILLON D C.
MITCHAM J L.
HARLOCKER S L.
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DAY C H.
VEDVICK T S.
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KALOS M D.
FANGER G R.
RETTER M W.
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WANG A.
SKEIKY Y A W
HEPLER W T.
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GR, Rette
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                       09-APR-1999;
13-JUL-1999;
18-NOV-1999;
14-JAN-2000;
27-MAR-2000;
29-MAY-2000;
13-JUN-2000;
27-JUN-2000;
21-JUN-2000;
21-JUN-2000;
10-AUG-2000;
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06-SEP-2000;
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3410 553 0 0 0 Length: Matches: Alignment Scores: Pred. No.: Score:

Conservative: Mismatches: Indels: 1.58e-218 2861.00 100.00% 100.00% Best Local Similarity: Query Match: Percent Similarity:

Н 284

(1-3410)

(1-553) x ABL94929

US-09-593-793A-113

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TACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGC 1243 240 320 380 100 140 703 160 763 180 823 200 883 220 943 463 523 120 80 09 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAjaThrLeuLeuValAlaGluGlu HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 104 1064 1184 1424 41 61 164 81 201 884 221 944 1304 1364 121 261 301 321 361 381 δý q ò q οy Q Qγ q ŏ Pp ò Q δy g οy Q ò q Óγ g οy QQ Qγ g Ω Q Qγ QQ δý pp δý d ρy qq à g

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        1603
                                                                                                             1723
                                                                                                                                                                    breast cancer; cytostatic;
                                                                                                                                            AGGGTGGTTCCGGGCCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTG 1783
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                                                              ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu
                                       AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro
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SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly
                                                                                                                                                            LeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal
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                                                                                                                                                                                                                                                                                                                         Human breast tumour polypeptide full length cDNA clone #3
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response -
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                                                                                                                                                                                                                                    ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
                                                                                                                                                                                                                                                                                                                                        breast tumour polypeptide; gene; ss;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           es encoding breast tumour or stimulating an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 143-144; 150pp; English.
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                                                                                                                                                                                                                                                                          ВР
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12-OCT-2000; 2000US-0687507.
06-FEB-2001; 2001US-0778381.
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                                                                                                                                                                                                                                                                          standard;
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cancer in a patient, comprises obtaining a biological sample from the patient, contacting the biological sample with a binding agent that bind to a breast tumour polypeptide, detecting in the sample an amount of polypeptide that binds to the binding agent, and comparing the amount of polypeptide to a predetermined cut-off value, therefore determining the presence of a cancer in the patient. Sequences ABK28920-ABK29025 represent cDNA clones encoding human breast tumour polypeptides of the
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                                                                                                                                                                                                                                                                       21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro
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Matches:
Conservative:
Mismatches:
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Query Match:
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                          ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla
                                                                                                         HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys
      SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu
                                                                                                GTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCA
                                                                                                                                                                         AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro
                                                                                                                                                                                             PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu
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                                                                                                                                                                                                                        SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly
                                                                                                                               SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla
                                                                                                                                                                                                                                                                                                                                                                                  cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                                                                                                                                                                                                                             ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
                                                                                                                                                                                                                                                                                                                                                                       Human prosate cDNA P553S splice variant #3.
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                                                                                                                                                                                                                                                                                                                                                                                  Human; prostate
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The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (for antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen-presenting cells are useful for stimulating and/or expanding of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for
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Carter D
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, JA, Day CH, Vedvick TS,
Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0 other;
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 483-484; 579pp; English.
                                                                                                                                                                                                                                                                                                                                                         Jillon DC, Mitcham JL,
SR, Retter MW, Stolk G
Wang A, Skeiky YAW, E
                                                                                                       2000us-0536857.
2000us-0568100.
2000us-0570737.
2000us-0593793.
2000us-0605783.
2000us-0651236.
2000us-0651236.
2000us-0657279.
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2716.50
70.09%
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                                                                        2001WO-US09919
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Best Local Similarity:
Query Match:
DB:
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WO200173032-A2
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10-AUG-2000;
29-AUG-2000;
06-SEP-2000;
02-OCT-2000;
10-OCT-2000;
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12-MAY-2000;
13-JUN-2000;
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Pred. No.:
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Fanger
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Qy Db	81	ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100 	•
Oy Dp	101	PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspP1 	
Qy Dp	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCySPhe 14	
Oy Dp	141	ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160	
Qy Dp	161	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180 	
Qy Dp	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200	
Qy Dp	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220 	
Oy Db	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240	
60 OX	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260	
oy Op	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280 	
Oy Dp	281	SerTrpMetalaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300 	
ر م	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 319	
a v	319	ANCASSOCIO CUCA CARRA CONTRA C	
QQ	1241	AAGGCCTTGGCAGCCAGGAGGCTGGTGTGGGAGCCGCCCAGAGAGGAGGAGGAGGAGGAGGAGAGAGAGAGAGAGAGAG	
ογ	319		
QQ	1301	GCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGG 1360	
οy	319	319	
QQ	1361	ATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCGTTTGCGGTTTC 1420	
οy	319	319	
Db	1421	AGGAAGGCCTCTGGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCCAGTTTGACAGAAG 1480	
ογ	319		
qq	1481	GAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGTTAAGGCTGGATTTCAGAT 1540	
٥y	319	319	
QQ	1541	CIGCCIGGITCCAGCCGCAGIGIGCCCTCTGCTCCCCAACGACTITCCAAAIAATCTCA 1600	
Qy	319	319	

RESULT 16 AAH93868

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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (II). (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340
                                                                                                                                                                                                                                                                                                                                                                               New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                   , Reed SG;
Skeiky YAW;
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                                                                                                                                                                                                                                                                                                     Harlocker SL, Jiang Y,
Retter MW, Stolk JA, S
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Conservative:
Mismatches:
Indels:
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                                                                                                                   therapy; metastasis; ss.
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                                                                            cDNA splice variant P553S-10
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BP.
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AAH93868 standard; cDNA; 4034
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2716.50
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                                                                                                                                                                                                                                                                                                   Xu J, Dillon DC, Mitcham
Kalos MD, Fanger GR, Day
                                                  (first entry)
                                                                                                                                                                                                                                                                           CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                            Meagher MJ
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Best Local Similarity:
Query Match:
                                                                                                     Human; prostate c
cytostatic; gene
                                                                                                                                                                    WO200151633-A2
                                                                                                                                             Homo sapiens.
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                                                  04-OCT-2001
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                                                                                                                                                                                                                                                                                                                               Wang A,
                                                                            P553S
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HisGlnLeuCysCysArgMetProArgThrLeuArgAigLeuPheValAlaGluLeuCys 280 1241 AAGGCCTTGGCAGCCAGCAGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGG 1300 AGGAAGGCCTCTGGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCCAGTTTGACAGAAG 1480 GAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGGATTTCAGAT 1540 ATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCTTGCGGTTTC 1420 ThrProLeuGlualaLeuLeuSerAspLeuPheArgaSpProAspHisCysArgGlnala 160 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu--- 319 100 TyrSerValTyrAlaPheMet11eSerLeuGlyGlyCySLeuGlyTyrLeuLeuProAla 180 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis TTTCTCATCCCAAGGGCCGGCTGGCTAGCAGGCTTGCTGTGCCCGGATCCCAGGCCCCTG IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe GCTGTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGG GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 1181 1481 761 181 221 941 1001 1121 1301 1361 1421 61 161 81 521 101 581 641 141 701 821 201 881 261 319 319 319 319 319 121 161 281 301 . q Op δ qq qq g QQ δy QQ Qγ q ŏ qq δλ qq QQ g g d q Db qq qq Qγ οy δλ δŏ δ δý ά δy à δ Qγ ò

GTGTTCCCTCTCACCCGCCTGTCTCACAGCTGAGACTCCAGGAAACCTACAGCTCACCCAGGAACCTCAGCAGCTCACCCAGCAGCTCACCCAGCAGCTCACCCAGCAGCTCACCCAGCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACCAGCTCACAGCACACTCCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACAGCTCACACACTCACACACTCACACACTCACACACA	. ,	319 319 5541 CTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCAACGACTTTCCAAATATCTCA 1600 319	Db 2621 GAGCGACTTGGCCAAATACTCAGCG 2645 RESULT 17 ABL95411 D ABL95411 standard; CDNA; 4034 BP.
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13 13 13 14 15 15 15 15 15 15 15		GTGTTCCCTCTCACGGCCTGTCCTCACAGCTGAGATCCCCAGGAAACCTTCAGACTACC	19-JuL-2002 (first entry)
###		6	Human P553S splice variant SEQ ID NO 704.
ACCTOCATECHAGORIANAMOGODANOGOTOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOC	-	21 TTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACTA	<pre>Human; cancer; prostate cancer; vaccine; cytostatic; gene therapy; gene; ss.</pre>
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		6	
CTTCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	$\overrightarrow{\rightarrow}$	AGGICTCGIGCAGCAGGTACCTGIGGTTCCGCCTTCTCATCTCCCTGAGACTGCTCCGAC	12-JAN-2001; 2
Trend year Tree T		GlyvalArgMetGlySe	25-FEB-1997; 01-AUG-1997;
	-	CCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCGTTCGGATGGGCAG	09-FEB-1998; 25-FEB-1998;
### 1979 1978		5 rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 	14-JUL-1998; 23-SEP-1998; 15-JAN-1999;
### 10.5000.000.000.000.000.000.000.000.000.	~	uValGinArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAl 	09-APR-1999; 13-JUL-1999; 12-NOV-1999; 18-NOV-1999;
14.000.000.000.000.000.000.000.000.000.0		alaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuTh	14-JAN-2000; 27-MAR-2000;
	Ñ	TGCCGGTGCCACATGCCTCTCTCTCTCTCTCTCTCTCTCT	12-MAY-2000; 13-MAY-2000; 13-MN-2000;
		rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 	27-JUN-2000; 10-AUG-2000; 29-AUG-2000;
	· `	gGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs 	06-SEP-2000; 02-OCT-2000; 10-OCT-2000;
	•	pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheproAshGlyHi	(XUJJ/)
SVAIGLYALGUIGUEGUPTOPTOPTOPTOPTOPTOPTOPTOPTOPTOPTOPTOPTOP	~		(MITC/) MITCHAM J L. (HARL/) HARLOCKER S
CGTGGGTGCTGGTGCTGCTCCCACCTCCCACCTCCCACCTCCCCCCCC	4	SValGlyAlaGlyGlyGerGlyLeuLeuProProProProProAlaLeuCysGlyAlaSerAl	(JIAN/) (KALO/) (FANG/)
A		CGTGGGTGCTGGAGGCAGTGGCTCCCACCTCCACCGCGCGCTCTGCGGGGCCTCTGC	(RETT/) (STOL/)
yArgGlyIleCysLeuAspLeuAlalleLeuAspSerAlaPheLeuLeuSerGlnValAl 505 Hargely IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	4 (acysasyalservalargvalvalvalvaldipprommedangvalvalpalprod 	(DAYC/) (VEDV/)
IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	4	vArqGlv1leCvsLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl	(LISX/)
aproSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThralaTyrMetVa 525	~		(SKEI/) (HEPL/)
CCCATCCCTGTTATGGGCTCCAGCTCAGCTGCTATATGGT 2560 PI Li SX, Wang A, Skeiky YAW, Hepler, WT, Henderson RA; ISERALABIAGIYLEUGIYUUGIYUGIYUGIYUGIYUGIYUGIYUGIYUGIYUGI	.,	aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa	(HEND/) HENDERSON K A. Yu. I. Dillon DC Mitcham II. Harlboker SI. Jiang V.
S ISSERAGATALALICITYPHEALTH XX XX XX XX XX XX XX	25	CCCATCCCTGTTPATGGGCTCCATTGTCCAGCCAGTCTGTCTCTCTCTTATTGT	Fanger GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Li SX, Wang A, Skeiky YAW, Hepler, WT, Henderson RA;
FT New prostate-specific polynucleotides for diagnosing and 5 sSerAspLeuAlaLysTyrSerAla 553	. 5	o iseralatasiyeedsiyeedsalatatteryrPhoAlaThrSinValValPhoAspLy 	WPI;
	4,	5 sSerAspLeuAlaLysTyrSerAla 553	New prostate-specific polynucleotides for diagnosing and diseases, in particular prostate cançer, and as markers f

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; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; therapy; gene; ss.
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Carter D;
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                                                                                                                                                                                                              P553S splice variant SEQ ID NO 704.
411 standard; cDNA; 4034 BP
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UKG-1997; 97US-0904804.
FEB-1998; 98US-002055.
FEB-1998; 98US-0115453.
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FEB-1999; 99US-02382149.
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DILLON D C.
MITCHAM J L.
HARLOCKER S L.
JIANG Y.
KALOS M D.
FANGER G R.
STOLK J A.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
SKEIXY Y A W.
HENDERSON R A.
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Г	progression of cancer -	Qy
X S S	Claim 1; SEQ ID NO 704; 87pp; English.	QQ
୍ଷ ଧ [୍] ଧ	The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment	Qy
ខេខ៖	s, particularly prostate cancer. The present sequence in the invention.	qa
XX SO	Sequence 4034 BP; 721 A; 1226 C; 1141 G; 946 T; 0 other;	oy G
Alignme Pred. N Score: Percent Best Lo	Alignment Scores: 6.72e-207 Length: 4034 Pred. No.: 2716.50 Matches: 553 Percent Similarity: 70.09% Conservative: 0 Best Local Similarity: 70.09% Mismatches: 0 Query Match: 94.95% Indels: 236	g o o
DB: US-09	24 Gaps: 1 93A-113 (1-553) x ABL95411 (1-4034)	qq
Qy Dp	rpValSerArgL 	Qy Db
Qy Dp	21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlylleThrTyrValPro 40	Qy Dp
Qy Dp	41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGly1leGly 60	Qy Dp
Oy Dp	61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80	Qy Db
Oy Dp	81 ArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100 	Qy Dp
Oy Dp	101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120 	oy Op
Oy Dp	121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140	Oy Dp
oy Dp	141 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGluAla 160 	Qy Dp
oy Ob	161 TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180 	Qy
Oy Db	181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200 	Qy Db
Qy Db	201 GlyLeuLeuThrLeuIlePheLeuThrCysValalaalaThrLeuLeuValalaGluGlu 220 	oy Db
Qy Dp	221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240	Qy Db
Oy Dp	241 CysCysProCysArgalaArgLeuAlaPheArgAsnLeuGlyalaLeuLeuProArgLeu 260 	Qy Db Qy

2y 26 0b 106	1 HisGlnLeuCysCysrgMetProArgThrLeuArgArgeuPheValAlaGluLeuCys 280
28	1 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
30	1 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 319
118	
31	
124	1 AAGGCCTTGGCAGCCAGCAGGCTGGTGTGGGAGC
31	6
130	1 GCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCC
31	
136	1 ATGGACCCCATCTGCATACACGGCTTCTCATGGGTG
31	6
142	1 AGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAK
31	6
Db 148	1 GAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGG
31	6
Db 154	1 CIGCCIGGIICCAGCCGCAGIGIGCCCICTGCICCCC
31	
160	1 CCAGCGCCTTCCAGCTCAGGCGTCTTAGAAGCGTCT7
31	
166	1 GTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGAC
31	6
172	1 TTCCTCTGCCTTCAGCAAGGGGCGTTGCCCCACATTC
31	
178	1 GACTCCCATTGCTAGAGGTAGAAAGGGGAAGGGTGC
31	6
184	1 AGGICTCGTGCAGCAGGTACCTGTGGTTCCGCCTTC
32	0
190	1 CCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCGTTCGGATGGGCA 1
Oy 32.	5 rLeuGlyLeuPheLeuGlnCysAlalleSerLeuValpheSerLeuValMetAs
196	1 CCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACGGCT
34	5 uValGinArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProV
202	1 GGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGC
36	5 aAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSe
208	1 TGCCGGTGCCACATGCTGTGTGTGTGTGTGTGTGTGTGTG
38	5 rGlyPheThrPheSerAlaLeuGlnIleLeuProTyr

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2200
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pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi
                                                                                     2441 CCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGC
                                                                                                                                                                                                                                                  aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa
                               gGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs
                                                                                                                     sValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAl
                                                                                                                                                              aCysAspValSerValArgValValGlyGluProThrGluAlaArgValValProGl
                                                                                                                                                                                                        yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl
                                                                                                                                                                                                                                                                      CCCATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thioredoxin; trxA; ubiquitin; P501S; tumour; prostate; antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; vaccine; therapy; human; gene; ds.
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Chimeric - Escherichia coli.
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The present sequence is that of a triple gene fusion comprising, from the 5' end, the trxA thioredoxin gene from Escherichia coli, the human ubiquitin coding sequence, the prostate antigen P501S (amino acids 55-53) coding sequence, the prostate antigen P501S tail. The triple fusion was constructed in plasmid pRIT15063, which included the Saccharomyces cerevisiae CUP1 promoter and yeast alpha prepro signal sequence. The triple fusion protein (see AAM50661) was produced in E. coli G7724 transformants. This is an example of the production of triple fusion proteins of the invention comprising ubiquitin (used between thioredoxin and a protein of interest, in this case P501S(aa55-553). A claimed method
                                                                                                                                                                                                                                                                                                                                        of producing a recombinant protein of interest involves: culturing a host cell (preferably E. coli) under conditions which allow for co-expression of the triple fusion and a ubiquitin-specific endoprotease (especially UBPI from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the ubiquitin-specific endoprotease in vivo. In the present case, a p501-like protein of 509 amino acids is generated. The recombinant protein can used as a vaccine for cancer therapy.
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Sequence 2133 BP; 384 A; 656 C; 614 G; 479 T; 0 other;

1144 TCGGCCCCTTCTTGTCGCCCCACTGCTGCTCCATGCCGGCCCGCTTGCCGAAC 1203

233 SerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsn

δλ g

Example 5; Fig 9a; 87pp; English.

Oy Dp	253 LeuGlyalaLeuLeuProArgLeuHisGlnLeuCysCysÄrgMetProArgThrLeuArg 272 	DE Humar XX KW Humar XX
Q Q	273 ArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyr 292 	OS HOMO XX WO200
03 Dp	93 ThraspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGlu 312 	PD 04-00 XX XX PF 27-M2
Oy Dp	13 AlaargargHisTyraspGluGlyValargMetGlySerLeuGlyLeuDheLeuGlnCys 33	PR 27-M2 PR 09-M5 PR 12-M3 PR 13-JI
Oy Dp	333 AlaileSerLeuValPheSerLeuValMetaspArgLeuValGlnArgPheGlyThrarg 352 	27 10 29 06
Oy Dp	353 AlavaltyrLeuAlaServalAlaAlaPheProvalAlaAlaGlyAlaThrCysLeuSer 372 	
Oy Op	373 HisservalalavalvalthralaseralaalaLeuthrGlyPheThrPheSeralaLeu 392 	XX PI Xu J, PI Fange PI Li S)
Oy Dp	393 GInileLeuproTyrThrLeualaSerLeuTyrHisArgGluLysGlnValPheLeuPro 412 	
Oy Dp	413 LysTyrargGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeu 432 	PT New P PT the C XX PS Clain
Oy Dp	433 ProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGly 452 	
Oy Dp	453 LeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgVal 472 	
Qy	473 ValValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeu 492 	
Qy Dp	493 AlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySer 512 	
Oy Dp	513 IleValGInLeuSerGinSerValThrAlaTyrMetValSerAlaAlaGIyLeuGlyLeu 532 	lignment red. No. core:
O.Y	533 ValalailetyrphealathrGlnValValPheaspLysSeraspLeualaLysTyrSer 552 	Percent Si Best Local Query Matc DB:
δy	553 Ala 553	US-09-593-
g	2104 GCG 2106	Qy 1
REST	19 8	Db 274
X X D	AAS64038 standard; cDNA; 4894 BP. AAS64038:	Oy 21
XX DT 29 XX	-JAN-	•

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invention relates to isolated prostate; specific

ynucleotides, polypeptides, fusion proteins of the polypeptides,
ibodies raised against the polypeptides (or antigenic epitopes
ilved from them) and antigen-presenting cells expressing the
ypeptides. The antibodies are useful for detecting the presence of
noer, especially prostate cancer. The polypeptides, polynucleotides and
sells specific for a tumour protein, and for inhibiting the development
cancer especially prostate cancer. Compositions comprising the
ynucleotide and/or polypeptide are useful for stimulating an immune
phonse, and for treating cancer. The oligonucleotide is useful for
ecting cancer. The present sequence is a prostate specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human prostate-specific polypeptides and polynucleotides useful for diagnosis and treatment of cancer, especially prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu----- 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalos MD;
Carter D;
                                       in; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
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Mismatches:
Indels:
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Matches:
in prosate cDNA P553S splice variant #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -793A-113 (1-553) x AAS64038 (1-4894)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .m 1; Page 480-482; 579pp; English.
                                                                                                                                                                                                                                   1.39e-192
2538.50
51.118
51.118
88.738
                                                                                                                                                                                                  JAR-2001; 2001WO-US09919
                                                                                                                                                                                                                                                                                                                                                                                                    2000US-0679426
2000US-0685166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDB; AAU69874, AAU69875.
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al Similarity:
tch:
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                                                                                 o sapiens.
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OCT-2000;
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SX, Wand
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3 3		רנד ניופניופניו מפששפיו שמשפפשפששפיו וראו מערראופניופניו - פפטופאפיי כ	7 .
; A	453	ACTACATCCTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGA 51	2
à	57		_
ą	513	CCTCTGCCCTGGGAGCTGCTTGGAGGGAGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 57	72
λ̈́α	57	55	_
q	573	GGAGGGTGACCCTGGGCTGAGGGGGCACACCAAGAGAAGAAGAAGAATACCAAGGACATA 63	32
λ̈́α	57	57	
q	633	CCCCAGTCACCTCTGGATCCCTGGTCCTGCAGAGCCTGGCTCATAGGAGACACTGGAG 69	92
7.7	57	57	
ą	693	AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC 75	52
ζ	57	57	
g	753	TTACAACCACCATTTGAGGTGATCCATTTTACAGAGGAAGGA	
λ	57	57	
ą	813	TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 87	72
λ̈́	57	57	
q	873	GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGAÇTCTGCA 932	32
λά	57	57	
q	933	GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCTCACC 99	32
λά	57	57	
qq	993	CCCAGGAAGAGGGGCCCCTGTGAGGATTGCAGGCTCTGGAGGCACACACTGCTTGTTGAAAC 105	152
ά	57	57	
q	1053	GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTCTTAGTTGCTCC 111	112
λά	57	57	
q	1113	ATGCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 117	172
λ	57	57	
ą	1173	AATTACAGCATCCCTGTGAAGACGTAGCACAGTTCGAGTACGGAATGTTATTTCCATCC 12	132
λ	57	57	
q	1233	TTCTCACGGAGCTTGGTTCCCCTTCCCCTTGCCTTTACTTGTCCCAGCCATTGACTCAT 12	292
λ̈́ς	58		
q	1293	ACTACTTCCCTTCTTGCAGGCATTGGTCCAGGCCTGGTCTGTGTTGTTGTTCTTAGTTGTCCTAGTGTTGTGGTCTGTGTTGTTGTTGTTGTTGTTGTTGTTGT	152
λ	7	GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 9	
ą	1353	GGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCA 1	412
λ q	92	LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 1 	11
λλ	112	LeuLeuCysproAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 1	31
ą	1473	CTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTCATCCTGGGCGTGGGGCTG 15	32

Qy	132	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe	151 1592
QY	152	ArgaspproasphisCysargGlnalaTyrSerValTyralaPheMetIleSerLeuGly	171 1652
Qy Db	172	JGlyTyrLeuLeuProAlaIleA 	191 1712
QY	192	GluGluCysLeuPh 	211
oy B	12	hrLeuLeuValAlaGluGluAlaA aLeuGlyProThrGluProAlaGl 	231
Oy Dp	0 0	roSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheAr 	251 1892
Qy	52	uGlyalaLeuLeuProArgLeuHisGinLeuCysCysArgMetProArgThr 	271 1952
QY	272	argLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeu 	291 2012
QY	292	PhraspPhevalGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGly 	311
οy	312	lualaargarghisTyraspGlu	\vdash
Dp	73	AGACACTATGATGAAGGTAAGG	H
٥y	31		319
g :		AGCCGCCCACAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGC	2192
g c	2193	CCATCTGCA	
Οy	319		319
qq	2253	GTGTGGAACATCTCTGCTTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC	2312
δλ	319		319
QQ	2313	AGAGTCGTTGCCCCAGTTTGACAGAAGGAAGGCGGAGCTTATTCAAAGTCTAGAGGAAG	2372
ΟŸ	319		319
qq	2373	TGGAGGAGTTAAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCT	2432
δλ	319		319
qq	2433	CCCCCAACGACTTTCCAAATAATCTCACCAGGGCCTTCCAGCTCAGGCGTCCTAGAAGCG	2492
δy	319		319
qq	2493	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGCCTGTCCTCACAGCTG	2552
Οy	319		319
Dp	2553	AGACTCCCAGGAAACCTTCAGACTACCTTCCTCTTCAGCAAGGGGCGTTGCCCACA	2612

Qy	319	
o q	TTCTCTGAGGGTCAGTGGAAGGAACCTAGACTCCCATTGCTAGAGGGTAGAAAGGGGAAAGG	
δλ	919	
qq	2673 TGCTGGGGAGCAGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCC 2732	
ΟŊ	319 319	
qq	2733 TICICATCICCCTGAGACTGCTCCGACCCTTCCCTCCAGGCTCTGTCTG	
οy	320GlyvalArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336	
QΩ	2793 TCCCTCTGCAGGCGTTCGGATGGGCAGCCTGGGGCTTCCTGCAGTGCGCCATCTCCCT 2852	
Oy Dp	336 uValPheSerLeuvalMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356 	
oy ob	356 ualaserValalaalapheProValalaalaGlyalaThrCysLeuSerHisserValal 376 	
ó	376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396	
qq		
Oy Dp	396 OTYTThrLeualaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGl 416 	
Š Š	416 yAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436	
a 2	m -	
g 5	450 STRONINTEROPRETEROSBOLLYBURSALELYBURSELSBURSELSBURSELDENEDER 456 3153 GCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGYTGGAGGCAGTGGCCTGCTCCCACC 3212	
Oy Dp	456 oProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGl 476	-
٥y	476 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs 496	
qa	3273 GCCACCGAGGCCAGGGTGGTTCCGGGGCGGGCATCTGCCTGGACTCGGCCATCCTGGA 3332	-
Qy Db	496 pSeralaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516 	
ΟŊ	516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy 536	
QQ	3393 CAGCCAGTCTGTCACTGCCTATATGGTGTCTCCCGCAGGCCTGGGTCTGGTCGCCCATTTA 3452	
Qy Db	536 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553 	
RESULT AAH938 ID A	RESULT 20 AAH93866 ID AAH93866 standard; cDNA; 4894 BP.	
X Y	AAH93866;	- '
LOX	04-OCT-2001 (first entry)	
X G	P553S cDNA splice variant P553S-14.	
M M X	<pre>Human; prostate cancer; prostate-specific; diagnosis; vaccine; cytostatic; gene therapy; metastasis; ss.</pre>	

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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I). (II), antibodies to (II), fusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93337 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    453 ACTACATCCTCCTTCCTTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        513 CCTCTGCCCTGGGAGCTGCTTGGAGGGAGGTGTGTCTGCTGGGAAGGCATTGCTGGGCA 572
                                                                                                                                                                                                                                                                New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                          SL, Jiang Y, Reed SG;
Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4894 BP; 928 A; 1448 C; 1354 G; 1163 T; 1 other;
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551
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2
526
526
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Conservative:
Mismatches:
Indels:
                                                                                                                                                                          Harlocker S
Retter MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-593-793A-113 (1-553) x AAH93866 (1-4894)
                                                                                                                                                                                                                                                                                                                        Claim 1; Page 457-459; 543pp; English.
                                                                                                                                                                      Xu J, Dillon DC, Mitcham JL,
Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.39e-192
                                                                                   16-JAN-2001; 2001WO-US01574.
                                                                                                                14-JAN-2000; 2000US-0483672.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2538.50
51.118
51.118
88.738
                                                                                                                                                                                                                                                                                             for use in vaccines
                                                                                                                                                                                                                                   WPI; 2001-425873/45.
                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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                            WO200151633-A2.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alignment Scores:
                                                        19-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
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۲۵ وړ	192 Le	euGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
3 8	12	23
Z qq	73	- 00
Qy	232 Le	uSerAlaProSerLeuSerProHisCyscySProCysArgAlaArgLeuAlaPheArg 251
qq	1833 CT	CHGICGCCCCCCTCCTTGTCGCCCCCCTCGTCCATGCCGGCCCGCTTGGCTTTCCGG 1892
Qy	252 AS	nLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
QQ	1893 AA	AACCTGGGGGCCCTGCTTCCCCGGCTGCTGCTGCTGCCGCGCTGCCCCCC
Qy	272 Ar	ArgargLeuPheValalaGluLeuCysSerTrpMetalaLeuMetThrPheThrLeuPhe 291
qq	1953 CG	CCGGCTCTTCGTGGCTGGGCTGTGTGTGTGTGTGTGTGT
QY	292 TY	IyrThrAspPheValGlyGluGlyLeuTyrG nGlyValProArgAlaGluProGlyThr 311
qq	2013 TA	GCCGAGGCCTGTACCAGGCCGTGCCCAGAGCTGAGCCGGG
οy	312 G1	GlualaargargargatisTyraspGlu 319
qq	2073 GA	CCGGAGACACTATGATG
Οy	319	319
QQ	2133 AG	CCGCCCACCAGAGACGACACTCGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGC 2192
δλ	319	319
QQ	2193 CC	CGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2252
Οy	319	319
qa	2253 GT	GTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC 2312
ΟY	319	
qq	2313 AG	AGTCGTTGCCCCCAGTTTGACAGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAG 2372
Οy	319	
Db	2373 TG	GAGGAGTTAAGGCTGGATTTCAGATCTGCTTGGTTCCAGCCGCAGTGTGCCCTCTGCT 2432
Oy	319	
QO	2433 CC	CCCAACGACTTTCCAAATAATCTCACCAGCGCTTCCAGCTCAGGCGTCCTAGAAGCG 2492
Οy	319	319
QQ	2493 TC	CTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGCCTGTCCTCACAGCTG 2552
δλ	319	
QΩ	2553 AG	ACTCCCAGGAAACCTTCAGACTACCTTCCTCTTCAGCAAGGGGGCGTTGCCCACA 2612
ΟÝ	319	319
QQ	2613 TT	CTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGG 2672
οy	319	319
qq	2673 TG	CTGGGGAGCAGGCTGGTCCACAGCAGGTCTCGTGCAGGTACCTGTGGTTCCGCC 2732
Οy	319	319
2	2733	CTCATCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGA

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                                                                                                                                                                                                                                 536
                                                                                                                                                                                                                                                                                                                                     cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
      2793 TCCCTCTGCAGGCGTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCCATCTCCCT
                            SProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr
                                                                                                                                                                                  uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy
                                                                                                                                                                                                                                     uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe
                                             uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl
                                                                                                                                                  GCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGYTGGAGGCAGTGGCCTGCTCCCACC
                                                                                                                                                                                                          pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe
------GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe
                                                                                                                                                                                                                                                            3453 CTITGCTACACAGGTAGTATTTGACAAGAGGGACTTGGCCAAATACTCAGCG 3504
                                                                                                                                                                                                                                                      rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
                                                                                                                                                                                                                                                                                                                          splice variant SEQ ID NO 702
                                                                                                                                                                                                                                                                                        ВР
                                                                                                                                                                                                                                                                                       ABL95409 standard; cDNA; 4894
                                                                                                                                                                                                                                                                                                                                                                                                  97US-0806099.
97US-0904804.
98US-0020956.
98US-0030607.
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01-AUG-1997;
09-FEB-1998;
25-FEB-1998;
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a cDNA described in the invention.
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, Vedvick TS,
Henderson RA;
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GR, Retter MW, Stolk J
14-JUL-1998; 98US-0115453.
23-SEP-1998; 98US-0158812.
09-APR-1999; 99US-0232149.
09-ANR-1999; 99US-028946.
13-JUL-1999; 99US-0355616.
12-NOV-1999; 99US-043313.
18-NOV-1999; 99US-0443686.
14-JAN-2000; 2000US-0536857.
09-MAY-2000; 2000US-0556100.
12-MAY-2000; 2000US-0556110.
13-UN-2000; 2000US-05593793.
27-JUN-2000; 2000US-0553783.
10-AUG-2000; 2000US-0553783.
10-AUG-2000; 2000US-0553783.
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HEPLER W T.
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HARLOCKER S
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RETTER M W.
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KALOS M D.
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	CCTCTGCCCTGGGAGCTGCTTGGAGGAGGAGGTCTGCTGGGAAGGCATTGCTGGGCA 572
	25
	GGAGGGTGACCCTGGGCTGAGGGGGCACACCAAGAAGAAGAAGAATACCAAGGACATA 632
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	CCCCAGTCACCTCTGGATCCCTGGTCCTGCACAGAGCCTGGCTCATAGGAGACACACTGGAG 692
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	AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC 752
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	TTACAACCACCATTTGAGGTGATCCATTTTACAGAGGAAGGA
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	TTAGGTAAGTCTTAGCCAAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 872
	22
	GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 932
	25
	GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCCTCACC 992
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	CCCAGGAAGAGGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 1052
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	GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTCTTAGTTGCTCC 1112
	25 57
	ATGCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1172
	57
	AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC 1232
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	TTCTCACGGAGCTTGGTTCCCCTTCCCCTTTACTTGTCCCAGCCATTGACTCAT 1292
	GlylleGlyProValLeuGlyLeuValCysValProLeuLeu 71
	ACTACTTCCCTTCTTGCAGGCATTGGTCCAGGCCTGGTCTGTTCTGTCTCTGTCTTTTTTTT
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	11
_	TIGICCTIGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCT

Qy Db	112 Leu 1473 CTG	LeuCysProAspProArgProLeuGluLeuAlaLeuLeutleLeuGlyValGlyLeu 131
Qy	132 Leu	AspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 15
qq	1533 CTG	GACTICIGIGGCCAGGIGIGCTICACICCACTGGAGGCCCTGCTCTGACCTCTT
Qy	15.	AspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
qq	Ō	GACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGG
ογ	<u> </u>	91
QQ	1653 GGC	sceredectacerecetecearteacregadacaceateceredecerac 17
Οy	192 Leu	GlyThrGlnGluGluCysLeuPheGlyLeuLhurLeuIlePheLeuThrCysVal 211
qq	- Ĕ	GGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCTCATCTTCCTCACCTGCGT
Qy	212 Ala	AlaThrLeuLeuValAlaGluGluAlaA
QΩ	1773 GCA	GCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCCACCGAGCCAGCAGAAGG
QY	232 Leu	uSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
qq	1833 CTG	CGCCCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCG
QY	252 Asn	LeuGlyAlaLeuLeuProArgLeuHis
Db	1893 AAC	TGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACC
Qy	272 Arg	ArgLeuPheValAlaGluLeuCysSer
qq	1953 CGC	CGGCTCTTCGTGGCTGAGCTGTGCAGCTGGGATGGCACTCATGACCTTCACGCTGTT
Oy	292 Tyr'	ThraspPheValGlyGluGlyLeuTyrGlnGlyValProArgA
qq	2013 TAC	acggatitcgiggccgagggcigiaccagggcgigcccagagcigagcgggcac
Οy	312 Glu	AlaArgArgHisTyrAspGlu 31
qq		gcccggagacactatgatgaaggtatggcatggcagcaggagg
Qy	319	316
qq	2133 AGC	CGCCCACCAGAGGACGACTCGGGGCTGTGTCTG
Оу	319	319
qq	2193 CCC	GACTICTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2252
δλ	319	
qq	2253 GTG	TGGAACATCTCTGCTTGCGGTTTCAGG
ογ	319	319
qq	2313 AGA	GTCGTTGCCCCAGTTTGACAGAAGGA
Qy	319	
QQ	2373 TGG	AGGAGTTAAGGCTGGATTTCAGATCTGC
QY	319	
ΩĐ	2433 CCC	CCAACGACTITCCAAAIAAICICACCAG
QY	319	
qq	2493 TCT	TGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGGCCTGTCCTCACAGCTG 2552
ΟY	319	319

ARDABO1220-AAD05282 represent CDNAs corresponding to 21 human secreted protein genes, and AAE01352-AAE01413 represent the protein stagements or variants. CC AAE01413. represent human secreted protein fragments or variants. The secreted proteins and their genes are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. The secreted proteins and their genes are useful for preventing, treating conditions can be diagnosed by determining the amount of the case of the issues in which they are most highly expressed, and include consection in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 21 genes, consect tumours for the diagnosis or treatment of proliferative developing products for the diagnosis or treatment of proliferative developing products for the diagnosis or treatment of proliferative concert, tumours, foetal and developmental abnormalities, disorders, diseases of the immune system, AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, alergies, neurological disorders (e.g., Alzheimer's disease, Parkinson's disease), cognitais, sepsis, diabetes, atherosclerosis, cardiovascular disorders, and indication organs condition controls of prequent of primary tissues, conditieration, to prevent skin aging due to subburn, to maintain organs contribers and and inchemotaxis, and can be used as a food additive or corresponding to modify storage properties. Antibodies specific for a preservative to modify storage properties. Antibodies specific for a Human; secreted protein; proliferative disorder; cancer; tumour; asthma; foctal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; inflammation; neurological disorder; Alzheimer's disease; food additive; angiogenic disorder; kidney disorder; paskrointestinal disorder; allergy; pregnancy-related disorder; endocrine disorder; infection; wound healing; cell culture; chemotaxis; vulnerary; binding partner identification; naturally occurring New nucleic acid encoding one of 21 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions, such as autoimmune disease and cancer, and used as a food additive or Baker KP; protein" /transl_except= (pos:209..211, aa:Xaa) /note= "Xaa corresponds to any of the protein" /product= "Mature human secreted Σ Fiscella /*tag= a /product= "Human secreted Claim 1; Page 388-389; 490pp; English. Location/Qualifiers Komatsoulis GA, Wei P, L-amino acids" 2000WO-US30654. 12-NOV-1999; 99US-0164835. 27-JUL-2000; 2000US-0221142. (HUMA-) HUMAN GENOME SCI INC /*tag= b 296..1264 U 152..295 /*tag= /*tag= WPI; 2001-308779/32. gene therapy; ss. P-PSDB; AAE01362. WO200134629-A1 08-NOV-2000; sapiens preservative 17-MAY-2001. sig_peptide nat_peptide Ruben SM, Homo

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S×S	une invention. Sequence 3878 BP; 709 A; 1164 C; 1044 G; 951 T; 10 other;
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Oy Dp	54 ThrMetValLeuGlyIleGlyProValLeuGlyLeuValCysValProLeuLeuĠlySer 73 ::::::::
Oy Dp	74 AlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPhelleTrpAlaLeuSer 93
Oy Dp	94 LeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeu 113
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oy ob	134 PheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAsp 153
Oy Dp	154 ProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyCys 173
Oy Dp	174 LeuGlyffyrLeuLeuProAlaileAspfrpAspfhrSerAlaLeuAlaProTyrLeuGly 193
Oy Dp	194 ThrGinGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValalaala 213
Qy	214 ThrLeuLeuValalaGluGluAlaalaLeuGlyProThrGluProAlaGluGlyLeuSer 233
oy Db	234 AlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArgAsnLeu 253
o d	254 GlyAlaLeuLeuProArgLeuHisGlnLeuCySCysArgMetProArgThrLeuArgArg 273
Oy Op	274 LeuPheValalaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPheTyrThr 293
Qy Db	294 AspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAla 313
δŏ :	4 ArgargHisTyrAspGlu 319
g	1013 CGGAGACACTATGATGAAGGTAAGGCCTTGGCAGCCAGCAGAGGCTGGTGGGGAGCCGC 1072

Óλ	Оу 319	319
Op	Db 1073 CCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCTCTCCATCCT	GGCCCCGAC 1132
ογ	Оу 319	319
Op	Db 1133 TTCTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCAT	GGGTGTGG 1192
Qy	319	319
qq	Db 1193 AACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTG	ATCAGAGTC 1252
Οy	оу 319	319
qq	Db 1253 GTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGG	AGTGGAGG 1312
Qy	оу 319	319
qq	Db 1313 AGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCCTCTGCTCCCCCA	CTCCCCCA 1372
Qγ	Оу 319	319
q a :	Db 1373 ACGACTTTCCAAATAATCTCACCGCCCTTCCAGCTCAGGCGTCCTAGAAGCGT	CGTCTTGA 1432
Qy	оу 319	319
qq	Db 1433 AGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAG	CTGAGACTC 1492
Qy	оу 319	319
qa	Db 1493 CCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCC	ACATTCTCT 1552
Οy	оу 319	319
Dp	Db 1553 GAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAA	GGGTGCTGG 1612
δy	Оу 319	918
qq	Db 1613 GGAGCAGGCTGGTCCACAGGTCTCGTGCAGCAGGTACCTGTGGTTCC	GCCTTCTCA 1672
Ωy	оу 319	319
qa	Db 1673 TCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG	crcrccrc 1732
Qy	Oy 320GlyvalArgMetGlySerLeuGlyLeuPheLeuGlnCysAlalleSe:	rLeuvalPh 338
qa	1733 rgcaggcgrrcggarggccrgcrgggccrgrrcrgcrgcrgccarcr	CTGGTC
δλ	338 eSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValT	yrLeuAlaSe 358
qq	1793 CTCTCTGGTCATGGACCGCTGGTGCAGCGATTCGGCACTCGAGCAGTCT	GCCA
δy	358	lAlavalva 378
Dp	1853 rerescaserrrecersisses de la recensione de la reconstrucción de la	SCCGTG
Οy	Oy 378 IThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeu	uProTyrTh 398
QQ	1913 GACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGAT	CCCT
δy	398 rLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrAr	gGlyAspTh 418
QQ	1973 ACTGGCCTCCTCTACCACGGGAGAGGAGGTGTTCCTGCCCAAATACC	GGGGACAC 2032
δy	418 rGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGly	ProLysProG1 438
qq	2033 IGGAGGIGCIAGCAGIGAGACAGCCIGAIGACCAGCTICCIGCCAGGC	AAGCCTGG 2092
Qy	438 yAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuF	28
QQ	2093 AGCTCCCTTCCCTAATGGACACGTGGTGCTGGAGGCAGTGGCCTGCTCC	CCTCCACC 2152

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cancer especially prostate cancer. Compositions comprising the ynucleotide and/or polypeptide are useful for stimulating an immune ponse, and for treating cancer. The oligonucleotide is useful for ecting cancer. The present sequence is a prostate specific ynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTÄTAGCGATTATCTCATTTAATGC 643
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                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro
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Matches:
Conservative:
Mismatches:
Indels:
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30.48%
30.48%
74.94%
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al Similarity:
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25	ICAGTTTGFCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1063	22	CAGCATCCCTGTGAAGACGTAGCACAGTGGTCGAGTACGGAATGTTATTTCCATCC 1123	25	CGGAGCTTGGTTCCCCTTCCCCTTGCC	GlylleGlyProValLeuGlyLeuValCysValProLeuLeu 71	CATTGGTCCAGTGCTGGCCTGGTCTGTGTCCCGCTCC	SeralaserasphistrpargGlyargTyrGlyargargargProPhe11=rrpala 91 	LeuGlylleLeuLeuSerLeuPheLeulleProArgAlaGlyTrpLeuAlaGl	TITITITITITITITITITITITITITITITITITITI	eucysProAspProArgProLeuGluLeuAlaLeuLeulleLeuGlyVaiGlyLeu 131 	GIJGInValCysPheThrProLeuGluAlaLeuLeuSerAshLeuPhe 15	CIGGAGGCCCIGCICIGGACCICIIC 140	, LÓ	SLEUGIYTYTLEULEUPTOAlatleAspTrpAspThrSerAlaLeuAláProTyr 191 	yThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211	TITITITITITITITITITITITITITITITITITITI	laAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlàGluGly 231 	251	7	AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCySCysArgMetProArgThrLeu 271	CAGCIGIGCIGCCGCATGCCCCGCACCCT	91	SCICTICGIGGCIGAGCIGIGCAGCIGGGIGGCACICAIGACCIICACGCIGIII 1903	1	rgtaccaggccgtgcccagagctgagccgggcacc 19	GluAlaArgArgHisTyrAspGlu	61	Ĉ
	ATGCCTCAGI		AATTACAGCA		TTCTCACGGA	-	ACTACTTCCC	GlySerAlas GCTCAGCCA	LeuSerLeuC	CTGTCCTTGG	LeuLeuCysF CTGCTGTGCC	LeuAspPheCys	ArdAsoPro	CGGGACCCGC	GlyCysLeuG 	LeuGlyThr	CTGGGCACC	AlaAlaThrI 	LeuSerAlaF	CTGTCGGCC	AsnLeuGlyA	AACCTGGGCG	ArgArgLeuP	CGCCGGCTC1	TyrThrAspP 	TACACGGATI	GluAlaArg? 		AGCCGCCCAC
57	1004	57	1064	57	1124	io d	4	72 (92	1304	112	132	52	84	172	192	1604	212	~ ~	24	52	1784	72	1844 (92	04	312 (319	2024
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ò	319	319
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QQ	2084	CCCGACTICTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2143
Oy	319	319
qq	2144	GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC 2203
Qy	319	319
qa	2204	AGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAG 2263
Qy	319	319
qa	2264	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCCTCTGCT 2323
Qy	319	319
qq	2324	CCCCCAACGACTTTCCAAATAATCTCACCAGGCCTTCCAGCTCAGGCGTCCTAGAAGCG 2383
Qy	319	319
qq	2384	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGCCTGTCCTCACAGCTG 2443
Qy	319	319
qq	2444	AGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACA 2503
QY	319	319
qq	2504	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGGTAGAAAGGGGAAGGG 2563
QY	319	319
qq	2564	TGCTGGGGAGCAGGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCC 2623
οy	319	319
qq	2624	TICTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG
Οy	320	GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336
QQ	2684	SCGTTCGGATGGCCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCC
οy	336	5
qq	2744	crecreredacedecederegrades procedes contracted and
Qγ	356	ualaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376
QQ	2804	GCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGACATGCCTGTCCCACAGTGTG
QY	376	avalValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 396
qq	2864	GTGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGC
Οy	368	TyrThrLeuAlaSerLeuTyrHisArgGluLys
qa	2924	GGGAGAAGC
QY	409	608
qq	2983	GGTCTGGGTTTTTGGGAGGCCAACTAGCTCAGAACCTG
δ	409	409
qq	3043	CTTT(
QY	409	409
Dρ	3103	GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT
δý	409	409
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3163	TCAGGACTGTGGTAGCACTTGAATGGATGATGGGAAATGCAAAATACGATAGTGGGAA	3222
409		409
3223	TCCCGAAGGGTCAGGCCAGCAGGAGCCCTAGGCTTCTAGGCTTGTTCTATGGAGGG	3282
409		409
3283	CAGGGCGCTGAATCAGATGACCCCTGGGCCATTCAGCCTCAGCAGACGGGAGTGGGAATG	3342
409		409
3343	GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC	3402
409		409
3403	TCTGGTCTCTGAGATGGGGCAGGCTCCTTCCTACCCCCTTTCTTT	3462
409		409
3463	TTTCTGTCTAATTCCCTTTTTCTTTTCCTGCATCCCTCCTTTGCCTCCTTTCCCTTTCTCCT	3522
409		409
æ	TCCCCTTCCCCTTCCCCTGTGGCAGATATCTGAGCTTGACACCTGACCCACTCACT	3582
409		409
583	CACTGTGTAAGTTGTGGGGACCTCCTTCTTGGTTGGCCCTACACATAACCAGCCCCTCCAG	3642
409		409
3643	GGGCCCCTTTCCTTGGGAAGCCACCTAACCCAGGTAGTGTGTCGTCATCCTTGTCCCCCCC	3702
409		409
3703	CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCCTTGAGGGGCATGAAGTTGG	3762
409		409
3763	GGTGTCCCAAGGGAGGAGGAGGATGCAGGACTGCTCATAGAGCTCTCAGACTGTAGGGA	3822
409		409
3823	AGACCTGCCCCTGCGTCTCGTAGCACTTGAGGAGAGGAG	3882
		409
3883	GGCTGGTTAACTGAGTAGGTAGCTGCAGGGGTGAGAGGTATGGAGGGGAGGGGCCTAAGGT	3942
409		409
3943	TTTGGTTGGGGGGGGCCTGGTCCCTGAGACCCCTGTTAGCCCACTGATAACCTTCTTCAGC	4002
409		409
4003	CTTCACTCTTCTGCTTGCCTGGGGGGGGGGGGGGGGCTGGCATCAGCGGCCAGGCCTGA	4062
409		409
4063	GTATGTGCTGTCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGAGC	4122
409		409
4123	ATGTCTGTCCTCGGACCACTCCAGACTCCAACCTCAGCGGACATTCCTGGGGTGGCAGGC	4182
409		409
4183	AGGGAGAGAAAGTCCTGGGAGGCCCCTTCCTAACAGCAGCTGATGGCAGACTTGGCACTG	4242
409		409

Db	4243 CAC	GCTGTCTGCCTGTTCCTTTGCCCACTTGTTGAGC
٥y	409	
οp	4303 CTG	CCATGGCTCCCACCTC
Qy	409	
QQ	4363 TTC	GATAAGACCTGGCCTTGTCCT'
QY	409	
qq	4423 GCC	CCAGTCA
ΟŸ	409	607
qq	4483 CAG	_A
Οy	409	408
QQ	4543 AGA	SGGTCTACTGGATTCT
Qy	409	409
qq	4603 AGG	PACCCTAGTGGCATCT
οy	409	409
QQ	4663 TCT	FTCCAGATGTCGGAG
Qy	409	409
qq	4723 GTT	၂၁၁
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Qy	409	409
Dβ	4963 CACT	ctggttagacttggaccaag <mark>tag</mark>
Qγ	409	604 408
qq	5023 GCT	CCTGATTCTCATGAAGTCCCCATTGCCCCTGGGATGGAGGCAAGGGTCTGTTCTCACA 5082
οy	409	608 408
qq	5083 GCT	CTGGGGTGGTGCCAGTGCTGGGTACACACCTGTCCTTTCCCCTTTTCTTCACCCCTCT 5142
Qy	410	PheLeuProLysTyrArgGlyAspThrGlyGlyGlyAlaSerSerGluAspSe 426
QQ	5143 GCCTT	AGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTTAGCAGTGAGGACA
δλ	26	
qq	5203 CCTC	CTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATC
Qy Dp	446 1Gly 5263 GGGTG	yAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCySGlyAlaSerAlaCy 466
ò	9	2a Serva ArdVa Va Va G vG uDroThrG ua aArdVa Va DroG vAr 486
5 A	0	STCTCCGTACGTGGGTGGGTGGGCCCACGAGGCCAGGGTGCGGGCCG 53

486 gGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506	Score: Percent
CATCHGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 5442	Ouery Ma
oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526 	69-80
	QY Db
CCGCAGGCCTGGGTCTCGCTCTTTACTTTTGCTACACAGGTAGTATTTGACAAGAG 5562	ò
rAspLeuAlaLysTyrSerAla 553 	QQ .
	Ολ
869 AAH93869 standard; cDNA; 6976 BP.	qq
	Qy
04-OCT-2001 (first entry)	qa
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==	qa
cytostatic; gene therapy; metastasis; ss.	0y
Homo sapiens.	qα
WO200151633-A2.	Qy
9-JUL-2001.	qa
6-JAN-2001; 2001WO-US01574.	Qy
4-JAN-2000; 2000US-0483672.	qq
(CORI-) CORIXA CORP.	οy
Xu J, Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, Reed SG; Kalos MD, Fanger GR, Day CH, Retter MW, Stolk JA, Skeiky YAW; Mang A. Meacher MI:	qq o
	. q
New polynucleotide encoding a prostate-specific protein, for diagnosing, monitoring and treating prostate cancer in a patient and for use in vaccines -	٥٧ م
Claim 1; Page 461-463; 543pp; English.	Qy
esent invention describes polynuclectide sequences (I) which encode	qq
prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II),	Qy
<pre>11</pre>	QQ
(1) and the antibodies are also used in the detection of cancer in a particularly the cancer that is diagnosed or treated is particularly contact of the cancer that is diagnosed or treated is particularly and the cancer that is a diagnosed or treated is particularly as the cancer that is a contact to the cancer that is a contact to the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is particularly as the cancer that is a diagnosed or treated is a diagnosed or treated in the cancer that is a diagnosed or treated is a diagnosed or treated in the cancer that is a diagnosed or treated in the cancer that is a diagnosed or treated in the cancer that is a diagnosed or treated in the cancer that is a diagnosed or treated in the cancer that is a diagnosed or treated in the cancer that is a diagnosed or treated in the cancer that is a diagnosed or treated in the cancer that the cancer that is a diagnosed or treated in the cancer that the canc	δλ
The cancer. (1) and (11) can be used in vactimes. The allthoughes of the used for monitoring the progression of cancer in a patient.	qq
(11) can also be used to imploye diagnostic and theirapeutic for prostate cancer. They can indicate the level of metastasis as the prostate volume abuddate; to abuddad and abuddits to	Qy
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Sequence 6976 BP: 1312 A: 1996 C: 1961 G: 1706 T: 1 other:	Qy
	106

9/69

Length:

6.81e-161

Alignment Scores: Pred. No.:

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ATGCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAAATGCCTGTGTTATGAGGAGTA 1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1064 AATTACAGCATCCCTGTGAAGACGTAGCACÁGTGTCGAGTACGGAATGTTATTTCCATCC 1123
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                                                                                                                    44 ACTACATCCTCCTTCCTGCTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 403
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 Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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2144.00
30.48%
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74.94%
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Aatch:
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qq	1124 TTCTCACGGAGCTTGGTTCCCCTT	CCCCTTGCCCTTTACTTGTCCCAGCCATTGACTCAT	1183	
οy	9 85	ValProLeuL		
qq	1184 ACTACTTCCCTTCTTGCAG	GCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTA	1243	
g G	y 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 	GlyargTyrGlyargArgArgProPheIleTrpAla 	91 1303	
Oy Db	92 L 1304 C	yTrpLeuAla 	111 1363	
Oy Dp	112	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeulleLeuGlyValGlyLeu 	131 1423	
Qy Db	132 LeuaspPheCysGlyGlnVa 	1CyspherhrproLeuGlualaLeuLeuSeraspLeuPhe 	151 1483	
Q Op	152 ArgaspProAspHisCysArc 	III	171 1543	
S S	172 GlyCysLeuGlyTyrLeuLe 	auproalaileaspirpaspihrSeralaieualaprotyr 	191 1603	
O.y Db	192 Le 11 1604 CT	uGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 	211 1663	
Oy Dp	212		231 1723	
Qy Dp	232	HiscysCysProCysArgAlaArgLeuAlaPheArg 	251 1783	
Oy Dp	252 AsnLe 1784 AACCT	uGlyalaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 	271 1843	
oy Op	272 ArgAr 1844 CGCCG	ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe	291 1903	
oy O	292	GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 	311 . 1963	
οχ	312 GluAla	1	19	
qq	1964 GAGGCC		2023	
οy	319		319	
QQ	2024	AGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGGCTGGTGCCTCCTCCATCCTGGC	2083	
٥y	319		319	
QO	2084 CCCGACTTCTCTGTCAGGAA	SGAT	2143	
οy	у 319у		319	
QQ	2144 GTGTGGAACATCTCTGCTTG	CGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC	2203	
οy	у 319		319	

qq	2204	AGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTA	ATTCAAAGTCTAGAGGGAG 2263
Qy	319		319
qa	2264	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCT	CCCCAGTGTGCCCTCTGCT 2323
0y	319		319
qq	2324	CCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGCTCAGGGGTCCT	CTCAGGCGTCCTAGAAGCG 2383
ΟŽ	319		319
qq	2384	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACC	CACCCGCCTGTCCTCACAGCTG 2443
ογ	319		319
qq	2444	AGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAG	TCAGCAAGGGGCGTTGCCCACA 2503
ΟŊ	319		319
qq	2504	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAG	GCTAGAGGTAGAAGGGGAAGGG 2563
Qγ	319		319
qa	2564	TGCTGGGGAGCAGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCC	AGGTACCTGTGGTTCCGCC 2623
ΟŊ	319		319
qq	2624	TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG	CTCTGTCTGATGGCCCCTC 2683
Qγ	320	GlyValArgMetGlySerLeuGlyLeupheLeuGlnCysAlaIleSerLe	euGlnCysAlaIleSerLe 336
qq	2684	– to	rgcagrgcgccarcrccr 2743
Qy	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe	lyThrArgAlaValTyrLe 356
qq	2744	GGTCTTCTCTCTGTCATGGACCGGCTGGTGCAGCGATTCGG	SCACTCGAGCAGTCTATTT 2803
Qy	356	uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHiSSerValAl	ysLeuSerHisSerValAl 376
qq	2804	Geccaererecertrecerereceserecedare	scererccacacacrerece 2863
δλ	376	aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr	erAlaLeuGlnIleLeuPr 396
qa	2864	cereereacatricacceccercacceeerreaceirere	SAGCCCTGCAGATCCTGCC 2923
δλ	396	oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal	409
qq	2924	ACACACTGGCCTCCTCTACCACCGGGAGAAGCAGGT-	ACTCATTGGCCAGTGGGTGG 2982
QY	409		409
qq	2983	AGTCAGGGTGGGGGGGGTGGTTTTTGGGAGGCCAAC	AACTAGCTCAGAACCTGGTAT 3042
QY	409		604 408
qq	3043	CTGGCAAGCAACTTTGGAGAATGCTTCTTTGAATCAGAGAAGAAGCTTATCCTAGCCCCA	SAAGCTTATCCTAGCCCCA 3102
ΟŊ	409		409
qq	3103	GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT	AGALTCTGGGAATGACTTCCTGGGG 3162
QY	409		409
qq	3163	TCAGGACTGTAGCACTTGAATGGATGATTGCAGGAAATGC	GCAAAATACGATAGTGGGAA 3222
δy	409		604 408
qq	3223	TCCCGAAGGGTCAGGCCAGCAGGAGCCCTAGGCTTCTAGGCTC	CTGGTTGTTCTATGGAGGG 3282
δŏ	409		409
qq	3283	CAGGGCGCTGAATCAGATGACCCCTGGGCCATTCAGCCTCAGCAGACGGGAGTGGGAATG	SCAGACGGGAGTGGGAATG 3342

604 408	09	90
3343 GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402	qa —	3 GCCATCAAGGGCAGGGGTTGGGGGGATGGTGGTCGACCAGTCACTCTGATCTAAGTCAGA 4
607	O.	***************************************
3403 TCTGGTCTCTGAGATGGGGCAGGCTCCTTCCTACCCCTTTCTTT	მ	CAGCAGGAAGGAAGTGAGAAGCCTTCAACATTAGCACAGCTGGGGCTGGGGAGGTGGGA 4
604 608	Qy	7
3463 TTTCTGTCTAATTCCCTTTTCTTTTCCTGCATCCCTCCTTTGCCTTCCCTTTCCTTTCTCT 3522	q a	AGAGGGACATTCCTCCTGCTTGGGGTCTACTGGATTCTCCCTGCCCCAAGGCTGGGGACA.
607	O.	
3523 TCCCCTTCCCCTTCCCCTGTGGCAGATATCTGAGCTTGACACCTGACCCACTCACT	අධ	AGGGAGCTCATGGCAGGCAGCTACCCTAGTGGCATCTGGGACCCCAGAGAGGCAGAGCT 4
607	Oy	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3583 CACTGTGTAAGTTGTGGGGACCTCCTTGGTTGGCCCTACACTAACCAGCCCCTCCAG 3642	ପ୍	TCTCTGCACCGGGCAATGAGGATTTCCAGATGTCGGAGTGGAGGGCAGGCA
	δλ	6
3643 GGGCCCCTTTCCTTGGGAAGCCACCTAACCCAGGTAGTGTGGTCATCCTTGTCCCTCCA 3702	qa ko	4723 GTTAGGAGAGCCTGCGTGGGCTTTGGGCCATCAGGGGCCCTGCCTTGGTTTTGTTCCTC 478
409	<i>4</i> 8) ジャンジルホンスキホホンンホホホルンドジホントンファルキップはジンマンフマルルンホマンチマンかびかってはない。
3703 CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCCTTGAGGGGCATGAAGTTGG 3762	a à	00 V
607	42	
3763 GGTGTCCCAAGGGAGGAGAGGAGATGCAGGACTGCTCATAGAGCTCTCAGACTGTAGGGA 3822	an i	CICIGIICICICIGAICIGAIAIIGAGAIIICICICCCICIIIACCIGIICIAAGAGGCT
607	δō	00 t Company Commence of the c
3823 AGACCTGCCCTGCGTCTCGTAGCACTTGAGGAGGAGGAGGTAGGT	an o	AGAGGAGACTIAGACTICTGGGTTCACATTIGICCCCGCCCTACCCGTTACCCTTCTCCC
607	δō -	
3883 GGCTGGTTAACTGAGTAGGTAGCTGCAGGGGTGAGGTATGGAGGGGAGGGGGTAAGGT 3942	ag ·	CACICCIGAGGAGGGICCIGGITAGACTIGGACCAAGIAGGGICICCCAICITCICICC
607	ς i	
3943 TTTGGTTGGGGGAGCCTGGTCCCTGAGACCCCTGTTAGCCCACTGATAACCTTCTTCAGC 4002	a :	5023 GCTCCTGATTCTCATGAAGTCCCATTGCCCCTGGGGATGGAGGGCAAGGGGTCTGTTCTCACA 5005
607	S t	単い出している。 *** *** *** *** *** *** *** *** *** *
CTTCACTCTTCTGCTTGCCTGGGCTGGGGGGGGCTGGCATCAGGGGCCAGGCCTGA 4062	gr :	GCIGGGGIGGCGGGIGCCIGGGIACACACCIGICCICCITIIICIICACCCCICI 314
608	λ dd	410PneLeuProLysiYrArgoLyAsDinfoLyoLyAlaserSeroLuasDse 420
GTATGTGCTGTGCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGAGC 4122	^o	, rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa
	i qa	
4.09	Qy	6 1GlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCy 466
4183 AGGGAGGAGAAGTCCTGGGAGGCCCCTTCCTAACAGCAGCTGATGGCAGTTGGCACTG 4242	අු	GGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCACCGGGGCCTCTGCGGGGCCTCTGCCTG
604	λo d	466 sAspValSerValArgValValValQllyGluProThrGluAlaArgValValProGlyAr 486
4243 CACGCTGTCTGCCTGTTCCTTTGCCCACTTGTTGAGCTGCATGGTGAGCCGTGGGCTTCC 4302	9 io	5 Tealestelectestatestelectedstatestelectedstatestelectedstatestelectedstatestelectedstatestelectedstatestelectedstatestelectedstatestelectedstatestelectedstatestelectedstatestelectedstatestatestelectedstatestele
608	∂ 6	9 GOLY THE CYSTER OF THE PROPERTY OF THE PROPE
CTGGTGTCAGGTTTGAGCTCTGCCATGGCTCCCACCTCGCAAATGCAGCCAACTCAACTC 4362) }	6 oSerIeuDheMatGluSerTleValGluIeuSerGluSerValThrAlaTurMetValSe 526
608	7 A	ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCATATGGTGTC
TTCTGGCATGGGACAATGTTGGATAAGACCTGGCCTTGTCCTTAAATAGGGGCTCTGG 4422	Qy	
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
                                                                                                                                                                                                                                                                        165 AIGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTG 224
                                                                                                                                                                                                                                                                                                                                                                                                            344 ACTACATCCTCCTTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                     04 CCTCTGCCCTGGGAGCTGCTTGGAGGAGGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              524 CCCCAGTCACCTCTGGATCCCTGGTCCTGCACAGAGCCTGGCTCATAGGAGACACTGGAG 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                704 TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763
                                                                                                                                                                                                                                                                                                                                              1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu
                                                                                                                                                                                                                                                                                                      21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              584 AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTÄTAGCGATTATCTCATTTAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCCTCACC
                      treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          764 GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGGTGGACTCCTGACTCTGCA
                                and as markers for the
                                                                                                                                     1706 T; 1 other;
                      for diagnosing and
                                                                                                                                                                 6976
551
0
2
                                                                                                                                                                                      Conservative:
Mismatches:
                                                                                                                                                                  Length:
Matches:
                                                                                                                                                                                                           Indels:
                                                                                                                                     C; 1961 G;
                                                                                                                                                                                                                                         US-09-593-793A-113 (1-553) x ABL95412 (1-6976)
                  New prostate-specific polynucleotides for diseases, in particular prostate cancer, progression of cancer
                                                             Claim 1; SEQ ID NO 705; 87pp; English.
                                                                                                                                    BP; 1312 A; 1996
                                                                                                                                                                 6.81e-161
2144.00
30.48%
30.48%
74.94%
WPI; 2002-255649/30
                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                     Sequence 6976
                                                                                                                                                          Alignment Scores:
                                                                                                                                                                                                           Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                       57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                            cancer; prostate cancer; vaccine; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalos MD;
Carter D;
5503 TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dillon DC, Mitcham JL, Harlocker SL, Jiang Y, GR, Retter MW, Stolk JA, Day CH, Vedvick TS, Wang A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                       Human P553S splice variant SEQ ID NO 705.
                                         5563 CGACTTGCCCAAATACTCAGCG 5584
                                                                                           ABL95412 standard; cDNA; 6976
                                                                                                                                                                                                                                                                                                                                  980S-0115453.
980S-0159812.
990S-028946.
990S-0352616.
990S-0439313.
                                                                                                                                                                                                                                                                                                                                                                                                          2000US-058857
2000US-058857
2000US-0568100
2000US-0593193
2000US-0593793
2000US-0593783
2000US-0651236
2000US-0651236
2000US-0651236
2000US-0651236
                                                                                                                                                                                                                                                                                                      97US-0904804.
98US-0020956.
98US-0030607.
                               rAspLeuAlaLysTyrSerAla
                                                                                                                                                                                                                                                                       2001US-0759143
                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     XU J.
DILLON D C.
MITCHAM J L.
HARLOCKER S L.
                                                                                                                                                                                       gene therapy; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKEIKY Y A W.
HEPLER W T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HENDERSON R A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KALOS M. FANGER G R. RETTER M W. STOLK J A. DAY C H. VEDVICK T S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARTER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JIANG Y.
                                                                                                                                                                                                                            US200202248-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LI S X.
WANG A.
                                                                                                                                                                                                                                                                                                                                                                                                                              09-MAY-2000;
12-MAY-2000;
13-JUN-2000;
27-JUN-2000;
10-AUG-2000;
                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                      12-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                           14-JAN-2000;
27-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2000;
10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                09-APR-1999;
13-JUL-1999;
12-NOV-1999;
18-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-AUG-2000;
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                                                                                                                                                                                                                                                                                                      01-AUG-1997;
09-FEB-1998;
25-FEB-1998;
                                                                                                                                                                                                                                                   21-FEB-2002
                                                                                                                                                                                                                                                                                                                                                         15-JAN-1999
                                                                                                                                                                                                                                                                                           25-FEB-1997
                                                                                                                ABL95412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (XUJJ/)
(DILL/)
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(HEPL/)
(HEND/)
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(FANG/)
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Li SX,
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0y	57	25	ź	1064
QQ	884	CCCAGGAAGAGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 943	<u>a</u>	1304
δy	57	57	À	6T£
qq	944	GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTMTTAGTTGCTCC 1003	qa	2024 #
Οÿ	57	75	ΟŸ	319
οp	1004	ATGCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1063	qq	2084
οy	57	15	δλ	319
Op	1064	AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC 1123	ad s	2144 (
ογ	57	15	ò	₹T\$
qq	1124	TTCTCACGGAGCTTGGTTCCCCTTCCCCTTTACTTGTCCCAGCCATTGACTCAT 1183	qa (2204 4
δý	58		λο :	2264 1
අු	1184		QY	319
ઠે ક	72	GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPhe1leTrpAla 91 	οqα	2324 (
3 8	92	111	Qy	319
; 음	1304		qa	2384 1
ò	112	131	ΟY	319 -
. d	1364		qa	2444 P
ò	132	15	δy	319
r q	1424		qq	2504 1
οy	152	ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171	Oy	319
QQ	1484		qa	2564 1
Qy	172	1	δy	319
q	1544		QQ	2624 1
ογ	192	LeuGlyThrGlnGluGluCysLeuPheGlyLeuThrLeuIlePheLeuThrCysVal 211	οy	320
o qo	0		qu	2684 T
δ	212	AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly 231	ογ	336 u
qq	1664	7	qu	2744
^ 0	232	LeuSerAlaProSerLeuSerProHisCvsCvsProCvsArgAlaArgLeuAlaPheArg 251	δy	356 u
g q	1724		Dp	2804
ò	252	27	δy	376 2
. a	00	. œ	Db	2864
ò	272	291	Qy	396 c
. a	1844	ক	QQ	2924 0
Οy	292	TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311	οy	409
QQ	1904		QQ	2983 1
٥y	312	GluAlaArgArgHisTyrAspGlu319	Qy	409

qq	1964		2023
Qy	319		319
qq	2024	AGCCGCCCACCAGAGACGACACTCGGGGCTGTCTTGGGCTGGTGCTCTCCTTCCT	2083
Qγ	319	-	319
QQ	2084	CCCGACTTCTCTGTCAGGAAAGTGGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG	2143
οy	319		319
Dp	2144	GTGTGGAACATCTCTGCTTTGCGGTTTCAGGAAGGCCTCTGGCTGCTGTAGGAGTCTGATC	2203
Οy	319		319
QQ	2204	AGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAG	2263
ΟY	319		319
QQ	2264	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCT	2323
Qy	319		319
Op	2324	CCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCG	2383
δý	319		319
Dp	2384	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGCCTGTCCTCACAGCTG	2443
ΟÝ	319		319
pp	2444	AGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACA	2503
δy	319		319
qq	2504	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGGTAGAAAGGGGAAGGG	2563
Οy	319		319
qq	2564	TGCTGGGGAGCAGGGCTGGTCCACAGGTCTCGTGCAGGAGGTACCTGTGGTTCCGCC	2623
δy	319		319
Op	2624	TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTGGCCTCTGTCTG	2683
ΟY	320	Alailes	336
QQ	2684	AGCCTGGGGCTGTTCCTGCAGTGCGCCAT	2743
ΟY	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe	356
Dp	2744	TCTCTGGTCATGGACCGGCTGGTGCTGTTTTGGCACTCGACCACTCTATTTTTTTT	2803
yo q	356	ualaservalalaalapheprovalalaaladlyalaarhrCysLeuserHisservalal 	376
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25 A2	396 2924	OJYTITLEUNTASSELEUTYTHISATQUIUJYSLINVAL 	409 2982
οy	409		409
qq	2983	AGTCAGGGTGGGAGGGGTGGTTTTTGGGAGGCCAACTAGCTCAGAACCTGGTAT	3042
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Dp	3043	CTGGCAAGCAACTTTGGAGAATGCTTTTTGAATCAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA	_	
2	409		Qy	4
ු සු	3103	GGGCCAGAGGCTTGGGCTGCAGACAGTGTAGATTAGATT	qa	41
į	•		Qy	4
ò	404	607	qq	42
q	3163	TCAGGACTGTGTAGCACTTGAATGGATGATTGCAGGAAATGCAAAATACGATAGTGGGAA 3222		•
Qy	409	408	ζ, ζ	.
q	3223	TCCCGAAGGGTCAGGCCAGCAGGAGCCCTAGGCTTCTAGGCTGGTTGTTCTATGGAGAGG 3282	QQ -	4,
οy	409	607	oy Oy	4
qq	3283	CAGGGCGCTGAATCAGATGACCCCTGGGCCATTCAGCCTCAGCAGACGGGAGTGGGAATG 3342	qa	4
δy	409	409	δλ	4
qq	3343	GTCCAGCCITAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402	qa -	44
ΟŸ	409	608	δδ	4
a	3403	TCTGGTCTCTGAGATGGGGCAGGCTCCTTCCTACCCCCTTTCTTGGGCTATTTTTCT 3462	qq	4
οy	409	608	δλ	4
qq	3463	TITCIGICIAATICCCTITICTITICCTGCATCCCTTTGCCTCCTTCCCTTTCTCT 3522	QQ .	4.5
οy	409	607	δλ	4
qq	3523	TCCCCTTCCCCTTCCCCTGTGGCAGATATCTGAGCTTGACACCTGACCCACTCACT	gg —	4
δy	409	409	Οŷ	4
qq	3583	CACTGTGTAAGTTGTGGGGACCTCCTTCTTGGTTGGCCCTACACTAACCAGCCCCTCCAG 3642	QQ ,	40
δy	409	409	OY .	4
QQ	3643	GGGCCCCTTTCCTTGGGAAGCCACCTAACCCAGGTAGTGTGGTCATCCTTGTCCCTCCA 3702	qq	47
οy	409	409	Qy .	4 ;
QQ	3703	CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGGCGGGGGGGG	αn	4
Óγ	409	608	Ολ	4
qq	3763	GGTGTCCCAAGGGAGGAGGAGGACTGCTCTCATAGAGCTCTCAGACTGTAGGGA 3822	qq	4
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QQ	3823	AGACCTGCCCCTGCGTCTCGTAGCACTTGAGGAGAGGAG	gg :	2. 4.
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qq	3943	TTTGGTTGGGGGGGCCTGGTCCCTGAGGCCCCTGTTAGCCCCACTGATAACCTTCTTCAGC 4002	ga d	, ,
δy	409	408	λα d	4. 0
qq	4003	CTTCACTCTTCTGCTTGCCTGGGCTGGGGGGGGGCTGGCATCAGCGGCCAGGCCTGA 4062	2	2
ογ	409	408	23	, r
qq	4063	GTATGTGCTGTCGTGCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCCAGATGGAGGAGC 4122	a a	7
ογ	409	409	Z 48	י י
QQ	4123	ATGTCTGTCGGACCACTCCAGACTCCAACCTCAGGGGACATTCCTGGGGTGGCAGGC 4182		1

5262	CCTTCCCTAATGGACACGT	CCTGATG	5203	qq
446	ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 4	rLeuMet	426	ΟŊ
2	TGCTAGCAGTGAGGACAG	GCCTTAGG	5143	QQ Dp
5142	GCTGGGGTGGTGGTGCCAGTGGTGGGTACACACTGTCCTCTTCCCCTTTTCTTCACCCCTCT 5	GCTGGGG	5083	q à
409	7		409	ΟŸ
5082	GCTCCTGATTCTCATGAAGTCCCATTGCCCCTGGGATGGAGGCAAGGGTCTGTTCTCACA 5	GCTCCTG	5023	qq
409			409	QY
5053	CTGAGGAAGGGTCCTGGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCCT	CACTCCT	4963	qq
409	,		409	Οy
4962	AGAGGAGACCTAGACTTCTGGGTTCACATTTGTCCCCGCCTACCCCGTTACCCTTCTCC	AGAGGAGI	4903	qq
409			409	οy
490	CTCTCTGATCTGTGATATTGAGTTTGTCTGCCTCTTACCTGTTCTAAGAGGCT 4	CTCTGTT	4843	pp
409			409	Οy
484	GTGCATCTCTTACCACCGTCTTCATTCCCCCTGTGTCTTTTCCTTACCTTGGAG	TGTTCTG	4783	qq
409			409	Qy
4782	TAGGAGAGCCTGCGTGGGGTTTGGGCCATCAGGGG¢CCTGCCTTGGCTTTTGTTCTCCTC	GTTAGGA	4723	qq
409		1	409	δy
4723	ACCGGGCAATGAGGATTTCCAGATGTCGGAGTGGAGGGCAGGAAGGA	TCTCTGC	4663	Dp
409		1	409	Qγ
466	AGGGAGCTCATGGCAGGCAGCTACCCTAGTGGCATCTGGGACCCCAGAGAGGCAGAGCT	AGGGAGC	4603	Dp
409		1 1 1	409	Qy
460	AGAGGGACATTCCTCCTGCTTGGGGTCTACTGGATTCTCCCTGCCCCAAGGCTGGGGACA	AGAGGGA	4543	Dp
409		1	409	οy
4542	AGGAAGGAAGTGAGAAGCCTTCAACATTAGCACAGGCTGGGGGTGGGGAGGTGGGA	CAGCAGG	4483	Dp
409			409	δλ
4483	GCCATCAAGGGCAGGGGTTGGGGGGGATGGTGGTCGACCAGTCACTCTGATCTAAGTCAGA	GCCATCA	4423	qq
409			409	δy
4422	TCTGGCATGGGGACAATGTTGGATAAGACCTGGCCTTGTCCTTAAATAGGAGGCTCTGG 4	TTCTGGC	4363	qq
409		1 1 1 1 1 1	409	δy
4362	AGGTTTGAGCTCTGCCATGGCTCCCACCTCGCAAATGCAGCCAACTCAACTC	CTGGTGTC	4303	QQ
409			409	Οy
4302	CACGCTGTCTGCCTGTTCCTTTGCCCACTTGTTGAGCTGCATGGTGAGCCGTGGGCTTCC 4	CACGCTG	4243	QQ
409			409	Óγ
424	AGAAGTCCTGGGAGGCCCCTTCCTAACAGQAGCTGATGGCAGACTTGGCACTG	AGGGAGGAGAAGT	4183	Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful
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Carter D;
        5263 GGGTGCTGGAGGCGATGCCTCCCACCCCCCGCGCTCTGCGGGGCCTCTGCCTG
                                                                                                                                           rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe
                                            OSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe
                                                                                                                 5503 TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG
446 1GlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAlaCy
                                  466 sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr
                                                                     gGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPr
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                                                                                                                                                                                                                                                                                                           tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human prostate-specific polypeptides and polynucleotides diagnosis and treatment of cancer, especially prostate or
                                                                                                                                                                                                                                                                                                          cancer; ss; cytostatic; immunostimulant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   on DC, Mitcham JL, Harlocker SL, Jiang Y, Retter MW, Stolk JA, Day CH, Vedvick TS, J A, Skeiky YAW, Hepler WT, Henderson RA;
                                                                                                                                                                                                                                                                                         prosate cDNA P553S splice variant #2.
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                                                                                                                                                                                                                                   AAS64039 standard; cDNA; 2904 BP
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2000US-0558100.
2000US-0570737.
2000US-0655783.
2000US-0655783.
2000US-0651236.
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06-SEP-2000; 2
02-OCT-2000; 2
10-OCT-2000; 2
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09-MAY-2000; 2
12-MAY-2000; 2
13-JUN-2000; 2
27-JUN-2000; 2
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cancer, especially prostate cancer. The purypertures, project the antigen-presenting cells are useful for stimulating and/or expanding the antigen-presenting cells are useful for stimulating the development of cancer especially prostate cancer. Compositions comprising the polyprotide and/or polypreptide are useful for stimulating an immune response, and for treating cancer. The oligonocleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
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                     PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg
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-- ArgMetGlySerLeuGlyLeu
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                                                                                                                                                                                                CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu
                                                                                                                                                                                                                                                                                                                                         Human; prostate cancer; prostate-specific; diagnosis; vaccine;
cytostatic; gene therapy; metastasis; ss.
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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I), (II), and the antibodies to (II), tusion proteins comprising (II), and isolated T cells prepared using (I) or (II) are used treat cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) and (II) can be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. Analys337 to Analys344 and AaM01115 to exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                               or
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Stolk JA, Skeiky YAW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAsp
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treating prostate cancer in a
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Conservative:
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                                       Harlocker
Retter MW,
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                                                                                                                                                                                                                                                    Claim 1; Page 459-460; 543pp; English.
                                       GE,
                                                                                                                                                                  polynucleotide encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.52e-143
1920.50
77.23%
77.23%
67.13%
                                     Mitcham GR, Day G
                                                                                                                                                                                      diagnosing, monitoring and
                                                             Fanger GR,
                                                                                                                                                                                                              for use in vaccines -
                                                  Kalos MD, Fanyer Tanger MJ;
                                                                                                                         WPI; 2001-425873/45.
(CORI-) CORIXA CORP
                                       Dillon DC,
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Best Local Similarity:
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DB:
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	JT 28 5410	ABL9541	ABL/95410;	19-JUL-2002 (first entry)	Human P553S Splice Variant SEQ I	<pre>KW Human; cancer; prostate cancer; va KW gene therapy; gene; ss. vx</pre>	OS Homo sapiens.	AA PA US200202248-A1.	PD 21-FEB-2002.	AA PF 12-JAN-2001; 2001US-0759143.	25-FEB-1997; 01-AUG-1997;	09-FEB-1998; 25-FEB-1998;	14-JUL-1998; 23-SEP-1998;	13-JAN-1999; 09-APR-1999; 13-JHT-1999;	12-NOV-1999; 18-NOV-1999;	14-JAN-2000; 27-MAR-2000;	09-MAY-2000; 12-MAY-2000; 13-JIIN-2000:	FR 27-JUN-2000; 200020-055755. PR 27-JUN-2000; 2000US-0605783. PR 10-AUG-2000; 2000US-0636215. PR 29-AUG-2000; 2000US-0651236.	06-SEP-2000; 02-OCT-2000; 10-OCT-2000;	c ux (/ccux)	(MITC/) MITCHAM J L.	(JIAN/) JIANG Y.	(KALO/) (FANG/) (RETT/)	(STOL/) STOLK J A. (DAYC/) DAY C H.	(CART/	(LISX/) (WANG/) (SKEI/)	PA (HEPL/) HEPLER W T. PA (HEND/) HENDERSON R A.	XX YI Xu J, Dillon DC, Mitcham JL, Ha: PI Fanger GR, Retter MW, Stolk JA, DI Ti SY Gang A Chailer VM Honl	WPI; 2002-255649/30.	The New prostate-specific polynucleotic pt diseases, in particular prostate or progression of cancer xx	
b 421 GGCGTGCCCAGAGCTGAGCCGGGCACCGGAGACACTATGATGAAGGAAG	321	b 480 TCTGGCTGCTGTAGGAGTCTGATCAGAGTCGTTGCCCCCAGTTTGACAGGAAAGGCGG 539	у 321 321	b 540 AGCTTATTCAAAGTCTAGAGGGAGTGGAGGTTAAGGCTGGATTTCAGATCTGCCTGGT 599	у 321 321	Db 600 TCCAGCCGCAGTGTGCCCTCTGCTCCCCAACGACTTTCCAAATAATCTCACCAGCGCCT 659	у 321 321	Db 660 TCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCT 719	Qy 321 321	Db 720 CTCACCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGC 779	322ArgMetGlySerLeuGlyLeu 32	780 CTTCAGCAAGGGGGGGTTGCCCACATTCTGAGGGGGGTTCGGATGGGCAGCCTGGGGCTG 83	Oy 329 PheLeuGInCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGInArg 348	ore increased and increased an	900 TTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCC	369 ThrCysLeuSerHisS	096	Oy 389 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGlütysGln 408	409 ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet 428	1080 GIGTICCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATG 1	429 ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAla 448	1140 ACCACCTTCCTGCCAGGCCCTAGGCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGCT 1	y 449 typelyster(lybeubeuProProProProProProProProProProProProProP	y 469 ServalArgValvalValvalGlyGluProThrGluAlaArgValValProGlyArgGlyIle 488	1260	489 CysLeuAspLeuAlalleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeu 508	1320 TGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCCTG	y 509 PheMetGlySerILeValGLnLeuSerGLnSerValThrAlaTyrMetValSerAlaala 528 	y 529 GlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValValPheAspLysSerAspLeu 548 	549 AlaLysTyrSerAla 553 	
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nan; cancer; prostate cancer; vaccine; cytostatic; immunostimulant; ne therapy; gene; ss.
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Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ry prostate-specific polynucleotides for diagnosing and treating seases, in particular prostate cancer, and as markers for the sgression of cancer
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                                                                 nan P553S splice variant SEQ ID NO 703.
                                                                                                                                                                                                                                                                                5-FEB-1997; 97US-0806099.
1-AUG-1997; 97US-0804804.
9-FEB-1998; 9BUS-0020956.
3-SEP-1998; 9BUS-0115453.
3-SEP-1998; 9BUS-0115453.
3-MR-1999; 9BUS-0159812.
3-JUL-1999; 9BUS-0159112.
3-JUL-1999; 9BUS-0132149.
9BUS-0132149.
3-JUL-1999; 9BUS-0135616.
3-JUL-1999; 9BUS-0135616.
3-JUL-1999; 9BUS-0135616.
3-JUL-1999; 9BUS-0135616.
3-JUN-2000; 2000US-0558100.
2-MAY-2000; 2000US-0558100.
3-JUN-2000; 2000US-055813.
3-JUN-2000; 2000US-055813.
3-JUN-2000; 2000US-055813.
3-JUN-2000; 2000US-055813.
3-JUN-2000; 2000US-055813.
3-JUN-2000; 2000US-055813.
4-JUN-2000; 2000US-055813.
5-ZCT-2000; 2000US-055713.
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                                (first entry)
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DILLON D C.
MITCHAM J L.
HARLOCKER S L.
JIANG Y.
KALOS M D.
FANGER G R.
STOLK J A.
DAY C H.
VEDVICK T S.
CARTER D.
LI S X.
WANG A.
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            The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
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Matches:
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Mismatches:
Indels:
Gaps:
                                            542 A; 875 C; 773 G; 714 T;
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NO 703; 87pp;
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/note= "Xaa not given in amino acid sequence of
Figure 12b (AAM50662), which has a Val
residue at amino acid position 208 not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antigen;
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    Homo sapiens.
    Escherichia coli.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine;
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The present sequence is that of a triple gene fusion comprising, from the 5' end, the trxA thioredoxin gene from Escherichia coli, from the 5' end, the trxA thioredoxin gene from Escherichia coli, and the man ubiquitin coding sequence, the prostate antipen PSOIS (amino acids 1-320) coding sequence, and DNA encoding a histidine tail. The triple fusion was constructed in plasmid pRITIS115, under the control of the lambda pL promoter. Triple fusion protein (see AAMSOG62) was production of triple fusion proteins of the invention comprising ubiquitin fused between thioredoxin and a protein of interest, in this case PSOIS(aal-320). A claimed method of producing a recombinant protein of interest involves: culturing a host cell (preferably E. coli) under conditions which allow conceptease (especially UBPI from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial
                                                                                                                                                                                                                                                                                                                                                              Novel DNA sequence encoding triple fusion protein comprising ubiquitin fused between thioredoxin and polypeptide of interest, useful for producing recombinant polypeptide of interest suitable for medicinal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ubiquitin-specific endoprotease in vivo. In the present case, expression was controlled by addition of tryptophan. The recombinant protein can used as a vaccine for cancer therapy.
not encoded by the present sequence"
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                                                                                                                    19-JUN-2001; 2001WO-EP06952
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30-OCT-2000; 2000GB-0026484
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P-PSDB; AAM50662.
                                       WO200200892-A1
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783 1593 320 Conservative: Mismatches: Indels: Length: Matches: US-09-593-793A-113 (1-553) x ABA91284 (1-1593) Gaps: 5.84e-126 1696.00 100.00% 100.00% 59.28% Percent Similarity: Best Local Similarity: Alignment Scores: Pred. No.: Query Match: 41 724 61 Score: QQ ò g ò ŏ q õ g

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Qy Db	81	ArgTyrGlyArgArgArgProPheIleTrPAlaLeuSerLeuGlyIleLeuLeuSerLeu 100
Qy	101	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
Qy	121	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140
Qy Db	141	ThrProLeuGluAlaLeuLeuSerAspLeuPhergAspProAspHisCysArgGlnAla 160
Qy Dp	161	TyrSerValTyralaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180
Qy	181	IleAspTrpAspThrSerAlaLeuAlaProTyLeuGlyThrGlnGluGluGysLeuPhe 200
Qy Dp	201	GlyLeuLeuThrLeuIlePheLeuThrCysValaalaThrLeuLeuValalaGluGlu 220
Qy Db	221	AlaAlaLeuGlyProThrGluProAlaGluG yLeuSerAlaProSerLeuSerProHis 240
Qy Db	241 1324	CysCysProCysArgAlaArgLeuAlaPheA [†] gAsnLeuGlyAlaLeuLeuProArgLeu 260
Oy Dp	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280
Oy :	281	SerTrpMetalaLeuwetThrPheThrLeuPheTyrThraspPheValGlyGluGlyLeu 300
Oy Db	301	TyrGlnGlyValProargAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
RESU ABN8 ID XX AC	LT 30 1320 ABN81 ABN81	320 standard; cDNA; 3663 BP. 320;
X L	30-AU	G-2002 (first entry)
DE	Human	mast cell related gene MC14 SE
X X X X X	Human vasot gene;	.; mast cell; MC; antiallergic; antiinflammatory; antiasthmatic; ropic; dermatological; allergy; hypersensitivity; rhinitis; asthma; ss.
SO	Ношо	sapiens.
FH FT	Key	lon/Qualifie 146 - a
rr rr X	CDS	/product= "MC14-1" 1238218 /*tag= a /product= "MC14-2"
PN	W0200	1246389-A2.

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The invention relates to isolated nucleic acid (ABN81319-ABN81324),

corresponding to genes differentially expressed in mast cells following

activation or in patients with allergic hypersensitivity disease. (I)

that encodes proteins (AB877569-AB877575) [II] or a protein fragment of

that least 6 amino acids. (II) is useful for identifying binding

constant or (II) if at least 6 amino acids. (II) is useful for identifying binding

constant or atopic dermatitis or mastocytosis) in a subject which

constrain or atopic dermatitis or mastocytosis) in a subject which

constrain or atopic dermatitis or mastocytosis) in a subject which

constrain or atopic dermatitis or mastocytosis) in a subject which

constrain or atopic dermatitis or mastocytosis) in a subject which

constrain or atopic dermatitis or mastocytosis in a subject which

constrain or atopic dermatitis or mastocytosis in a subject which

constrain or atopic dermatitis or identify the relative expression level of

constraint or monoclonal antibodies. (II) is useful for identifying

agonists or antagonists or activity and as an antigen to raise

collating biological activity and function of (II) and thus are useful

constraint or monoclonal antibodies in a plergic hypersensitivity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seasonal rhinitis, asthma, urticaria, atopic dermatitis or mastocytosis.
                                                                                                                                                                                                                                                                                         Novel isolated nucleic acids that are differentially expressed in mast cells in patients with allergic hypersensitivity, encoding proteins associated with mast cell regranulation and allergic hypersensitivity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3663 BP; 740 A; 1058 C; 985 G; 880 T; 0 other;
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43.118
56.068
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14-MAR-2001; 2001US-275479P.
28-MAR-2001; 2001US-279115P.
02-APR-2001; 2001US-280143P.
                                                07-DEC-2001; 2001WO-US46180
                                                                                                                                                                                                                                                         P-PSDB; ABB77570, ABB77571.
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Best Local Similarity:
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                                                                        553 CCCCAGTCACCTCTGGATCCCTGGTCCTGCAGAGCCTGGTAGGAGACACTGGAG 712
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                        533 CCTCTGCCCTGGGAGCTGCTTGGAGGGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA
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0y 0y 0y 473 ACTACATCCTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 532

ArgaspProaspHisCysargGlnalaTyrSerValTyrAlaPheMetIleSerLeuGly
GGCTGCCTGGGCTACCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTAC LeuGlyThrGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrysVal [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]
AlaalaThrLeuLeuValalaGluGlualaAlaLeuGlyProThrGluProalaGluGly
LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg
AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu
ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe
$\tt TyrThraspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrapperspheres and \tt TyrThrapperspheres and \tt TyrThrappersp$
${\tt GlualaargargHisTyraspGluGlyValargMetGlySerLeuGlyLeuPheLeuGlugluglugluglugluglugluglugluglugluglugl$
alleSerLeuValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThr
ArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThr
HisSerValAlaValVhrAlaSerAlaAlaLeuThrGlyPheThrPhe
LeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheL
ProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPhe
LeuProGlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySer
GlyLeuLeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArg
ValValValGlyGluProThrGluAlaArgValValProGlyArgGlyTleCysLeuAsp
Leuala IleLeuaspSeralaPheLeuLeuSerGlnValalaProSerLeuPheMetGly
SerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGly

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uncleotides, polypeptides, fusion proteins of the polypeptides, odies raised against the polypeptides (or antigenic epitopes ediform them) and antigen-presenting calls expressing the epitides. The antibodies are useful for detecting the presence of intigen-presenting calls are useful for detecting the presence of intigen-presenting calls are useful for stimulating and/or expanding. Is specific for a tumour protein, and for inhibiting the development uncleotide and/or polypeptide are useful for stimulating an immune note, and for treating cancer. The oligonucleotide is useful for intign cancer. The present sequence is a prostate specific for the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uman prostate-specific polypeptides and polynucleotides useful for iagnosis and treatment of cancer, especially prostate cancer -
                                                                      Kalos MD;
Carter D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; prostate cancer; ss; cytostatic; immunostimulant; tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /M. tuberculosis fusion protein RA12-P501S-E2 cDNA.
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                                                                                                                                                                                                                                                                                                                       153 standard; cDNA; 1203 BP.
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2000US-0651236.
2000US-0657279.
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G; 245 T; 0 other;

ice 1203 BP; 175 A; 415 C; 368

ment Scores: 9.07e-103 Length: 1203 No.: 1403.50 Matches: 267 it Similarity: 97.45% Conservative: 0 Local Similarity: 97.45% Mismatches: 2 Match: 49.06% Indels: 5 Caps: 1 1	XX XX XX XX XX XX XX
-793a-113 (1-553) x AaS64153 (1-1203) ValCysLeuAlaAlaGly	N X A A A
49	XX PX
LeuvalCysvalProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArg 84 	XX Id Id
ArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeuPheLeuIlePro 104 	XX DR TY
ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124 	PT PT XX PS
LeulleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144 	× 888
AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr 164 	8888
AlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAsp 184 	8888
ThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCySLeuPheGlyLeuLeuThr 204	888X
LeullePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGly 224 	SQ Aligo Pred
ProthrGluProhlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244	Score Perce Best Query
ArgalaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264 	DB: US-0
CysargMetProArgThrLeuargargLeuPheValalaGluLeuCysSerTrpMetala 284	da
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7 standard; cDNA; 1203 BP.	Oy Dp
7;	y g
-OCT-2001 (first entry)	an an

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The present invention describes polynucleotide sequences (I) which encode prostate-specific proteins (II). (I) and (II) have cytostatic activity, and can be used in vaccine production and gene therapy. (I). (II), antibodies to (II), fusion proteins comprising (II), and isolated the antibodies are also used in the detection of cancer in a patient. (I) and the antibodies are also used in the detection of cancer in a patient. The cancer that is diagnosed or treated is particularly prostate cancer. (I) and (II) can be used in vaccines. The antibodies or (I) can be used for monitoring the progression of cancer in a patient. (I) and (II) can also be used to improve diagnostic and therapeutic methods for prostate cancer. They can indicate the level of metastasis as well as the prostate volume. AAH93357 to AAH93944 and AAM01115 to AAM01318 represent polynucleotide and amino acid sequences used in the exemplification of the present invention.
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Retter MW, Stolk JA, Skeiky YAW;
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Ral2-P501S-E2 construct cDNA sequence.
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Kalos MD, Fanger GR, Day CH,
Wang A, Meagher MJ;
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                                                                                                                                                                                       ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu
                LeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu
                                                                               AlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAlaTyrSerValTyr
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Chimeric - Homo sapiens.
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14-JUL-1998,
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The present invention provides prostate-specific coding sequences and their encoded proteins. These can be used in the diagnosis and treatment of cancers, particularly prostate cancer. The present sequence is a CDNA described in the invention.
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A, Day CH, Vedvick TS,
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GR, Retter MW, Stolk JA, Da
Wang A, Skeiky YAW, Hepler
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14-JAN-2000; 2000US-0483672.
27-MAR-2000; 2000US-0536857.
29-MAY-2000; 2000US-0568100.
12-MAY-2000; 2000US-0593733.
27-JUN-2000; 2000US-0593793.
27-JUN-2000; 2000US-0593793.
29-AUG-2000; 2000US-0551236.
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Stroupe SD,
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Billing-Medel PA, Klass MR, Roberts-Rapp L,
Kratochvil JD, Russell JC, Hodges SC;
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The present invention is related to a number of partial coding and protein sequences for the human prostate tissue protein PS108. These sequences can be used in the diagnosis and prognosis of prostate diseases, particularly prostate cancer. They can also be used to produce antibodies which can be used in treatment. The present sequence is one of the PS108 partial coding sequences.
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ncer), comprising detecting sequences in a test sample
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 prostate (e.g. prostate cancer), any of PS108 nucleic acid sequence
                                                                                                                                                                  Length: | Matches: | Conservative: Mismatches:
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                                                                                                                                 C; 561 G;
                                 English.
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                                                                                                                                 BP; 414 A; 618
                               77-80; 55pp;
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eases of the presence of
                                 Column
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                                Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence tag (EST) consensus sequence. The sequence was produced from overlapping PSIOB ESTs sequences to produce a full length consensus sequence. This sequence was then used to produce PSIOB polypeptides which are useful in assays for detecting antibodies to prostate tissue, and as immunogens to produce antibodies. The polypeptide is useful for screening compounds which specifically bind to the polypeptide is useful for screening for drugs, compounds, or any other agent which can be used to treat diseases associated with PSIOB. The antibody is useful to detect, or for image localisation of, PSIOB antigen in a patient, for detecting or diagnosing a disease or condition, as delivery agents for therapeutic agents as well as for diagnostic tests and for screening for diseases or conditions associated with PSIOB, especially cancer. The antibody is also useful for generating chimeric antibodies for therapeutic uses for inhibiting the biological activity of PSIOB, in therapy (for e.g. to the prostate tissue disease including prostate cancer and its metastases), and to detect the presence of any polypeptide in a test sample which shares one or more antigenic determinants with the PSIOB
                                                                                                                                                                                                                                                                                                                          Prostate; PS108; immunogen; drug screening; image localisation; diagnostic; therapeutic; prostate tissue disease; cancer; metastasis; expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4, Colpitts TL, Friedman PN, Gordon J;
Klass MR, Kratochvil JD, Roberts-Rapp L;
Yu H;
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/product= "Prostate-specific protein PS108"
                                                                                                                                                                                                                                                                        Prostate gene PS108-specific cDNA (EST) consensus sequence
561 G; 540 T; 0 other;
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1..799
                                                                                                                        AAS07155 standard; cDNA; 2133 BP
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97US-0850713
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Stroupe SD,
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02-MAY-1997;
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Russell JC,
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2133 255 0

Length: Matches: Conservative:

3.78e-93 1287.00 100.00%

Percent Similarity:

Alignment Scores:

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                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                            299 GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp
                                                                                                               2 GGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGAT
                                                                                                                                                                              62 GAAGGCGTTCGGATGGGCAGCCTGGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTC
                                                                                                                                                                                                                                                                                           362 GGAGGTGCTAGCAGTGAGGACAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGA
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                                                                                                                                                              319 GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe
                                                                                                                                                                                                                              339 SerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             542 GAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCC
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                 Indels:
                                                               US-09-593-793A-113 (1-553) x AAS07155 (1-2133)
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               44.988
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diseases of the prostate (e.g. prostate cancer), comprising detecting the presence of any of PS108 nucleic acid sequences in a test sample
ACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACA 301
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                                                                                                                   PheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGln
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention is related to a number of partial coding an protein sequences for the human prostate tissue protein PS108. Th sequences can be used in the diagnosis and prognosis of prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate cancer; PS108; antibody; tumour; metastasis; ds.
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roupe SD, Yu
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s MR, Roberts-Rapp L, S
JC, Hodges SC;
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Russell JC, I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is derived from overlapping clones AAV71166-79. The clone sequence is derived from overlapping clones AAV71166-79. The clone sequences are PS108 gene-specific. They are used in the method of the invention. The specification describes a method for detecting the presence of a target PS108 polynucleotide in a test sample. The method comprises contacting the test sample with at least 1 PS108-specific polynucleotide or complement, and detecting the presence of the target PS108 polynucleotide. The products can be used for detecting, ps108 polynucleotide. The products can be used for detecting, proposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (PBH), prostatic intrappithelial neoplasia (PIN) and cancer. In particular the products can be used in drug screening and gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated prostate-specific polynucleotides - used to develop products for the diagnosis and treatment of prostate diseases, e.g. benign hyperplasia, prostatic or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents the consensus sequence for a PS108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPhe
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                                                                                                                                                                                                                                                                                                                       Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN;
Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;
Roberts-Rapp L, Russell JC, Stroupe SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2152 BP; 419 A; 622 C; 569 G; 542 T; 0 other;
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                       Location/Qualifiers
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  sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            663 GCCTATATGGTGTCTGCCGCAGGCCTGGGTCGCCATTTACTTTGCTACACAGTA
                                                                                                                                                                   GlnGlyvalProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyval
                                                                                                                                                                                        3 CAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTT
                                                                                                                                                                                                                                                                                                                                                 SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe
                                                                                                                                                                                                                                                                                                                                                                                                                                  442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522 AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal
                                                                                                                                                                                                                                                                                                                                       AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423 CCTAATGGACACGTGGGTGCTGCAGGCCAGTGCCTGCTCCCACCTCCACCGCGCTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         502 SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482 ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu
   can also be used to
diseases, particularly prostate cancer. They can also be used to antibodies which can be used in treatment. The present sequence of the PS108 partial coding sequences.
                                                                       2124
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                                                                       Length:
Matches:
Conservative:
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                                          G; 539
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                                          411 A; 616 C; 558
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                                                                       8.56e-92
1270.00
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                                          BP;
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Best Local Similarity:
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                                                            Alignment Scores:
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The sequence represents the coding sequence of prostate gene PS108-
specific expressed sequence tag (EST) CDNA clone 171346fH. The sequence
was used along with other overlapping CDNA clones to produce a full
length consensus sequence (see AASO7155). This sequence could then be
used to produce PS108 polypeptides which are useful in assays for
detecting antibodies to prostate tissue, and as immunogens to produce
antibodies. The polypeptide is useful for screening compounds which
specifically bind to the polypeptide and for screening for drugs,
compounds, or any other agent which can be used to treat diseases
compounds, or any other agent which can be used to treat diseases
compounds, or any other agent which can be used to treat diseases
compounds, or any other agent which can be used to treat diseases
compounds, or any other agent which can be used to treat diseases
compounds, or any other agent which for detecting or diagnosing a
disease or condition, as delivery agents for therapeutic agents as well
as for diagnostic tests and for screening for diseases or conditions
associated with PS108, especially cancer. The antibody is also useful for
generating chimeric antibodies for therapeutic use, for inhibiting the
tissue disease including prostate cancer and its metastases), and to
detect the presence of any polypeptide in a test sample which shares one
                                                                         Prostate; PSIO8; immunogen; drug screening; image localisation; diagnostic; therapeutic; prostate tissue disease; cancer; metastasis; expressed sequence tag; EST; ss.
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                                                                                                                                                                                                                                                                                                                                                                                 PN, Gordon J;
Roberts-Rapp
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Nte tissue, and as immunogens to produce PS108 antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or more antigenic determinants with the PS108 polypeptide.
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Klass MR, Kratochvil JD,
Yu H;
                                            Prostate gene PS108-specific cDNA clone 1711346IH
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97US-0850713.
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Hodges SC,
Stroupe SD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-424488/45.
                                                                                                                                                                                                                                                                                                                                                  LAB.
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                 Billing-Medel
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02-MAY-1997;
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AAS07601;

us-09-593-793a-113.rng

MetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAla 	36	
ATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTTGGCCAGTGTGGCGAGTT PheProvalAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAlaSer 		
TreceigleGergeeGergeeAcalGeergeeCargreeCagregeeGergergeAcargereA AlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSer 	CA 242 er 401 	
LeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAla 		
SerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPhe 	he 441 	
ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCys 	ys 461 	
GlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAlaArg 	rg 481 G 542	
ValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeu 	eu 501 	Pred. No. Score: Percent S Best Loca
SerGlnValAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr 	hr 521 CT 662	Query Mat DB: US-09-593
AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal 	al 541 TA 722	QQ Dp
ValPheaspLysSerAspLeualaLysTyrSerAla 553 	-	QY Db
standard; cDNA; 2143 BP.		QY
		δy
(first entry)		qq
Clone 1711346IH, the PS108 gene contig full length sequence.		QY
PS108 gene; prostate disease; benign prostatic hyperplasia; BPH; prostatitis; prostatic intraepithelial neoplasia; PIN; cancer; drug screening; gene therapy; ss.		d y
sapiens.		qq
WO9850567-A1.		δý
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(ABBO) ABBOTT LAB.	-	οy
Billing-Wedel PA, Cohen M, Colpitts TL, Friedman PN; Gordon J, Granados EN, Hodges SC, Klass MR, Kratochvil JD;		
troupe SD;	_	Οy

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The present sequence represents the full length contig of the PS108 gene, as represented by clone 171346IM. This clone is the contig of overlapping clones AAV1166-79. The clone sequences are PS108 gene-specific. They are used in the method of the invention. The specification describes a method for detecting the presence of a target PS108 polynucleotide in a test sample. The method comprises contacting the test sample with at least 1 PS108 specific polynucleotide or complement, and detecting the presence of the target PS108 polynucleotide. The products can be used for detecting, diagnosing, staging, monitoring, prognosticating, in vivo imaging, preventing or treating, or determining predisposition to diseases or conditions of the prostate such as benign prostatic hyperplasia (PPH), prostatitis, prostatic intraeplithelial neoplasia (PIN) and cancer. In particular the products can be used in drug screening and gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 GlyAlaSerAlaCySAspValSerValArgValValGlyGluProThrGluAlaArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * isolated prostate-specific polynucleotides - used to develo
oducts for the diagnosis and treatment of prostate diseases,
nign hyperplasia, prostatic or prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                            pence 2143 BP; 418 A; 621 C; 563 G; 541 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                             aim 1; Fig 1A-E; 122pp; English.
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1270.00
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(; 1999-034731/03
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The present sequence is derived from a prostate cancer-associated gene, and is represented by Incyte clone number 1864683. The sequence is used in the method of the invention. The specification clescribes a method for identifying biomolecules for the diagnosis or treatment of diseases associated with cell proliferation. The method comprises examining polymolecules, consisting of prostate cancer-specific genes, and genes of unknown function, expressed in CDNA libraries. The patterns of both gene sets are compared to identify genes of unknown function with similar expression patterns to the prostate cancer-specific genes. The biomolecules identified by the method form pharmaceutical compositions useful for the diagnosis and treatment of diseases associated with cell proliferation. Such diseases include cancer. The method may also be applied using other diseasers brostate cancer. The method may also be applied using other diseasers.
                602
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663 GCCTATATGCTGCCGCAGGCCTGGGTCGCCGTTTACTTTGCTACACAGGTA
                                             SerGlnvalAlaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThr
                                                                            603 TCCCAGGTGGCCCCATCCCTGTTTATGGCCTCCATTGTCCAGCTCAGCTCAGTCTGTCACT
                                                                                                          AlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnVal
                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
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                                                                                                                                                                                                                                                                                                                                                                                            Prostate cancer-associated gene; Incyte clone 1864683; bone cell proliferation; cancer; adrenal gland cancer; bladder ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Identifying biomolecules for the diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                               cDNA sequence of a novel prostate cancer-associated gene.
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                                                                                                                                                                                        723 GTATTTGACAAGAGGGACTTGGCCAAATACTCAGGG 758
                                                                                                                                                                      542 ValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/product= "prostate c
376..516
/*tag= b
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376..1071
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GlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAsp 318
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                                                                                                                                                                              310 GAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGC
                                                                                                                                                                                                ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu
                                                                                                                                                                                                                                   ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla
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proliferation disorders.
                 0 other;
                                           2462
241
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23
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Mismatches:
                632 G; 621 T;
                                           Length:
Matches:
                                                                                Indels:
                                                                                                         US-09-593-793A-113 (1-553) x AAZ45677 (1-2462)
                                                                                        Gaps:
diagnosis and treatment of cell
                 BP; 483 A; 726 C;
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                                        9.08e-84
1170.50
88.288
88.288
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Best Local Similarity:
                  Sequence 2462
                                    Alignment Scores:
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303 CTCCCACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTG
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919.00
96.50%
96.00%
32.12%
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Best Local Similarity:
                                                                                                                                                                                                                                                                 Homo sapiens
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01-AUG-1997;
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                                                                                                                                                                                                                                               therapy;
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DB:
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                                                                                                                                                                            The present sequence is a new DNA which encodes an immunogenic portion of a prostate tumour protein. The encoded immunogen, or the DNA itself, can be used as a vaccine for the treatment of prostate cancer. The DNA was identified by analysis of a subtracted cDNA library obtained by subtracting a prostate tumour cDNA expression library with a normal tissue cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                  ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis 373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides comprising immunogenic portions of prostate proteins used in a vaccine for the treatment of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerValAlaValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln
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                                                          SS.
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192
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                                                         Prostate; cancer; tumour; vaccine; immunogen; clone;
                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
Indels:
                                         cDNA sequence of prostate tumour clone L1-12
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Matches:
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                                                                                                                                          98US-0020956.
97US-0806099.
97US-0904804.
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919.00
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                        (first entry)
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01-AUG-1997;
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                        06-JAN-1999
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Pred. No.:
                                                                                                          27-AUG-1998
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        AAV61144;
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prostate
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                                                                                       513
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542 CC-ATTTACTTTGCTACACAGGTANTATTTGACAAGAACGANTTGGCCAAATACTCAGCG
                                                                                                                                                                                                 534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla
                                                                                       IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle
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    fragment of prostate tumour specific gene L1-12.

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Matches: |
Conservative:
Mismatches:
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Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                     BP
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97US-0806596.
97US-0904809.
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Query
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            (1-553) x AAV58487
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The present invention describes isolated polypeptides, comprising an immunogenic portion of a prostate tumour protein (PTP). The polypeptides and polymucleotides encoding them have cytostatic activity and can be used in vaccines and in gene therapy. The polypeptides and polymucleotides encoding them, antigen presenting cells which express comprising them can be used for inhibiting the development of prostate cancer in a patient. The polypeptides can be used to generate antibodies or anti-idiotypic antibodies for inhibiting the development of prostate the polymucleotides encoding the polypeptides can be used to generate antibodies or anti-idiotypic antibodies for passive immuno therapy. A portion of the polypeptides can be used as a probe or to modulate the expression of the polypeptides. AAA06541 to AAA06591 and AAAV82000 to AAAV8200 represent sequences used in the exemplification of
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an immunogenic portion of
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                                                                 New polypeptide useful comprises an immunogeni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to isolated prostate-specific polynucleotides, polypeptides, fusion proteins of the polypeptides, antibodies raised against the polypeptides (or antigenic epitopes derived from them) and antigen-presenting cells expressing the polypeptides. The antibodies are useful for detecting the presence of cancer, especially prostate cancer. The polypeptides, polynucleotides and the antigen presenting cells are useful for stimulating and/or expanding T cells specific for a tumnour protein, and for inhibiting the development of cancer especially prostate cancer. Compositions comprising the polynucleotide and/or polypeptide are useful for stimulating an immune response, and for treating cancer. The oligonucleotide is useful for detecting cancer. The present sequence is a prostate specific polynucleotide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human prostate-specific polypeptides and polynucleotides useful diagnosis and treatment of cancer, especially prostate cancer -
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Carter D;
cancer; ss; cytostatic; immunostimulant; tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harlocker SL, Jiang Y,
V, Day CH, Vedvick TS,
spler WT, Henderson RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G; 182 T; 14 other;
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Fanger GR, Retter MW, Stolk JA, Day CH
Li SX, Wang A, Skeiky YAW, Hepler WT,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 122 A; 250 C; 221
                                                                                                                                                     Human prostate cDNA sequence #10.
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                                                                                                                                                                                                                                                                                                                       2000US-0536B57.
2000US-056B100.
2000US-0593793.
2000US-0605783.
2000US-0651236.
2000US-0651236.
2000US-0657279.
2000US-0657279.
                                                                    AAS63458 standard; cDNA; 789
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                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                          29-JAN-2002
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                                                                                               AAS63458;
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(1-789)Gaps:

US-09-593-793A-113 (1-553) x AAS63458

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                                                                 ServalAlavalValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln 393
                                                                                          TyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433
                                                                                                                                                                                                                                                                                                                                                    GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel polynucleotide encoding polypeptide comprising a portion of prostate tumour protein useful for inhibiting development of prostate cancer or for treating prostate cancer in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            534 AlaileTyrPheAlaThrGinValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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3 GTCTATNIGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTATCCCAC
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Example 1; Column 32-33; 105pp; English

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                                                                                                                                  IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle
                    The sequence is a human prostate tumour cDNA which encodes a partial tumour protein. The DNA is useful for inhibiting the devol prostate cancer or for treating prostate cancer in a patient.
                                                Sequence 789 BP; 122 A; 250 C; 221 G; 182 T; 14 other;
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Matches:
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	.9 4403765 4 .9 4411529 4	.9 4833 4 .9 4391 4 .8 2571 4	8 3511 3 8 1765 1 8 1765 2 8 2304 1	.8 2304 4 .8 2304 4 .8 2304 4 .8 111282 4	. 000ct 8.	RESULT 1 US-09-020-956-110 ; Sequence 110, Application US/09020956	1562 MATION: Xu, Jiangchun Dillin, Davin C.	SWITON: COMPOUN SUENCES: 178 SEED and BERRY	ttle USA	6 20	OPERATING SISTEMS: PC-DOS/NN-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/020,956	CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: MAKI, DAVId J. NAME: MAKI, DAVID J.	RECISIONAL NOMBER: 31.92 RECISIONAL NOMBER: 21 TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 622-4900	INFORMATION FOR SEQ ID NO: 110 SEQUENCE CHARACTERISTICS: LENGTH: 310 base pairs	nucieic acid CDNESS: single SY: linear TYPE: CDNA	Homo sapiens	9.55e-264 2861.00 7: 100.00\$	100.008	US-US-US-US-UZU-928-110 QY 1 MetValGlnArgLeuTrpValSerArgLeuLeuArg
			2 3 109 109 109			r 1 -020-956-110 Jence 110, Ap	GENERAL INFORMATION: APPLICANT: Xu, Ji APPLICANT: Dillin	7 7 8 8	ET: SC E: SC TRY:	COMPUTER READ/ MEDIUM TYPE COMPUTER:	SOFTWARE: PATENT SOFTWARE: PATENT SURRENT APPLICATION NUMBER	CLASSIFICATION: CLASSIFICATION: ATTORNEY/AGENT IN DECTEMBER MAKI, Da	REFERENCE/D FELECOMMUNICA TELEPHONE:	FORMATION FOR SEQUENCE CHAR LENGTH: 34	TIPE: NUCLEIC STRANDEDNESS: TOPOLOGY: line MOLECULE TYPE:		Allymment Scores: Pred. No.: Score: Percent Similarity:	Query Match: DB:	-393-793A-113 1 MetValGl
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¹ MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20

TYPE: nucleic acid STRANDEDBESS: single STRANDEDBESS: single TOPOLOGY: linear T	Oy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20	Oy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80	Db 584 TTTCTCATCCCAAGGCCGGCTAGCAGCAGCCCGGTTCCCTCCTCTCTCT	Oy 181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCySLeuPhe 200
Db 1364 GCTTTCCCTGTGGCTGCCGTGCCTGTCCCACAGTGTGGCCGTGGTGACAGCT 1423 Oy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400 1424 TCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCACACACTGGCC 1483 Oy 401 SerLeuTyrHisArgGluLySGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420 1424 TCCCTCACCGGGGAGAGAGTGTTCCTGCCCAATACGGGGGACACTGGGC 1483 Oy 401 SerLeuTyrHisArgGluLySGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420 1424 TCCCTCACCGGGGAGAGGGGTTCCTGCCCAATACGGGGGACACTGGAGGT 1543 Oy 421 AlaSerSerGluAspSerLeuMeThrSerPheLeuProGlyProLysProGlyAlaPro 440 1111111111111111111111111111111111	Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGlubroThrGluAla 480 Db 1664 TGCGGGCCTCTGCCTGTCATCTCCGTACGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTG	rPheAla	Sed Pat GE GE	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: Date of the compatible COMPUTER: Date of the compatible SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: APPLICATION NUMBER: US/09/030,607 FILLING DATE: 25-FEB-1998 CLASSIFICATION: NAME: MAKI, David J. REGISTRATION NUMBER: 31,392 REFERENCE/DOCKET NUMBER: 210121.427C3 FELEPANE: (206) 682-6031 INFORMATION FOR SEQ ID NO: 110: SEQUENCE CHARACTERISTICS: LENGTH: 3410 base pairs

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Patent No. 6321716
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
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       APPLICANT: Carter, Darrick
APPLICANT: Li Samuel
APPLICANT: Wang, Aliun
APPLICANT: Weig, Aliun
APPLICANT: Hepler, William
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APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANTON: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 110
LENGTH: ANA 410
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ORGANISM: Homo sapien
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## APPLICANT: Xu, Jiangchun ### APPLICANT: Mitcham, Davin C. ### APPLICANT: Mitcham, Davin C. ### APPLICANT: Harlocker, Susan Louise ### APPLICANT: Harlocker, Susan Louise ### APPLICANT: Railos, Michael ### APPLICANT: Railos, Michael ### APPLICANT: Railos, Michael ### APPLICANT: Railos, Michael ### APPLICANT: Railos, Michael ### APPLICANT: Railos, Michael ### APPLICANT: Railos, Michael ### APPLICANT: Railos, Michael ### APPLICANT: Railos, Mark ### APPLICANT: Bay, Crail ### APPLICANT: Bay	Alignment Scores: Pred. No.: Pred. No.: 2861.00 Matches: 553 Score: 100.00\$ Matches: 553 Percent Similarity: 100.00\$ Mismatches: 0 Ouery Match: 100.00\$ Mismatches: 0 Gaps: 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Db 344	Db TITCTCATCCCAAGGCCGCTAGCAGCTGCTGTGTGTGTGTGT
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L INFORMATION:
CANT: Dillon, Davin C.
CANT: Harlocker, Susan Louise
CANT: Harlocker, Susan Louise
CANT: Jiang, Yuqui
CANT: Vi, Jiangchun
CANT: Mitcham, Jennifer Lynn
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Qy Db	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240 	; GENER; ; APPL; ; APPL; ; APPL
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QY Dp	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280 	
Oy Dp	281	SerTrpWetalaLeuWetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 30 	
Qy Dp	301	TyrGlnGlyvalProArgalaGluProGlyThrGlualaArgArgHisTyrAspGluGly 320 	Alignme Pred. N Score:
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oy Db	461	CysGlyAlaSerAlaCysAspValSerValArgValValGlyGluProThrGluAla 480 	Db 5 Qy 1
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Matches:
Conservative:
Mismatches:
                                 APPLICANT: Reed, Steven G.
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANG
TITLE OF INVENTION: AND DIAGNOSIS OF BREAST CANG
TITLE OF TREPLICATION WUBBER: US/09/602,877A
CURRENT APPLICATION WUBBER: 2000-06-22
CURRENT FILING DATE: 2000-06-22
SOFTWARE: FASTED for Windows Version 3.0
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	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 	HisGinLeuCysCysrgMetProArgThrLeuArgArgLeuPheValAla 	SerTrpMetalaLeumetThrPheThrLeuPheTyrThrAspPheValGly 	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 	ValargMetGlySerLeuGlyLeuPheLeuGlnCysalaIleSerLeuVal 	ValMetAspargLeuValGlnArgPheGlyThrArgalaValTyrLeuAla 	AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 	SeralaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyr 	SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAsp 	AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysPro	PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProPro	TTCCCTAATGGACACGTGGGGGTGCTGGAGGCAGTGGCCTGCTCCCACCTCCA CysG1yAlaSerAlaCysAspValSerValArgValValValG1yGluPro		ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSer 	LeuserGlnvalAlaProSerLeuPheMetGlySerIleValGlnLeuSer 	ThralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlalileTyrPhe	ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553	TGACAAGGGACTTGGCCAAATACTCAGCG 194	plication US/09232149

AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240 180 823 200 883 343 403 463 523 20 40 9 80 leAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe roLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly CANT: Xu, Jiangchun
CANT: Dillon, Davin C.
CANT: Mitcham, Jennifer Lynn
OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE
OF INVENTION: COMPOUNDS FOR THEIR USE
REFERENCE: 210121.427C6
NT APPLICATION NUMBER: US/09/232,149A
NT APPLICATION NUMBER: US/09/232,149A
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NT APPLICATION NUMBER: US/09/232,149A
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Matches:
Conservative:
Mismatches:
Indels:
Gaps: 9.55e-264 2861.00 100.00% 100.00% M: Homo sapien 49A-110 ilarity: Similarity: 3410 cores: ΝĀ 221 á

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APPLICANT: Mitcham, Jennifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqui APPLICANT: Harlocker, Susan L. APPLICANT: Harlocker, Susan L. APPLICANT: Harlocker, Robert A. APPLICANT: Kalos, Michael D. APPLICANT: Ranger, Gary R. APPLICANT: Ranger, Cary R. APPLICANT: Stolk, John A. APPLICANT: Carter, Darrick APPLICANT: Carter, Darrick APPLICANT: Carter, Darrick APPLICANT: Carter, Darrick APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Skeiky, Yasir A.W. APPLICANT: Wang, Allian APPLICANT: Skeiky, Yasir A.W. APPL	US-US-193-1936-113 (1-352) x US-US-US-193-1934-1934, US-US-193-1936-113 (1-352) x US-US-US-US-US-US-US-US-US-US-US-US-US-U
4 GCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTTGTCGCCCCAC 100 1 CysCysProCysargAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgleu 260 1 Hill	421 AlaserSerGluAspSerLeumetThrSerPheLeuproGlyProLy 1544 GCTAGCAGGACAGCCTGATGACCAGGCTTCTTGCTGCTGCTGTGTGTG

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181 IleaspTrpaspThrSeralaLeualaProTyrLeuGlyThrClnGluGluCysLeuPhe	221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSepProHis	DD 1001 TGCTGTCCGGGGCCCGGTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCGGGCTG 1050 Qy 261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGlüLeuCys 280 [Db 1121 AGCTGGATGGCACTCATGACGTTTTACACGGATTTCGTGGGGGGGTG 1180 Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 319 Db 1181 TACCAGGGCGTGCCCAGAGCTGAGGCGGGCACCGAGGCCCGGAGACACTATGATGAAGGT 1240	Qy 319 319 Dh 1241 aaggogganggaagaagagagagagagagagagagagaga	319	Db 1301 GCTGTGTCTGGGCTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAGTGGGG 1360 Qy 319	1361 ATGGACCCCATCTGCATACACGCCTTCTCATGGCTGTGGAACATCTCTGCGTTTC 14	Qy 319 319 Db 1421 AGGAAGGCCTCTGGCTGTTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAG 1480	QY 319	Qy 319 319	319	1601 CCAGGGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTT 16	OY 319	Qy 319 319	1721 TTCCTCTGCCTTCAGCAAGGGGGGGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTA 17	Oy 319	319	Db 1841 AGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGACTGCTCCGAC 1900

Z E i	APPLICANT: Hepler, William TILLE OF INVENTION: TILLE OF INVENTION: COMPOSITIONS AND	qa	993 CCCAGGAAGAGGGGG
	TLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER LE REFERENCE: 210121, 427012	OY	57
	RRENT FILLION NUMBER: US/U9/6US, /85 RRENT FILLION 2000-06-27	qα	1053 GCTGCCTCTTACCCT
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6 AO	nArgLeuTrpValSerArgLeuLeuArgHisArgLySAlaGlnLeuLeuLeuLeullull	Qy	72 GlySerAlaSerAspertasper 1353 GCTCAGCCAGTGAG
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QY	57	25
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Οŷ	57	25
Op	1113	GCC
Qy	57	25
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Οy	57	25
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Qy	58	GlylleGlyProValLeuValCysValProLeuLe
QQ	1293	restccagrecrescrescresta 1
Qy	72	TyrGlyAr
qq	1353	TCAGCCAGTGACCACTGGGTGGACGCTATGGCGCGCCGCCGCCCTTCATCTGGGCA 1
Qy	92	LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
qq	1413	STCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCT
Qy	\forall	31
qq		TETECCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTG 15
QY	m	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
qq	1533	TGGACTICITGIGGCAGGIGIGCTICACICCACTGGAGGCCCTGCTCTGACCTCTTC 15
QY	152	ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
QQ	1593	GGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGGG 16
QY	172	GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
qq	1653	TECCTEGGCTACCTCCTGCCTTGACTGGGACACCAGTGCCCTGGCCCCTAC 17.
Qy	192	LeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
QQ	1713	rescraccassassas eccretits conscrace concateric conscraces 17
Oy	212	AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly 231
qq	1773	CACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGCAGAAGGG 18
Qy	232	LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
Db	1833	STCGGCCCCCTCTTGTCGCCCCACTGTCCATGCCGGGCCCGCTTGCCTTTCCGG 18
Qy	252	LeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLe
qa.	1893	SCCTGCTTCCCCGGCTGCAGCTGTGCTGCTGCTGCTCCCCGCACCTG 19
QY	272	LeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 29
qq	1953	CCGCCTCTTCGTGGCTGTGGCTGGGTGGGACTCATGACCTTCACGCTGTT
ΟŸ	292	TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
qq	2013	ACACGGATTTCGTGGGCGGGGGTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGC
QY	312	GlualaargargHisTyraspGlu319

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See See See See See See See See See See	APPLICANT: TITLE OF II TITLE OF II TITLE REFERENCEURENT APPCORRENT FIN NUMBER OF SEQ ID NO 71 LENGTH: 6 LENGTH: 6 LENGTH: 6 LENGTH: 6 CORGANISM: ORGANISM:	ANT: OF INV OF INV OF EFEREN T APPI T APPI OF SE OF SE NO 705 H: 697 DNA ISM: H	Heple IVENTIO IVENTIO IVENTIO ILICATI ING DA SEQ ID SEX EQ SEX EQ SAST SEQ 176 HOMO S	H, William CON NO. DI. CON NUN. DI. CON NUN. CON NUN. CON NUN. CON NUM. CON NUM. CON NUM. CON CONTRACT	lliam MPOSITI IAGNOSI 1AGNOSI 1AGNOSI MBER: (2300-06 835 Windows	IONS AN 66 02/09/66-27 s Versi	APPLICANT: Hepler, William TITLE OF INVENTION: COMPOSITIONS AND METHODS FC TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANG TILE REPERENCE: 210121.427C16 CURRENT APPLICATION NUMBER: US/09/605,785 CURRENT FILING DATE: 2000-06-27 NUMBER OF SEQ ID NOS: 835 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 705 LENGTH: 6976 TYPE: DAA ORGANISM: Homo sapiens USGANISM: Homo sapiens	S FOR T	НБ ТНБRAРY	APY AND		
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qa	2264 TGG	AGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCGCAGTGTGCCCTCTGCT 2323
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2504	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGGTAGAAAGGGGAAGGG 2563	
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2744	GGTCTTCTCTCTGGGTCATGGACCGGCTGGTCGTCGGCACTCGAGCACTCGAGCACTCTATTT 2803	
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2864	CGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTCCAGATCCTGCC 2923	
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3103	GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT	
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3163	TCAGGACTGTGTAGCACTTGAATGGATGATTGCAGGAAATGCAAAATACGATAGTGGGAA 3222	
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3343	GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402	
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3403	TCTGGTCTCTGAGATGGGGCAGGCTCCTTCCTACCCCCTTTCTTT	
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APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqui APPLICANT: Henderson, Robert A. APPLICANT: Kalos, Michael D. APPLICANT: Kalos, Michael D. APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Carter, Day, Craig H. APPLICANT: Carter, Darrick APPLICANT: Stolk, Yasir A.W. APPLICANT: Skelky, Yasir A.W. APPLICANT: Skelky, Yasir A.W. APPLICANT: By Aljun APPLICANT: Wang, Aljun APPLICANT: Wang, Aljun APPLICANT: Wang, Aljun APPLICANT: Worker, Vasir A.W. APPLICANT: Wang, Aljun APPLICANT: Wang, Aljun APPLICANT: Wang, Aljun APPLICANT: Hepler, William APPLICANT: Holer, William APPLICANT: Wang, Aljun APPLICANT: Holer, William APPLICANT: Holer, William APPLICANT: Holer, William APPLICANT: Homo sapiens UNREWN HOMO sapiens UNSUMMENT OF APPLICANT APPLIC	Alignment Scores: Pred. No.:	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	
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Sequence 16, Application US/09071710 Patent No. 6130043 GENERAL INFORMATION:

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LICANT: COHEN, MAURICE
LICANT: COHEN, MAURICE
LICANT: COLITTS, TRACEY L.
LICANT: GORDON, JULIAN
LICANT: GORDON, JULIAN
LICANT: RAANADOS, EDNARD N.
LICANT: KLASS, MICHAEL R.
LICANT: KRATOCHVIL, JON D.
LICANT: ROBERTS-RAPP, LISA
LICANT: ROBERTS-RAPP, LISA
LICANT: ROBERTS-RAPP, LISA
LICANT: ROBERTS-RAPP, LISA
LICANT: ROBERTS-RAPP, LISA
LICANT: ROBERTS-RAPP, LISA
LICANT: FOR DETECTING DISEASES OF THE PROSTATE
RESPONDENCE ADDRESS:
RRESPONDENCE ADDRESS:

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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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PER GOOGA 32800
UTER READBLE FORM:
DIUM TYPE: Diskette
MMPUTER: IBM Compatible
ERRATING SYSTEM: DOS
PETWARE: FastSEQ for Windows Version 2.0
RENT APPLICATION DATA:
LING DATE:
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NG DATE: 02-MAY-1997
EY/AGENT INFORMATION:
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NCE CHARACTERISTICS:
GTH: 2152 base pairs
E: nucleic acid
ANDEDNESS: single
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STRATION NUMBER: 35,441
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AMUNICATION INFORMATION:
PHONE: 847/935-1729
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Db 182 GTGCCACTTTCCCTGTGCCTGCCGGTGCCACTGCCTGTCCCACAGTGTGGCGTGGTG 241	Oy 379 ThralaseralaalaLeuThrGlyPheThrPheSeralaLeuGlnIleLeuProTyrThr 398 11111111111111111111111111111111111	Qy 399 LeualaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThr 418	Qy 419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438 LIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 439 AlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProPro 458	Qy 459 AlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThr 478 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 479 GlualaargValValProGlyargGly1leCysLeuAspLeuAlaIleLeuAspSerAla 498 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 499 PheLeuLeuSerGlnValalaProSerLeuPheMetGlySerIleValGlnLeuSerGln 518	Qy 519 SerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAla 538 	539 Thrdinvalvalvasorosososososososososososososososososos	722 ACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTCAGCG 76	RESULT 13 IIS-00-525-307-16	Sequence 16, Application US/09525397	GENERAL INFORMATION: APPLICANT: BILLING-WEDEL PATRICIA	; APPLICANT: COHEN, MAURICE ; APPLICANT: COLPITTS, TRACEY L.			SPPLICANT: KLASS, MICHEL R. SPPLICANT: KRANCHVII. AND D. SPRINGHVII. AND D. SPRINGHVII. AND D. SPRINGHVII. AND D. SPRINGHVII.	APPLICANT: ROBERTS-RAPP, LISA APPLICANT: RUSSELL, JOHN C.	; APPLICANT: STROUPE, STEPHEN D. : TITLE OF INVENTION: PEACETHE AND METHODS INSPETIT	TITLE OF INVENTION: ALTOUR DISEASES OF THE PROSTATE NUMBER OF SPOTFULES. 41	CORRESPONDENCE ADDRESS ADDRESCEPT. A PACKET TASK TO THE TASK TO T	ADDRESSE: ADDOLL LABORATORIES CTTWV. Abbott Park Road CTTWV. Abbott	6	COMMITTED DEPARTMENT D	CONDIUM TURBLE DISCONS. COMPUTER. TRA Commatth	OPERATING SYSTEM: DOS SOFTWARE: FastsEO for Windows Version 2.0	CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/09/525,397

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                                                                                                                                                                                     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                            6083.US.P1
     PRIOR PAPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REGISTRATION NUMBER: 6083.US.
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFEAX: 847/935-1729
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FORMATION FOR SEQ ID NO: 16.
SEQUENCE CHARACTERISTICS:
LENGTH: 2152 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
-525-397-16
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cal Similarity:
CLASSIFICATION:
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RESULT 15
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                         APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
CORRESPONDENCE ADDRESS:
                                                                                          539 ThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
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Mismatches:
Indels:
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APPLICATION NUMBER: US/09/071,710
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Matches:
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REFERENCE/DOCKET NUMBER: 6083.US.Pl
                                                                                                                                                                                          BILLING-MEDEL, PATRICIA
COHEN, MAURICE
COLPITTS, TRACEY L.
FRIEDNAN, PAULA N.
GORDON, JULIAN
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APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      Sequence 15, Application US/09071710 Patent No. 6130043
                                                                                                                                                                                                                                                                                                                                                                                                       1: Abbott Laboratories
100 Abbott Park Road
                                                                                                                                                                                                                                                          GRANADOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
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1270.00
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
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TYPE: nucleic acid
STRANDEDNESS: single
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TELEFAX: 847/938-2623
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COMPUTER READABLE FORM:
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                                                                                                                                                                  Patent No. 6130043
GENERAL INFORMATION:
APPLICANT: BILLING
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Best Local Similarity:
Query Match:
DB:
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US-09-071-710-15
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REAGENTS AND METHODS USEFUL
FOR DETECTING DISEASES OF THE PROSTATE
US-09-593-793A-113 (1-553) x US-09-071-710-15 (1-2143)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BILLING-MEDEL, PATRICIA
APPLICANT: COHEN, MACRICE
APPLICANT: COLDITTS, TRACEY L.
APPLICANT: GORDON, JULIAN
APPLICANT: GORDON, JULIAN
APPLICANT: GRANDOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: KRATOCHVIL, JON D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 15, Application US/09525397 Patent No. 6252047
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RUSSELL, JOHN C.
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TITLE OF INVENTION:
TITLE OF INVENTION:
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APPLICANT: BILLING
APPLICANT: COHEN,
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GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillin, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS
NUMBER OF SEQUENCES: 178
                                                                                                                                                                                                                                                            442 ProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCys 461
                                                                                                                                   GlyAlaSerAlaCysAspValSerValArgValValValValGlyGluProThrGluAlaArg
                                                                                          ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/020,956
FILING DATE: 09-FEB-1998
                                                                                                                                                                                                                                                                                                                           542 ValPheAspLysSerAspLeuAlaLysTyrSerAla
                                                                                                                                                                                                                                                                                                                                         723 GTATTTGACAAGGGGACTTGGCCAAATACTCAGG
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NAME: WAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.427C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/09020956 Patent No. 6261562
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TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
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919.00
96.50%
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TYPE: nucleic acid
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COUNTRY:
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Matches:
Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches:
                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
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                                                                                                                                                                                                                                                                                                                                                        6083.US.P1
                                                                                                                                                                                                             APPLICATION NUMBER: US/09/525,397
FILING DATE:
CLASSIFICATION:
            CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                       NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
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1270.00
100.00%
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                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2143 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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NUMBER OF SEQUENCES: 41
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                                                                                      COUNTRY: USA
ZIP: 60064-3500
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Best Local Similarity:
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Mismatches:
Indels:
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Harlocker, Susan L.
Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
622-4900
        INFORMATION FOR SEQ ID NO: 10 SEQUENCE CHARACTERISTICS: LENGTH: 789 base pairs TYPE: nucleic acid STRANDEDNESS: single
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919.00
96.50%
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
                                                                                                          MOLECULE TYPE: CDNA
 (206)
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Best Local Similarity:
Query Match:
                                                                                            TOPOLOGY:
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                                                                                                          542 CC-ATTTACTTTGCTACACAGGTANTATTTGACAAGAACGANTTGGCCAAATACTCAGCG
                                     354 ValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHis
                                                                                          374 ServalAlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln
                                                                                                                                               394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys
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APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY C
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP .
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Version #1.30
             (1-789)
            (1-553) x US-09-020-956-10
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COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Ve.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/030,607
FILING DATE: 25-FEB-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09030607
Patent No. 6262245
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NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
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            US-09-593-793A-113
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Alignment Scores:
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LENGTH: 789
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                              APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Relay, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REPERENCE: 210121.427016
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: FASTSEQ for Windows Version 3.0
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192
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Mismatches:
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Matches:
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Fanger, Gary R.
Retter, Marc W.
Stolk, John A.
Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
Li, Samuel
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                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapien
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COTHER INFORMATION: n
US-09-605-785-10
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Best Local Similarity:
Query Match:
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Pred. No.:
                                                                                                                                                                                                   SEQ ID NO 10
LENGTH: 789
                        APPLICANT
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                  534 AlaIleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla
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APPLICANT: Harlocker, Susan Louise
APPLICANT: Read, Steven G.
APPLICANT: Reade, Steven G.
APPLICANT: Fanger, Gary
APPLICANT: Fanger, Gary
APPLICANT: Colly, John APPLICANT: Colly, John APPLICANT: Day, Craig
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
FILE REFERENCE: 210121.42709
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT APPLICATION NUMBER: US/09/439,313
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEO ID NOS: 575
SOFTWARE PRESED FOR WINDOWS VERSION 3.0
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                                                                                          US-09-439-313-10
Sequence 10, Application US/09439313
Pattent No. 6329505
GENERAL INFORMATION:
APPLICANT: XU, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
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OTHER INFORMATION: n = A,T,C
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LOCATION: (1)...(789)
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Best Local Similarity:
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Db 303 CTCCCACCTCCACCGGC	0y 474 ValGlyGluProThrGlu 	Oy 494 IleLeuAspSerAlaPhe	Qy 514 ValGlnLeuSerGlnSel	Qy 534 AlalleTyrPheAlaTh 	RESULT 21 US-09-232-149A-10 ; Sequence 10, Application (; Patent No. 6465611 ; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; APPLICANT: Mitcham, Jenn ; APPLICANT: Mitcham, Jenn ; TITLE OF INVENTION: COMPC	; TITLE OF INVENTION: CAN ; FILE REFERENCE: 210121.4. ; CURRENT APPLICATION NUMBI ; CURRENT FILING DATE: 199 ; NUMBER OF SEQ ID NOS: 338 ; SOFTWARE: FASLSEQ for Will ; SEQ ID NO 10 ; LENGTH: 789	TYPE: DNA CORGANISM: Homo sapien FEATURE: NAME/KEY: misc_feature CORTETE INFORMATION: 01.	ruckag o	DB: US-09-593-793A-113 (1-553) > Ov 354 ValTVTFENDALASETVA	374	63 394	Db 123 ATCTGCCCTACACACTC Qy 414 TyrArgGlyAspThrGl)	Db 183 TACCGAGGGACACTGG7	Db 243 GGCCTAAGCCTGGAGCI
Db 363 GTGGGTGAGCCCACCGANGCCAGGGTGGTTCCGGGCCGGG	Oy 494 IleLeuaspSeralaPheLeuLeuSerGlnValalaProSerLeuPheMetGlySerIle 513	Oy 514 ValGinLeuSerGinSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal 533 	Oy 534 AlalleTyrPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553	SSULT 20 S-09-352. Sequence	GENERAL INFORMATION: APPLICANT: Dillon, Davin C. APPLICANT: Harlocker, Susan Louise APPLICANT: Harlocker, Susan Louise APPLICANT: Micham, Jang, Yuqui APPLICANT: Micham, Jennifer Lynn TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS TITLE OF INVENTION: OF PROSTATE CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.42708	CURRENT APPLICATION NUMBER: US/09/352,616A CURRENT FILING DATE: 1999-07-13 NUMBER OF SEQ ID NOS: 472 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10 LENGTH: 789 TYPE: DNA ORGANISM: Homo sapien	FEATURE: NAME/KEY: misc_feature LOCATION: (1)(789) OTHER INFORMATION: n = A,T,C or G US-09-352-616A-10	Alignment Scores: 6.14e-79 Length: 789 Score: 919.00 Matches: 192 Score: 546.50% Conservative: 1 Best Local Similarity: 96.00% Mismatches: 7 Query Match: 32.12% Indels: 2 DB: 100.00 Mismatches: 7 Mi	US-UY-593-7938-113 (1-553) x US-U9-352-616A-10 (1-789) Qy		Oy 394 IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys 413	<pre>Qy 414 TyrargGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuPro 433</pre>	Qy 434 GlyProLysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeu 453 	<pre>Qy 454 LeuProProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal 473</pre>

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182
SECTUTECEGEGCUTCTGCCTGTGATGTCTCCGTACGTGTGGTG 362
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TCCTGCTGTCCCANGTGGCCCCATCCTGTTTATGGGCTCCATT
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nnifer Lynn |
POUNDS FOR IMMUNOTHERAPY OF PROSTATE
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419 GlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGly 438
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APPLICANT: HODGES, STEVEN C.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRACCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUGE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
CORRESPONDENCE ADDRESS:
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Mismatches:
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                                    /note= " N' represents
T or C polymorphism at
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Matches:
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FastSEQ for Windows Version 2.
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FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Abbott Laboratories
1: 100 Abbott Park Road
Abbott Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/09525397 Patent No. 6252047\,
base_polymorphism
                                                                                                                                        7.37e-34
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MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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OTHER INFORMATION:
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APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note= " N' represents an A or G or OTHER INFORMATION: T or C polymorphism at this position"
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                            Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
                                                              NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083.US.Pl
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BILLING-MEDEL, PATRICIA
PRIOR APPLICATION DATA: APPLICATION NUMBER: 09/071,710
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COLPITTS, TRACEY L.
FRIEDMAN, PAULA N.
GORDON, JULIAN
GRANNDOS, EDWARD N.
HODGES, STEVEN C.
KLASS, MICHAEL R.
KRATOCHVIL, JON D.
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                                                                                                                                                                                                                                                                                             NAME/KEY: base_polymorphism
LOCATION: 215
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                              FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 255 base pairs
TYPE: nucleic acid
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242 GCGCTCTGCGGG 253
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TOPOLOGY: linear
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Best Local Similarity:
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US-09-071-710-1
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Indels:
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Matches:
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Patent No. 6252047
GENERAL INFORMATION:
APPLICANT: BILLING-MEDEL, PATRICIA
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbort Laboratories
STREET: 100 Abbort Park Road
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
                                                                                                                                               COMPUTER: IBM Compatible
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100.00%
100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 258 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
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                                                          Abbott Park
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                                                                                       COUNTRY: USA
ZIP: 60064-3500
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Best Local Similarity:
                                                                                     USA
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                                                                           STATE:
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APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROPE, STEPHEN D.
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
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Conservative:
Mismatches:
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SOFTWARE: FastSEQ for Windows Version 2.[0
CURRENT APPLICATION DATA:
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APPLICANT: COHEN, MARRICE
APPLICANT: COLPITYS, TRACEY L.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRASS, MICHAEL R.
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STREET: 100 Abbott Park Road
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APPLICATION NUMBER: 08/850,713
FILING DATE: 02-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                     US-09-071-710-4; Sequence 4, Application US/09071710; Patent No. 6130043
                                                                                                                                                                                                                                                                                                                               ROBERTS-RAPP, LISA
RUSSELL, JOHN C.
STROUPE, STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 601
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
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OPERATING SYSTEM: DOS
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LENGTH: 247 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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Best Local Similarity:
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                                                                                                                                                                      TITLE OF INVENTION: REAGENTS AND METHODS USEFUL TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE CORRESPONDENCE ADDRESS:
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Indels:
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Matches:
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
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                                                                                                                                                                                                                                           E: Abbott Laboratories
100 Abbott Park Road
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APPLICANT: COLPITTS, TRACEY L.
APPLICANT: GRIDMAN, PAULA N.
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: HODGES, STEVEN C.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRASCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STEPHEN D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Becker, Cheryl L. REGISTRATION NUMBER: 35,441
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ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATED
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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Best Local Similarity:
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STREET: 10
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GluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAla	Query Macchi: DB:
	US-09-593-793
499 PheLeuLeuSerGinValalaProSerLeuPheMetGlySerIleValGinLeuSerGin 518 	Oy 439 Ala Db 1 GCT
519 Serval 520 241 mrggr 246	2y 459 Alal
J	479
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atent No. 625204/ GENERAL INFORMATION: ADDITIONAL BITITION: DAMBIGITA	Qy 499 Phe
	Db 181 TTC
APPLICANT: COLFILIS, IMACEL D. APPLICANT: COLFILIS, TITTING APPLICANT: COLFILIS, TITTING	Oy 519 Ser'
APPLICANT: GORLON, JULIAN APPLICANT: GENARADOS, EDWARD N.	Db 241 TCT
AFFLICANT: KLASS, MICHAEL R. APPLICANT: KRATOCHVIL, JON D.	RESULT 28 US-09-071-710
	; Sequence 2, ; Patent No. (
APPLICANT: STROUPE, STEPHEN D. TITLE OF INVENTION: REAGENTS AND METHODS USEFUL	GENERAL IN APPLICAN
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE NUMBER SEQUENCES: 41	; APPLICAN; APPLICAN; APPLICAN
ADDRESSE: Abbott Laboratories STREET: 100 Abbott Park Road	, APPLICAN ; APPLICAN
α	, APPLICAN' , APPLICAN'
COUNTRY: USA ZIP: 60064-3500	; APPLICAN ; APPLICAN
E E	APPLICAN
COMPUTER: IBM COMPATIBLE	TITLE OF
OFFINATION SISTEMS. DOS SOFTWARE: FASTSES FOR Windows Version 2.0 CHEMPENT ADDITIONATION DATE.	NUMBER OF
PAPLICATION NUMBER: US/09/525,397	, ADDRES
CLASSIFICATION:	CITY:
APPLICATION NUMBER: 09/071,710	COUNTR
FILING DATE: ATTORNEY/AGENT INFORMATION:	; ZIP: ; COMPUTER
NAME: Becker, Cheryl L.	, MEDIUM
REFERENCE/DOCKET NUMBER: 6083.US.P1	; OPERAT
TELECOMMUNICATION INFORMATION: TELEPHONE: 847/935-1729	; SOFTWA; CURRENT
	; APPLICA ; FILING
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:	; CLASSI ; PRIOR API
LENGTH: 247 base pairs TYPE: nucleic acid	; APPLIC ; FILING
STRANDEDNESS: single TOPOLOGY: linear	; ATTORNEY ; NAME:
-09-525-397-4	, REGIST ; REFERE

Alignment Scores:

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LICANT: COHEN, MAURICE
LICANT: COLPITTS, TRACEY L.
LICANT: FIEDMAN, PAULA N.
LICANT: GORDON, JULIAN
LICANT: GRANADOS, EDWARD N.
LICANT: GRANADOS, EDWARD N.
LICANT: GRANADOS, EDWARD N.
LICANT: HONGES, STEVEN C.
LICANT: RATOCHVIL, JON D.
LICANT: KRATOCHVIL, JON D.
LICANT: ROBERTS-RAPP, LISA
LICANT: STROUPE, STEPHEN D.
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Length:
Matches:
Conservative:
Mismatches:
Indels:
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THE READABLE FORM:
THE READABLE FORM:
FRUIDM TYPE: DISKETTE
FRUIDM TYPE: DISKETTE
FRATING SYSTEM: DOS
TWARE: FASTSEQ FOR WINDOWS VERSION 2.0
THE APPLICATION DATA:
                                                                                                                                                                                                                                3A-113 (1-553) x US-09-525-397-4 (1-247)
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T: 100 Abbott Park Road
Abbott Park
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CATION NUMBER: 08/850,713
G DATE: 02-MAY-1997
:Y/AGENT INFORMATION:
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REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 60
TELECOMMUNICATION INFORMATION:
8.93e-32
418.00
100.00%
100.00%
14.61%
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imilarity:
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PRIOR APPLICATION DATA:
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APPLICANT: COHEN, MAURICE
APPLICANT: COLETTS, TRACEY L.
APPLICANT: GORDON, JULIAN
APPLICANT: GORDON, JULIAN
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL N.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: RUSSELL, JOHN C.
APPLICANT: STROUPE, STEPHEN D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
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71
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SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/525,397
FILING DATE:
                                                                                                                                                                       Length:
Matches:
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Gaps:
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100 Abbott Park Road
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Patent No. 6252047
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100.00%
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
847/935-1729
                                                                   LENGTH: 217 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                       SEQUENCE CHARACTERISTICS:
                                        INFORMATION FOR SEQ ID NO:
           TELEFAX: 847/938-2623
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CORRESPONDENCE ADDRESS:
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Best Local Similarity:
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TELEPHONE:
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STREET: 10
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STATE:
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Query Match:
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APPLICANT: FROMMER, Wolf-Bernd
APPLICANT: RIESWEIER, JOSG
TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE
TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA AND PLANTS CONTAINING A
TITLE OF INVENTION: TRANSPORTER AS WELL AS A PROCESS FOR THE PREPARATION AND
TITLE OF INVENTION: TRANSFORMATION OF YEAST STRAINS FOR THE IDENTIFI.
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
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Mismatches:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,340
FILING DATE: 21-DEC-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-593-793A-113 (1-553) x US-09-525-397-2 (1:217)
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1: 1180 Avenue of the Americas
New York
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Matches:
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                                                                                      6083.US.P1
APPLICATION NUMBER: 09/071,710
 APPLACE.

FILING DATE:
ATONNEY, SAGET INFORMATION:
NAME: BECKEY, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083
TELECOMMUNICATION INFORMATION:
""TEPHONE: 847/935-1129
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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100.00%
100.00%
12.48%
                                                                                                                                                                                                      LENGTH: 217 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                              TOPOLOGY: linear
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Best Local Similarity:
Query Match:
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US-08-356-340-3
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530 AGGATGAGAAACAGCAAATGCTTTTTTCTTCATTCTTCATGGCCGTCGGAAACATTCTGGGG
                        TyrLeuLeuProAlaIleAspTrp--
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                            Sequence 3, Application US/0878655B
Fatent No. 5981181
GENERAL INFORMATION:
APPLICANT: FROMMER, Wolf-Bernd
APPLICANT: FROMMER, Wolf-Bernd
APPLICANT: FROMMER, Wolf-Bernd
TITLE OF INVENTION: DLASHIDS, BACTERIA AND PLANTS CONTAINING A TRANSPORTER;
TITLE OF INVENTION: OF YEAST STRAINS FOR PREPARATION AND TRANSFORMATION
TITLE OF INVENTION: OF YEAST STRAINS FOR THE IDENTIFICATION
FILE REPERENCE: Frommer
CURRENT APPLICATION NUMBER: US/08/786,555B
CURRENT FILING DATE: 1997-01-21
EARLIER FILING DATE: 1997-12-21
EARLIER APPLICATION NUMBER: PCT/EP93/01604
EARLIER FILING DATE: 1993-06-24
EARLIER APPLICATION NUMBER: DE P4220759.2
EARLIER PILING DATE: 1992-06-24
NUMBER OF SEQ ID NOS: 11
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CAATTGCTCGGAATTCCTCATAAATTTGCCTCTTTATTTGCTGGACCGATTTTT
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Matches:
Conservative:
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11.53%
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US-08-786-555-3
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710 AGCTTAACAACCATAACCTTAATCCGGGAAAACGAGCTCCCGGAGAAAGACGAG
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1135 ATGTCGTTGAGTTTGAAGGTTTGGCTCGTAGGGGGGTGCTAAAAGGTTATGGGGA 1194
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                                                                                                                                SerAspHisTrpArgClyArgTyrGlyArgArgArgProPheIleTrpAlaLeuSerLeu
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                                                                                                                                            TITLE OF INVENTION: DNA SEQUENCES WITH OLIGOSACCHARIDE
TITLE OF INVENTION: TRANSPORTER, PLASMIDS, BACTERIA AND PLANTS CONTAINING A
TITLE OF INVENTION: TRANSPORTER AS WELL AS A PROCESS FOR THE PREPARATION AND
TITLE OF INVENTION: TRANSFORMATION OF YEAST STRAINS FOR THE IDENTIFI...
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                     2: Ostrolenk, Faber, Gerb & Soffen 1180 Avenue of the Americas
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Matches:
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/EP93/01604
FILING DATE: 22-JUN-1993
PRIOR APPLICATION NUMBER: DE P42 20 759.2
FILING DATE: 24-JUN-1992
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 24,735
REFERENCE/POCKET NUMBER: P/951-106
TELECOMMUNICATION INFORMATION:
TELEFAX: (212) 382-0700
TELEFAX: (212) 382-0888
TELEFAX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1969 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/356,340
FILING DATE: 21-DEC-1994
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOC NOT
SOFTWARE: Patrii
                                                   Sequence 1, Application US/08356340 Patent No. 5608146
                                                                                                              Wolf-Bernd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Spinacia oleracea
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39.50%
23.16%
11.34%
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STRANDEDNESS: single
                                                                                       GENERAL INFORMATION:
APPLICANT: FROMMER, WO
APPLICANT: RIESMEIER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: 70..1644
OTHER INFORMATION:
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                              New York
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                       ADDRESSEE:
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QY 4		ProPheProAsnGlyH	LysProGlyAlaProPneProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuPro	ySerGlyLeuLeuPro	455	Qy	7
7		1 1 1 1 1 1 1 1 1 1 1 1	99	-eecreceecerece	1302	QQ	35
		LeuCysGlyAlaSerA 	ProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGly 	<pre>lArgvalvalvalGly :</pre>	475	δ	
Db 13	303 cceccecrecr	GGTGTTAAGG	-GGTGTTAAGGGTGGCGCTTTGGCTATCTTTGCCGTTCTTGGT	crrrccccrrcrrgcr	1356	. d	41
0y 4	476 GluProThrGluAlaArgVal	V	ro		484	3 (• •
Db 13	357 ATCCCTCTTGCG	::: ATCACTTTCAGTATTC	 ATCCCTCTTGCGATCACTTTCAGTATTCCTTTGGCCTTGGCGTCAATCTTTTCAGCATCT	AATCTTTTCAGCATCT	1416	ογ	11
Qy 4	485GlyArgGly	IleCysLeuAspLeuA	-GlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGln	aPheLeuLeuSerGln	503	qq	4 6
Db 14	1417 TCCGGTTCAGGAC	CAAGGTCTTTCTCTAG	::: ::: GAGTTCTCAACCTCGC		1476	Qy	12
S AO	504 Val			Alapro	506	QO	52
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į		GGAGC IGTAGCAGCAA	ACAGCCAGTGCAGTTCT	TTCATTT 138/		ΩD	64
US-08-71	US-08-786-555-1	499990000000000000000000000000000000000				QY	18
; Paten	Sequence 1, Application Patent No. 5981181	Aprication os/00/00/30358 981181 SENATON:	•			qq	70
APPL	ICANT: FROMMER,	Wolf-Bernd			-	QY	19
TITE:	TITLE OF INVENTION: DAY SEQUENCES WI	DIA SEQUENCES W	IITH OLIGOSACCHAR	IDE TRANSPORTER,	444	qa	16
TITLE	E OF INVENTION:	AS WELL AS A PROCESS OF VEAST CHEATNE FOR	IEKTA AND FLANIS CONIAINING A IKAI PROCESS FOR PREPARATION AND TRANSI PRO DOD WHE INDMINITERATION	ONIAINING A TRANS ATION AND TRANSFO EICAMION	TRANSFORMATION	QY	21
FILE	FILE REFERENCE: Frommer	OF IEASI SIRAIN NIMBER 12 00 77	IS FOR THE LUBBLE	FICHILON		qa	82
CURR	ENT FILING DATE:	1997-01-21	90,7778		,	Qy	23
EARL	IER FILING DATE:	1994-12-21	340			qa	88
EARL	IER APPLICATION IER FILING DATE:	1993-06-22	PCT/EP93/UI004 i-22			Qy	25
EARL	EARLIER APPLICATION NUMBER: DE P4220/59	NUMBER: DE P4220/59 : 1992-06-24	7.66/0			qa	92
SOFT	WARE: PatentIn V	s: 11 Ver. 2.0				QY	27
LEN(LENGTH: 1969					Dp	97
, ORG	; ORGANISM: Spinacia	oleracea				QY	29
	T-000-00					qq	103
Pred. No.:	. No.:	1.81e-21	Length:	1969		0y	31
Percent Sim	Similarity:	39.50%	ative:	129 91 196		qq	107
Query Match	atch:	11.348		141		Qy	33
	DS.	1 - 30 - 30 - 50 - 511	10501-17	2		qa	113
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23 LeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyr------

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33 ACAGCCCTAAATTGGATCGCATGGTTCCATTCTTGTTGTTGTTCGATACTGATTGGATGGGT 1032
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                                                                                                                                                                                                                                                                      95 GlylleLeuLeuSerLeuPheLeuIleProArgAlaG|yTrpLeuAla-----GlyLeu 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----TrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCys 198
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                                                                                                                   32 CAGCICICCCTACTGACCCCGTACGICCAACTACTGGGCATTCCCCACACTTGGGCCGCC 291
                                                                                                                                                                                                                                                                                                                                                                                                                    12 CTAGTGGCCGTAGCGGTGGGGCTAATC-----GGATTCGCCGCCGATATCGGCGCA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 LeuCysProAspPro------ArgProLeuGluLeuAlaLeuIleLeu 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeu 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGGTTTTGGATCCTCGACGTGGCTAACAACACCCTGCAAGGCCCATGCAGGCCGTTGTTA 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SerAspLeuPheArg---AspProAspHisCysArgGlnAlaTyrSerValTyrAlaPhe 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 AlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeu 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 ProArgLeuHisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAla 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 GGCGCTCTCAAAGATCTA-----CCAAAACCAATGCTAATCCTATTACTAGTA 972
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyr 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspGluGlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuVal 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 PheSerLeuValMetAspArgLeuValGlnArgPheGly-----ThrArgAlaValTyr 355
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55 MetValLeuGlyIleGlyProValLeuGlyLeuValCÿsValProLeuGlySerAla 74
                                                                39 -------ValProProLeuLeuGluValG|yValGluGluLysPheMetThr 54
                                                                                                                                                                                                   GCGTCGGGTGATCCAACGGGAAACGTGGCAAAACCCCGGGCCATCGCGGTGTTTGTGTGGC
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-	; CLA	, APP	; ATTOR	; REF	; TEL	; TEL	LEN	STR	6 E	Pred. No.: Score: Percent Sin	Best Local Query Matc	US-09-593-	Qy 496	Db 3 (Qy 516 1	Dp 63 (771 QQ	RESULT 35 US-09-525 ; Sequence ; Patent N ; GENERAL ; APPLIC	; APPLIC	APPLIC APPLIC APPLIC APPLIC	APPLIC ; APPLIC	APPLIC APPLIC APPLIC APPLIC	TITLE TITLE	CORRES	STRI	; COUI	MED COMPO
- 1105 ATT ATT ATT ATT ATT ATT ATT ATT ATT AT	DD 1195 ATTGTCAATATTCTTGCTGTTTGTTTAGCTATGACGGTG 1236	Oy 376 AlaValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeu 395 :::	Db 1237TAGTTACTAAGTCCGCCGAA	Oy 396 ProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArg 415 :: ::	<pre>Qy 416 GlyAspThrGlyGlyAlaSerSerGluAspSerLeuWetThrSerPheLeuProGlyPro 435</pre>	Db 1284 1284	Oy 436 LysProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlyGlySerGlyLeuLeuPro 455	1285GGCTCCGCCGTCCTCCG	<pre>Qy 456 ProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGly 475</pre>	476 GluproThrGluAlaArgValValPro		1	Oy 504 ValAlapro 506	Db 1477 ATGTTTGTGGGTAACAAGTGGGCCATGGGATGCAATGTTTGGTGGAGGAAATTTGCCA 1536	507 SerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyr	Db 1537 GCATTCGTGGTGGGAGCTGTAGCAGCAACAGCCAGTGCAGTTCTTTCATTT 1587	RESULT 34 US-09-071-710-5 Commence & Annilostics Heynboritain	; Sequence 3, Application US/USU/1/10 ; Patent No. 6130043	GENERAL INFORMATION: APPLICANT: BILLING MEDEL, PATRICIA APPLICANT: COHEN, MAURICE APPLICANT: COLPITS, TRACEY L. APPLICANT: FRIEDMAN, PAULA N. APPLICANT: GORDON, JULIAN		; APPLICANT: KLASS, MICHAEL R. ; APPLICANT: KRATOCHVIL, JON D. ; APPLICANT: ROBERTS:RAPP, LISA	JOHN C. STEPHEN D.	; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL ; TITLE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE ; NUMBER OF SEQUENCES: 41	ENCE ADDRESS E: Abbott I 100 Abbott		; ZIP: 60064-1500 ; COMPUTER READABLE FORM: ; MEDIUM TYPE: Diskette		SOFTWARE: FASTELY OF WINGOWS VERSION 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/071,710 FILING DATE:

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APPLICANT: COLETTYS, TRACEY L.
APPLICANT: COLETTYS, TRACEY L.
APPLICANT: GORDON, JULIAN
APPLICANT: GORDON, JULIAN
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: GRANADOS, EDWARD N.
APPLICANT: KLASS, MICHAEL R.
APPLICANT: KRATOCHVIL, JON D.
APPLICANT: REATOCHVIL, JON D.
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: ROBERTS-RAPP, LISA
APPLICANT: STROUPE, STEPHEN D.
ITILE OF INVENTION: REAGENTS AND METHODS USEFUL
ITILE OF INVENTION: FOR DETECTING DISEASES OF THE PROSTATE
OF SEQUENCES: 41
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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CLASSIFICATION:

IOR APPLICATION DATA:

APPLICATION NUMBER: 08/850,713

FILING DATE: 02-MAY-1997

TORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.

REGISTRATION NUMBER: 35,441

REFERENCE/DOCKET NUMBER: 6083.US.P1

LECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-1729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nce 5, Application US/09525397
t No. 6252047
RAL INFORMATION:
PLICANT: BILLING-MEDEL, PATRICIPEDICANT: COHEN, MAURICE
PLICANT: COLPITTS, TRACEY L.
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DRESSEE: Abbott Laboratories
REET: 100 Abbott Park Road
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98.28%
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DIUM TYPE: Diskette
MPUTER: IBM Compatible
ERATING SYSTEM; DOS
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PE: nucleic acid
RANDEDNESS: single
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ENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 93, Application US/08056200
Patent No. 5616500
GENERAL INFORMATION:
APPLICANT: Lee, Seung-Chul
APPLICANT: Kim, In-Gyu
APPLICANT: Chung, Soo-11
APPLICANT: Park, Sang-Chul
TITLE OF INVENTION: Trichohyalin and Transglutaminase-3 and
TITLE OF INVENTION: Mehods of Using Same
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive, Sixteenth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/056,200
                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
Indels:
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FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps:
                                                                                                                                                     6083.US.P1
                           US/09/525,397
                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/071,710
FILLING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                        NAME: Becker, Cheryl L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 6083
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/938-1729
TELEFAX: 847/938-2623
                                                                                                                                                                                                                                                                                                                                                   1.84e-15
247.00
98.28%
98.28%
8.63%
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              DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
           CURRENT APPLICATION DA APPLICATION DA APPLICATION NUMBER: FILING DATE:
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Best Local Similarity:
Query Match:
                                                     CLASSIFICATION:
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Pred. No.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 GlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluVal 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 ValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPhe 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6471 CTGACGCAGTTGCTCGCGCTCCTCGAGGCGCAGCTGCTGCTCCTC---CTTAAGGAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----CTCGGGCAGCCGCTGTTCCTC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6175 GCCTTTTGGCTTTTGCTCTTCTCGCTCCAGCTGTTCTTCCTCTGGGAAATGCCTGT
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GlyLeuLeuAspPheCysGlyGlnValCysPheThrPro
                       ATTORNEY/AGENT INFORMATION:
NAME: Fedrick, Michael F.
REGISTRATION NUMBER: 36,799
REFERENCE/DOCKET NUMBER: NIH054.001A
TELECOMMUNICATION INFORMATION:
TELECAX: (714) 760-0404
TELEFAX: (714) 760-0404
TELEFAX: (714) 760-0502
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISTICS:
LENGTH: 9551 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels:
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35.78%
25.65%
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2512..8070
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                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA HYPOTHETICAL: NO
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             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
                                                                                                                                                                                                                                                                       ANTI-SENSE: NO FEATURE:
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                     LOCATION:
FEATURE:
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QQ	6055 GGTGCTGCAGATCTTGCTGGGATTGTCTGTCGCGCACCTGGGAATCTTCCAACTGCCGGA 5996	e and a drawd a less to a resident and a second a second and a second and a second and a second and a second and a second and a second and a second and a second and a second a second and a second and a second and a second and a second and a second a second and a second and a second a second a second a s
ò	143LeuGluAlaLeu	ergluaspserbeumetiniserrnebeurioslykiolyskioslyaiakiokliekion
qq	::: :::	Db 5010 CTCCTGATCCTCCTGGAGGCCGTCCTCCTCCTGGAGCTG 4969
δý	ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMet	443 snGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyA
QQ	5935 CTGGTTCCCACTGCCATTCAGATCACTGCGCTGATCCTCATCCCGGTATCGCT 5882	4968 TIGGGCACGCTCCCCCCCTGGAGCTGCTCCTCTTCCTCCAGGAA
δο i	IleSerLeuGlyGlyCysLeuGly-TyrLeuLeuProalaIleAspTrpAspThrSerA	Oy 463 LaserAlaCysAspValserValArgValValValValUu
å å	GTTTCCTTTTCTGGCGCTGAAGCTCTTCCTCCTCCCGATATTGCCTCTCCAGCTCCTGGC	Oy 477 roThrGluAlaArgValValProGlyArgGly 487
දු පු	187 aLeuAlaProTyTLeuGlyThrGinGluGluCJySLeuPheGlyTLeuLeuThrLe 205 	Db 4866 CTCCGGGAGAAACCGTTGTTCCCGCTGCTGGC 4835
Οy	ullePheLeuThrCysValAlaAlaThrLeuLeu	
QQ	5767 CCTCTTCCTCCCGACATTGCCTCTCCCGGCTCTTCTTCTTCTCGGTTCCTCTC 5708	; Sequence 93, Application US/U8BUU644 ; Patent No. 2595875.
Οý	218 aGluGluAlaAlaLeuGlyProThrGluProAl 229	; APPLICANT: Lee, Seurg-Chul
g	5707 TCAGCA-GCTGCTCTTCCTCCTGCTGCAGCTCCTTTCCTT	APPLICANT: Kim, In-Gyu
Oy Y	aGluGly	; APPLICANT: Park, Sang-Chul ; TITLE OF INVENTION: TICHODyalin and Transglutaminase-3 and
3 3	ictiescentificiestricters in the contract of t	NUMBER OF SEQUENCES: 117
à c	SPIOCYSAIGALAAIGLEUALAPheArgAsnLeuGlY	DENCE ADDRESS:
Q C	recrementations and recognifications are recognificated and recognification	; STREET: 620 Newport Center Drive; Sixteenth Floor :; CITY: Newport Beach
o d	AlaLeuLeuProArgLeuHisGlnLeuCysCysArg-MetProArgThrL	STATE: CA
9	CICASCASCISCICITOTICOISCISCASCIUSTITITITITAGGIACISCOIQUOCAC	ABL
y g	271 eu	MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible . ODBODATING CVCTEW. DATACLOG
3 8	יינייסייסייסייסייסייסייסייסייסייסייסייסי	SOFTWARE: Patentin Release #1.0, Version #1.25
3 6	200 ysseriipmetalaleumetrirreneinteurneiytrintasprnevalolyGluclyL 300 	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/800,644 FILING DATE: 14-FFR-1997
3 8	GIOGRAFIA CONTROLOCATO CONTROLLA CON	CLASSIFICATION: 424
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3 8	יוניוניניניון יוניוניוניוניוניון יוניוניון יוניוניון יוניוניון יוניוניון יוניוניון יוניוניון יוניוניון יוניון YAGENT I	
<u> </u>	340 IVValAtgMetGLySerLeuGlyLeuPhe	NAME: Feditick, Michael F. REGISTRATION UNDER: 36,799
3 8	ATATIOCCITICCCOCTCTTCTTTTTTTTTTTTTTTTTTT	N:
<u> </u>	eucincysAlaileserLeuvalPheserLeuvalmeCASpArgLeuvalGinArgPhes	; TELEFAX: (714) 760-9502
3 3	TICCICCICCIGCAGCIGCTCTICCTCGCGGIATIGICTCTCCTGFTCTIGGGGCCTTCT	SEQUENCE CHARACTERISTICS:
<u> </u>	1911II ATATAVALIYI LEUALIASELYAIAIAALIARINEKTOVALALAALIAALIATIILC ::::	ic.
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දු දු	370 ysLeuSerWisSerValAlavalValThrAlaSerAlaAlaLeuThrGlybheThrPhe- 389 	MOLECULE TYPE: CDNA ; HYPOTHETICAL: NO ANTI-SENSE: NO
		. ,
à á	GTACAGGGGGGGGGTTTTTTTTTTTTTTTTTTTTTTTTT	NAME/REI: CDS
3 8	vrHisAraGluLwg]nValPhelenProLwsTvraraGlwsphrGlwGlwlwlaSerS	: NAME/KEY: intron : LOCATION: 1645.2511
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; US-08	LOCATION: 2-800-644-93	5128070				QY	
Alignm Pred. Score: Percen Best L Query DB:	ent Scores: No.: t Similarity: ocal Similari Match:	0.000289 155.50 35.78% ty: 25.65% 2.44%	Length: Matches: Conservative: Mismatches: Indels: Gaps:	9551 157 62 1198 198 31		oy do oy	242 SPIC 242 SPIC 11 5588 TCC 255
us-0	US-09-593-793A-113 ((1-553) x US-08-800-644-93	(1-9551	<u>.</u>		qq	
Oy Dp	7 ValSerArgL ::::::: 6471 CTGACGCAGT	ValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeuValAsnLeuLeuThrPhe :::::::	laGlnLeuLeuLeuVa ::CGCAGCTGCTGTTCCT	IASnLeuLeuThrPhe 	26 6415	Qy	
Qy Db	27 GlyLeuGluValC 6414 TCTCTCCCGTTC-	GlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValProProLeuLeuLeuGluVal 	leThrTyrValProProLeuLeuLeu CTCGCGCAGCCGCTGTTCCTC	roLeuLeuLeuGluVal CGCTGTTCCTC	46	QQ Dp	280 ysSe
Qy	47 GlyValGluGlu ::: 6381CTCGAGGAA	GlyValGluGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGlyLeuVal :::	alLeuGlyIleGlyPr CTGATGGAGCAGTTCC	ProValLeuGlyLeuVal ::: ::: CTCTTCGCGGAATTTTC	66 6326	Qy	
oy Og	67 CysValProL 6325 TGTCACGCTC	CysValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArg 	spHisTrpArgGlyAr	gTyrGlyArgArgArg	86 6293	Qy Db	
Oý Dp	87 ProPhe 6292 CCCTTTCCTG	ProPhe	IleTrpAlaLe ::: GCGGAATTTTCTGTCT	IleTrpAlaLeuSerLeuGlyIleLeu ::: GAATTTCTGTCTGTCTTGACGGCGTC	97 6233	QY	
Oy Dp	98 LeuSerLeuP 6232 TCTTCTCTT-	LeuSerLeuPheLeullePro	CAACTGCTTTTCCTCT		105 6176	Oy Dp	
Qy Db	106 AlaGlyTrpLeu 	AlaglyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu	ysProAspProArgPr TCCAGCTGTTCTTCC	OLeu	120 6116	do Ob	370 yste 5140
Qy Db	121 6115 TGGCCTGCTG		GluLeuAlaLe ::: ::: CTCACGATCTCTCTCT	-GluLeuAlaLeuLeuIleLeuGlyVal ::: ::: .CGATCTCTCTTGCTGTTCACCCAGCA	129 6056	Qy Db	
Qy Dp	130 GlyLeuLeuA 6055 GGTGCTGCAG	GlyLeuLeuAspPheCysGlyGlnValCysPheThrPro	ysPheThrPro 	TCTTCCAACTGCCGGA	142 5996	Qy Db	
Qy	143LeuGluAlaLeu ::: ::: 5995 ACTGTTCATTCTCTC	LeuGluAlaLeu		-LeuSerAspLeuPhe 	151 5936	QY	423 erG 5010 CTC
Qy Db	152 ArgaspPro- 5935 CTGGTTCCCA	ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAla 	ysArgGlnAlaTyrSe scGcTGATCCTCATCC	-AspHisCysArgGlnAlaTyrSerValTyrAlaPheMet AGATCACTGCGCTGATCCTCATCCGGTATCGCT	167 5882	Oy Dp	
Oy Dp	168 IleSerLeuG ::: 5881 GTTTCTTTT	IleSerLeuGlyGlyCysLeuGly-TyrLeuLeuProAlaIleAspTrpAspThrSerA	LeuLeuProAlaIleA TCCTCCGATATTGC	SpTrpAspThrSerAl	187 5822	QY	
Qy Db	187 aLeu 5821 GCCTTCTCTT	aLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLe 	3lnGluGluCysLeuP ::::: rcrcAGCAGCTGCTCT	rGlnGluGluGysLeuPheGlyLeuLeuThrLe :::::	205 5768	Qy Db	477 roth
Oy Dp	205 ullePheLeu ::: 5767 CCTCTTCCTC	ullePheLeuThrCysValAlaAlaThrLeuLeu	seuleu TCCTGGCGCCTTCTC	valAl ::::: TTCTCCGGTTCCTCTC	218 5708	REST US+(RESULT 38 US-09-199-737 ; Sequence 3, ; Patent No.
oy Op	218 aGluGluAla :::: 5707 TCAGCA-GCT	aGluGluAlaAlaLeuGlyPro···················ThrGluProAl :::: TCAGCA-GCTGCTCCTCCTGCTGCAGCTCCTTCCTTCCGATATTGCCTCTCCAGC	SCTCCTCTTCCTTCCG	ThrGluProAl	229 5649		GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT:

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					CTCCTTC		roAlaLe	CTCCTCC	lyAlaPr	CTCCTGT	hrGlyGl	 CC	hrLeuAl	hrGlyPh stagggct	CTGCA	\laAlaGl	TTCTTGG	TCTCAGC		CTTCTTA	rgHisTy	TCCTGGC	heValG1	TCCTCT	FACTGCC	:::!!	TTCTCC	1 1 1	TCCTCCT	uSerPro
IuGly				1. - -	yelu cccccrc	TCCA	OProPro	CCGTCCTC	o LysPro(GGGCGCTC	gGlyAsp1	 AGTTGCC	, uProTyr1	aAlaLeu1 TGCTCTTC	TCCTCCTC	eProval?	CICICCIC	CGTTCCTC		TGCTGCAC	uAlaArg	rereces	rThrAsp	SCTGCTCT		CysCysAı	GTCTTCT		GCTGCTC	ProSerLe
			483	: 11y 487	/alvalGl CTGGCGG	CTCTTCC	euLeuPr	LILLÍ	roglyPr	90	ysTyrAr	TTCTICT	SlnileLe	AlaSerAl :::	SCICCICC	laAlaPh	GTATTGT	TTTCTCC		TTCCTTC	lyThrGl	::: :: 3TATTTT	euPheTy	:: CTCAGCA	TCGTCTT	sGlnLeu:::	TCCTGGA	snLeuGly	II III	euSerAla
	Α.	99737	CGCTGCTC	-cecerci oglyArg(lArgvalvilli	AGCTGCT	ySerGly1)	rPheLeu	1	eLeuPro]	::: :TTCCTTT(rAlaLeu	lvalThri TGTTCCT	CTCTGTA	aSerVal	TCCTCGC	CGTCTTC	yLeuPhe	 :AGCTGCT	aGluPro	CCTCGCG	rPheThr	GTTCCTC	GCTGCAG	ArgLeuH	TCTCCCG	PheArgA	GTTCCTC	Ž
UuGly CCTGGCGCCTTCT CCTGGCGCCTTCT CAGCAGCTGCTCT CCTGGCGCTCTCT CCTGGCGCTTCTCTCCCGTTCTCTCTCCCGTTCTCTCTC	Beth li E. Theresa	o ;	GTTGTTCC	cccrcr ValValPr	ValSerVa CCCTCT	GCCGCTGG	AlaGlyGl		MetThrSe		GlnValPh	II GGCGTCTC	9SSe	ValAlaVa GCAGCTGC	CI	TyrLeuAl	GCTGCTCI	GCTCCTGC	SerLeuGl	II TCCCA-GC	ProArgAl	::: CTCCTCT1	LeuMetT	CTTCTCC	TTCTTCCI	euLeuPro	ATATTGC	rgLeuAla	CGTCTCC	
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ALR3 Receptors And Uses Thereof	Length: 1417 Qy Matches: 115 Conservative: 43 Mismatches: 178 Indels: 21	-199-737-3 (1-1417)	80	95 139	Oy -LeuLeuSerLeuPheLeuIleProArgAla 106 :::	0)	259	118 319	A 133 G 379	153 423	173	DE 123	193 441	RESERTED PROPERTY RESERVED PROPERTY	AlaGluGluAlaAlaLeuGlyproThrG 227	SerProHisCysCysProCysArgAlaA 247	GACAGGTAC
APPLICANT: Gerald, Christophe P.G. APPLICANT: Jones, Kenneth A. TITLE OF INVENTION: DNA Encoding Galanin G. FILE REFRENCE: 52241-D-PCT-US CURRENT APPLICATION NUMBER: US/09/199,737A CURRENT FILING DATE: 1998-11-25 NUMBER OF SEQ ID NOS: 59 SOFTWARE: PatentIn Ver. 2.0 - beta SEQ ID NO 3 LENGTH: 1417 TYPE: DNA ORGANISM: HOME Sapiens	ent Scores: 0.00618 No.: 128.50 t Similarity: 29.53% ocal Similarity: 21.50% Match: 4.49%	-593-793A-113 (1-553) x US-09	66 ValcysValProLeuLeuGlySerAlaSerAspHisTrpArgGly::111	81 ArgiyrGlyargArgargProPhelleTrpAlaLeuSerLeuGly 	96 Ile	106	200 CACTGGACAGCCCAGGGAGTGTGGGGGCCGTGGGCAGTGCCTGTGGTCTTTGCCC	107	118 rgProLeuGlu	133 spPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgA	153 spProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyC	423	173 ysLeuGlyTyrLeuLeuProAlaileAspTrpAspThrSerAlaLeuAlaProTyrLeuG 	193 lyThrGlnGluGluCysLeuPheGlyLeuLeuThr 	207 heLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThr ::	227 luProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAl	514CTGGCTGCTCTCCGTGGACAGGTAC
AAHEOOS SOO	Alignm Pred. Score: Percen Best L Query DB:	60-sn	Oy Dp	Oy Db	Oy Dp	ōy	QQ	0y 0p	Oy Op	Qy	δý	qq	Oy Dp	Qy Dp	Oy Db	οχ	g :

267 e 267 e 267 e 287 h 287 c 287 h 281 c 337 l 337 l 356 e 357 - 356 e 357 - 356 e 357 - 1052 c 404 - 1112 g 398 h 1112 g 435 r 1112 g 435 r 1129 c 435 r 1136 - 201-058-3 Sequence Patent N APPLIC APPLIC APPLIC APPLIC APPLIC

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    200 CACTGGACAGCCCAGGGAGTGTGGGGGCCGTGGCAGTGCCTGTGGTCTTTGCCCTAATCT 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 rgProLeuGlu--------LeuAlaLeuLeuIleLeuGlyValGlyLeuLeuA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  320 GTGCCTGGCAGCACCACGGACCTGTTCATCCTCAACCTGGCGGTGGCTG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           153 spProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyC 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----- 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 spPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 CTCTGCTCTCCCTCCTCCTCCCACGAGCTTCCAGGACCCAGACCC 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ValCysValProLeuLeu------GlySerAlaSerAspHisTrp---ArgGly 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 ArgTyrGlyArg------ArgArgProPhelleTrpAlaLeuSerLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106
                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/058,333A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-593-793A-113 (1-553) x US-09-058-333A-3 (1-1417)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 52241-E/JPW/KDB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 278 0400
TELEFAX: 212 391 0525
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 1417 base pairs
TYPE: nucleic acid
STRANDENNES: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.00618
128.50
29.538
21.508
                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA
               New York
: U.S.A.
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New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
                                           10036
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Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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           STATE: N
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Qy Db	173	ysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuG	193 441
Oy Db	193	nrGlnGluGluCysLeuPheGlyLeuLeuThr	207
Oy Db	207	aAlaLeuGly	227 513
QY	227	luProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaA	247
Qy Db	247	LeuAlaPheArgAsnLeuG CTGGCCGTGCGG	267 571
Qy Db	267	etProArgThrLeuArgArgLeuPheValAlaGluLeUCysSerTrpMetAlaLeuMetT 	287
δ d	287	rGlnGlyValProAr	
Oy Oy	i 0	Procedy Three Languages are the control of the cont	
Dp Oy	327	GCCTGGGAGGACGCGCCGCCGCCCTGGACGTGGCCACCTTGCTGCC GLeuGlnCysAla1leSerLeuValPhèSerLeuValMetAspArgLeu 111	751 346
QQ		craccracraccaraccrataracradaccracacacacacacacacacacacacacaca	
Qy Db	346	PheGly GTGGGTCCCGCGG	356 871
ōγ	356	srvalAlaAlaPheProvalAlaAla	366
qa &	872	GCGCGGGCGCCCATGCTGGCCGCTCGCCCCTCTACGCGCTCTGCTGGGGTCCCCACC	931
op o	o m	1 2	5
oy da	378	8 alThralaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrT	398
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qq	1052	5	1111
Qy dy	404		415
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QY Db	416	G1yAspThrG1yG1yAlaSerSerG1uAspSerLeuMetThrSerPheLeuProG1yP 	435 1228
Qy Db	435	lyalaProPhePr AGGGACCCGTCCA	454 1288
QY	454	laLeuCysGlyAlaSerAlaCysAspValSerVa	474
Dp	1289	CTCCGCCTGTGTCCGTCTGTCTCACTC	1335

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it çe i	
TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS: ADDRESSEE: Quarles & Brady STREET: 1 South Pinckney Street CITY: Madison STATE: WI COUNTRY: US ZIP: 53701-2113	
COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:	
APPLICATION NUMBER: US/09/453,702B FILING DATE: 03-06c-1999 CLASSIFICATION: «Unknown> PRIOR APPLICATION DATA: PRIOR APPLICATION NUMBER: 60/110,955 FILING DATE: 04-DEC-1998 ATTORNEY/AGENT INFORMATION: NAME: Seay, Nicholas J	
TELEC MATIO SEQUE MOLEC	
Alignment Scores: 0.0464 Length: 4021 Pred. No.: 126.50 Matches: 102 Best Local Similarity: 33.00% Conservative: 61 Best Local Similarity: 20.65% Mismatches: 153 Query Match: 4.42% Indels: 26 Best Local Similarity: 20.65% Mismatches: 163 DB: 4	
US-09-593-793A-113 (1-553) x US-09-453-702B-197 (1-4021) Qy 19 LeuLeuValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyr 38	
39 ValProProLeuLeuLeuGluValGlyValGluGluLySPheMetThrMetValLeuGly 58 1081TTCTACACGACGTTTTTGGA 110	
Oy 59 IleGlyPro	

87 1221	104	118	1320	134	54	4	170	1470	190	1524	10	n o	6 1	1611	Š	1653	270	1674	290	1701	310	1737	27	1782	345	1842	359	1902	377	6	0
8 ValProLeuLeuGlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgPro :::::	8 PheIleTrpAlaLeuSerLeuGlyI:::::	5 ArgalaGlyTrpLeulaGlyLeuLeu	2 GATGCCAGCATG	9 ProLeuGluLeuAlaLeuLeulleLeuGlyValGlyLeu	5 CysGlyGlnVal		5 AspHisCysArgGln	1 ATCTCCTGCCAGTCCTGGGGGATTCGTTCTCTGGGGGGGTAGGGGGGATTTCTGGTTTCGGT	1 GlyGlyC	1 GCTTACCGTGGATGGTAGCTCTTTCGGTCAGGGC	1 TyrLeuGlyThrGlnGluGluCysLeuPheGlyLeu	5 CAACTGGGCGTCGGGGTATTGTGCGCCATTGCCGTGGTGATGTTCCTGT	1 ValAlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaG	GTGAACGGGTG	1 GlyLeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPh ::: :::		1 ArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgT	4 cegalcaaceaccaactecte	1 LeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThr	-crearecregrearerrrecrecr	1 PheTyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgA	2 ATTAACGTCTTTAACATTCGCGGCGGTGGGTATATG	ThrGluAlaArgArgHsTyrAspGluGlyValArgMetGlySerLeuGly	,AC	8 LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeu	3 cigircircaccargarcaccircacricalitarcagcicagrafarasccafi	InArgPheGlyThrArgAlaValTyr	TTTCGATACCGTCAAAATTTATTACTACACCAACCTGC	0 AlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaVal 1 1 1 1 1 1 1 1 1 1	8 ValThrAlaSerAlaAlaLeuThrGlvPheThrPheSerAlaLeuGl	:::
1162	1223	10	1282	119	13	9	155	1411	17]	147]	6	C1 .	~ 1	157	m	1613	25]	1654	27.1	1675	291	1703	П	1738	328	1783	346	1843	360	7	ن ،
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Db 2023 TTTGCCGATGACTACGGCGAGT2044	Query Mato	-
Qy 414 rArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGl 434	60-SD	-09-593
Db 2045GGAAAACCCACGTACGTTCTTCCGGC 2070	Qy	269
434	qa -	1225
Db 2071 ATGAACTTCGCCTTCAATCTGTTTTCATCAGCTGGCCTGGG2113	QY	289
Qy 453 uLeuProProProAlaLeuCysGlyAlaSerAlaCys 466	qa	1174
Db 2114CTCCAGCGCCGGGATCATCAGCCTGC 2140	Qy	308
RESULT 41 IIS-08-404-007-13 /c	qa	1114
; Sequence 13, Application US/08494907 : Patent No. 595508	Qy	328
GOVERAL INC. 25.25.250. GOVERAL INC. 25.25.250. GOVERAL INC. 25.25. GOVERANT TENDERS. 15.25.	qa	1063
AFFLICANI: InduaSilow, Linda S ; APPLICANY: Bangera, Mahalaxmi : APPLICANY: Wellor David M	Qy	347
; APPLICANT: MCITET, DAYLU N ; APPLICANT: MCON, R. Jammes : TITIE OF INVENTION: Sequences for Droduction of	q -	1039
; TILE OF INVENTION: 2.4-Diacetylphloroglucinol and Methods NIMARR OF SECHENCES: 20	oy	367
CORRESPONDENCE ADDRESS:	qa	979
STREET: 800 Buchanan Street	δλ	387
STATE: CA COUNTRY. CA	QΩ	919
; ZIP: 25A	Qy	407
CONTOLER REALPROLE FORM: ** MEDIUM TYPE: Floppy disk ** COMMITTED: TEM PO COMMONTIALS	qq	876
CONTRACTING SYSTEM: PC-DOS/MS-DOS COPERATING SYSTEM: PC-DOS/MS-DOS CONTRADED: Datacattr Daloace #1 0 vorcion #1 25	QY	427
CURRENT APPLICATION DATA: APPLICATION NIMBER: 15,008,494,907	dα	820
FILING DATE: CONTROLL STATE OF THE STATE OF	Qy	439
ATTORNET TOTAL TOT	qa	160
; REGISTRATION WHEEK 30043 : REGISTRATION WHEEK 30043 : DEPENDENCE ACCOUNT ACCOUNT ACCOUNT	QY	453
. X	qa	700
; TELEFAX: (507) 559 500; ; TELEFAX: (510) 559 5777 ; TNEPRATTAL FOR STO 17 NO. 13.	Qy	471
; SEQUENCE CHARGETERISTICS:	qa	640
; TYPE: nucleic acid	٥y	491
; SIKANDEDNESS: Single ; TOPOLOGY: linear	qa	586
E ::	δŏ	510
ĸ	qa	529
	Qy	530
NAME/KEI: CUS LOCATION: complement (11269) OTHER INFORMATION: /note= "phlE DNA sequence. SEQ ID OTHER INFORMATION: No.14 is translation (nontein) of central No.12 in	qq	Db 469
907-13 Scores:	PCI	RESULI 42 PCT-US96-1 ; Sequence ; GENERAI
FIGU. NO.: 0.01/0 LENGIN: 1269 SOCIE: 127 00 Matches: 84	_	TITE

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----CGGGCTGGTAGGACTTGA 1175
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                                                                                                                                         GluProGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuGly 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 -LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGl 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLy 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GACAGACGTCTTGCACCTGAGCATTTCTCCATGGCCATGATCATCTCCGCGATCGGCCT 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nArgPheGlyThrArgAlaValTyrLeuAlaSerValĀlaAlaPheProValAlaAlaGl 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       yAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThrGlyPh 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 TCCCATCATCGGCCTGTGCCTGGGGCGCTGCTGGCGGCGTATTGTTTGAAATGTTCGG 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0 ATCGTGGCGCCCGTGTTCGCCATCATCTCGTTGCCGGGCCTGCTGGTGGCCTGGTATCT 701
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequences for Production of 2,4-Diacetylphloroglucinol and Methods 20
124
52
12
                                                                                             3-793A-113 (1-553) x US-08-494-907-13 (1-1269)
Mismatches:
Indels:
Gaps:
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|CCTCTTCATGGGCGTTGCTATC-------
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ce 13, Application PC/TUS9610986
AL INFORMATION:
LE OF INVENTION: Sequences for P
LE OF INVENTION: 2,4-Diacetylph1
BER OF SEQUENCES: 20
Similarity: 28.00%
1: 4.30%
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Db 979 CGCATCTGCCTTGATCTCAAGCCTGTGCTGCTGCTGCGCGCCTTGATGGGGAT 920 Qy 387 eThrPheSeralaLeuGlnIaLeuProTyrthrLeualaSerLeuTyrHisArgGluLy 407 (1) 11 11 11 11 11 11 11 11 11 11 11 11 1	Sequence 2, Application US/08494907
CORRESPONDENCE ADDRESS: ADDRESSEE: Stephan A. Pendorf, DOMINIK & STEIN STREET: 600 N. West Shore Boulevard, Suite 1000 CITY: Tampa CITY: Tampa CITY: Tampa COMPUTER READBLE FORM: ADDITION TYPE: PLORY GISK COMPUTER: TAMPA: PLORY GISK COMPUTER: TAMP COMPALIAN COMPUTER: TAMPA: COMPALIAN COMPUTER: TAMPA: PC-OMPALIAN COMPUTER: TAMPA: PC-OMPALIAN COMPUTER: TAMPA: PC-OMPALIAN COMPUTER: TAMPA: PC-OMPALIAN COMPUTER: PALCATION NUMBER: PCT/US96/10966 FILING DATE: CLASSIFICATION NUMBER: D265 REDERANCE/DOCKET NUMBER: A700.320 TELEPOND: (31) 289-2966 TELECAMONICATION NUMBER: A700.31 TELEPONENICATION NUMBER: A700.31 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NUMBER: A700.320 TELEPONENICATION NOMBER: A700.320 TELEPONENICATION NOMBER: A700.320 MATI-SENSE: Single STRANDEDESS: Single STRANDEDESS: Single STRANDEDES: NOMBER: NOMBER: NOMBER: PRATURE: PRESENCE NOMBER: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PRATURE: PR	Alignment Scores: Score: Score: 123.00 Matches: Rercent Similarity: 4.334 Conservative: 40 Best Local Similarity: 4.304 Mismatches: 5 Best Local Similarity: 4.304 Indels: 5 US-09-593-793A-113 (1-553) x PCT-US96-10986-13 (1-1269) QY 269 ArgThreuargArgLeupheValalaGluLeuCysSerTrpMetalaLeuweThrPhe 288 1174 125 AAGACGCATGGTCGTTTTTTGTCGCTGAGCTTCGGCTGGTAGGACTTGA 1175 QY 289 ThrLeuPheTyrThrAspPheValGlyGluGlyCalTyrGluGlyValargAla 307 1174 TGGTTCATTATACATGCCGTTGTTCCTGGCATGACAGCTGGACTATCA 1115 QY 289 ThrLeuPheTyrThrAspPheValGlyGluGlyValargMetGlySeftLeuGly 327 1114 TGGTTCATTATACATGCCGTTGTTCCGGTGGATGACTGGCTGG

INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:	Db 1064 CCTCTTCATGGGCGTTGCTATCAG 1041
TENERAL SOFT BEAUTY SOFT BEAUT	Qy 347 nArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGl 367
IIFE: NUCLEIC ACLU STRANDEDNESS: single TODDIACY. lines	Db 1040 GCGATTGGGCACCAAGCAACTGCTGGTGTTTCGATTACCTTGGTATCGCTCGTGGCGG 981
E ::	
ä	900 CGCA1CIGCG116A1CICAAGCCI1A1GG6CC116G1GC1CC1GCGCCGCC11GA1GG6GA1
FEATURE: NAME/KEY: misc feature	Db 920 CTGGGAAGGGGC
LOCATION: complement (42855076) OTHER INFORMATION: /note= "phlA, transcribed from OTHER INFORMATION: right to left"	407 sGlnValPheLeuProLysTyrArg-GlyAspThrGlyGlyAlaSerSerGluAspSerL
FEATURE: NAME/KEY: misc_feature	877 -GAAGTTTCGCAGCCGTGCCGGGGTCAACCTGGGCATCCAGCAGGCACTGTT
LOCALION: Comprement (2000) OTHER INFORMATION: /note= "phib, transcribed from OTHER INFORMATION: right to left"	Db 821 TCCCATCATCGCTGGGCCGCGCGCGCGCGCGTATTGTTTGAAATGTTCGG 762
FEATURE: MARE/KEY: misc_feature LOCATION: complement (30854251) OTHER INFORMATION: //note= "phil", transcribed from	Qy 439AlaproPheProAsnGlyHisValGlyAlaGlyGlySerGly 452
OTHER INFORMATION: IIGHT TO TELL NAME: NAME/KFV. misc foathro	Oy 453LeuLeuProProProProAlaLeuCysGlyAlaSerAlaCysAspValSerVal 470
LOCATION: complement (13982444) OTHER INFORMATION: /note= "phlD, transcribed from	
OTHER INFORMATION: right to left." FEATURE: NAME/KEY: misc_feature	471 ArgvalvalvaloligluproThrGluAlaArgvalvalPalProGlyArgGlyIleCysLeu 490 541 CAGCCAARGGGGAACAGCGCTGTCCAGCGCAACGGCGCTCAACAT1GCCTT 588
LOCATION: 35144767 OTHER INFORMATION: /note= "phlR, transcribed from left OTHER INFORMATION: to right"	491 Asp-LeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMe
PARIONE: NAME/KEY: misc_feature NAME/KEY: misc_feature LOCATION: complement (21270) OTHER INFORMATION: /note= "phlE, transcribed from OTHER INFORMATION: right to left"	DD 587 GAIGCTAIGCAIACTGACGTGCCAATTCGTCCTGTGCCCCTGCTCCCCAGCTACCT 531 QY 510 tGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLe 530 : :::::
30	Oy 530 uGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSerAsp 547
ORMATION: Phl."	RESULT 44 PCT-US96-10986-2/c ; Sequence 2, Application PC/TUS9610986
Alignment Scores: 0.143 Length: 5076 Pred. No.: 123.00 Matches: 84 Score: 41.33% Conservative: 40 Best Local Similarity: 28.00% Mismatches: 124 Ouery Match: 4.30% Tobals: 52	ATION: Sequences for Producti ENTION: 2,4-Diacetylphlorogluc QUENCES: 20 CE ADDRESS: CF ADDRESS: CF ADDRESS:
2 Gaps:	STREET: 600 N. West Shore Boulevard, Suite 1000
269 ArgThrLeuargargLeunheValAlaGluLeuCysSerTrpMetalaLeuwetThrPhe 288	STATE: FL COUNTRY: USA ; ZIP: 33609
AAGACCCATGGTCGTTTTGTCGCTGAGCTTCGGGCTGGTAGGACTTGA	COMPUTER READABLE FORM: ** MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible
289 ThrLeuPheTyrThraspPheValGlyGluGlyLeuTyrGlnGlyValProargAla 307 ::::::	; OPERATING SYSTEM: PC-DOS/MS-DOS ; SOFTWARE: PatentIn Release #1.0, Version #1.25 ; CURRENT APPLICATION DATA:
308 GlubroGlyThrGlualaargArgHisTyrAspGluGlyValArgMetGlySerLeuGly 327	AFFILATION NOMBER: FCI/USSO/IUSSO ; FILING DATE: ; CLASSIFICATION: ; ATTORNEY/AGENT INFORMATION:
328 -LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValG1 347 :::	; NAME: Pendorf, Stephan A. ; REGISTRATION NUMBER: 32665 ; REFERENCE/DOCKET NUMBER: A700.320

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702

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-LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGl 347
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                                                                                                                                                                        nArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                eThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         920 CTGCGAAGGCGCC------TTCACCCCGGTCAGCATCATTGTCACCGAT--
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APPLICANT: Thomashow, Linda S
APPLICANT: Bangera, Mahalaxmi
APPLICANT: Weller, David M
APPLICANT: Cook, R. James
TITLE OF INVENTION: Sequences for Production of
TITLE OF INVENTION: 2,4-Diacetylphloroglucinol and
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Margaret A. Connor, USDA-ARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             euMetThrSerPhe-LeuProGlyProLysProGly------
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS |
SOFTWARE: Patentin Release #1.0, version #1.25
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STREET: 800 Buchanan Street
CITY: Albany
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Patent No. 5955298
GENERAL INFORMATION:
                                                                                                      1064 CCTCTTCATGGGCGTTGCTATC---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 3514.4767
OTHER INFORMATION: /note= "phlR, transcribed from left
OTHER INFORMATION: to right"
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40
124
124
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OTHER INFORMATION: /note= "phlA, transcribed from OTHER INFORMATION: right to left"
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LOCATION: complement (3085..4251)
OTHER INFORMATION: /note= "phlC, transcribed from
OTHER INFORMATION: right to left"
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LCGATTON: complement (2606..3313)
OTHER INFORMATION: /note="phlB, transcribed from
OTHER INFORMATION: right to left"
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Matches:
Conservative:
Mismatches:
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LOCATION: complement (1398..2444)
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas fluorescens
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                              TELEPHONE: (813) 289-2966
TELEFAX: (813)289-2967
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5076 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TELECOMMUNICATION INFORMATION:
TELEPHONE: (813) 289-2966
                                                                                                                                                                                                                                                                                                             DNA (genomic)
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NAME/KEY: misc_feature
LOCATION: 1..5076
OTHER INFORMATION: /note
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123.00
41.33%
28.00%
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LOCATION: complement (2
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                                                                                                                                                                                                                                                                    TOPOLOGY: 11:
                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: /note= "phlF, truncated, OTHER INFORMATION: transcribed from left to right"
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OTHER INFORMATION: /note= "phlB, transcribed from
OTHER INFORMATION: right to left"
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LOCATION: complement (3085..4251)
OTHER INFORMATION: /note= "phlC, transcribed from
OTHER INFORMATION: right to left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: complement (1398..2444)
OTHER INFORMATION: /note= "phlD, transcribed from
OTHER INFORMATION: right to left"
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OTHER INFORMATION: /note- "phlR, transcribed from
OTHER INFORMATION: left to right"
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                               NAME: CONNOR, MARGARET A
REGISTRATION NUMBER: 30043
REFERENCE/DOCKET NUMBER: 000995
TELEPHONE: (510) 559-6067
TELEPHONE: (510) 559-577
INFORMATION: (510) 559-577
INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
LENGTH: 6170 base pairs
LENGTH: 6170 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,907
FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: complement (4285..5076)
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complement (2..1270)
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                        GluProGlyThrGluAlaArgArgHisTyrAspGluGiyValArgMetGlySerLeuGly 327
                                                                                                                                                                                                                                                                                                                                                                                                                               328 -LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGl 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       920 CTGCGAAGGCGCC------TTCACCCCGGTCAGCATCATTGTCACCGAT-- 878
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     · 347 nArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGl 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 367 yAlaThrCysLeuSerHisSerValAlaValThrAlaSerAlaAlaLeuThrGlyPh 387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 -----LeuLeuProProProProAlaLeuCysGlyAlaSerAlaCysAspValSerVal 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             289 ThrLeuPheTyrThrAspPheVal---GlyGluGlyLeuTyrGlnGlyValProArgAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                701 GTATCGAACCTACCAACCGAGCCAGGCGCCCCATCCAAGGCCGCTCGTAGAACCCTCCGG
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US-09-593-793A-113 (1-553) x US-08-494-907-4 (1-6170)
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Job time : 147 secs
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RESU US-0 ; Se ; Pu ; GE	RESULT 2 US-09-232-880-110 ; Sequence 110, Application US/09232880 ; Publication No. US20020182596A1 ; GENERAL INFORMATION:	
	APPLICANT: Xu, JiangGhu APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer Lynn	
	; TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF ; TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE	
·. ·. ·	; FILE REFERENCE: 210121.428C6 ; CURRENT APPLICATION NUMBER: US/09/232,880	
	CONNECT FILLING DAILS, 1999 OL 13	
SES :	SOFTWARE: FASTSEQ IOF WINGOWS VERSION 3.0 ; SEQ ID NO 110 . TENNAH, 3/10	
0-SD	; TYPE: DNA ; ORGANISM: Homo sapien US-09-232-880-110	
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Db 1484 TCCCTCTACCACCGGAGAAGCAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGT 1543 Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440 Db 1544 GCTAGCAGGAGAAGCCTGATGACTTTCTCTCCCCAGGCCCTAGAGCTCCCTGAGCTTGAGAACCTGATGACCACACACCCTGAAGCTTGAGAACCTGAAGACCTGATGACCACACACA	Oy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProPalaLeu 460 	Oy 461 CysGlyalaseralaCysAspvalSerValArgValValValQlyGluProThfGluAla 480 	Oy 481 argValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAläPheLeu 500 	Qy 501 LeuSerGlnValalaProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerVal 520 	Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAla 553 	RESULT 3 US-10-012-896-110 ; Sequence 110, Application US/10012896	; Publication No. US20020183251A1 ; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun	Dillon, Davin C Mitcham, Jennif Harlocker, Susa Jiang, Yuqiu	APPLICANT: RAIGS, MICHAEL DAPLICANT: Retter, Warc W. APPLICANT: Stolk, John A. APPLICANT: Day, Craig H.	APPLICANT: APPLICANT: APPLICANT:	Skeiky, rasir A.W. Hepler, William T. Henderson, Robert Hural, John		APPLICANT: Wantanabe, Yoshihiro APPLICANT: Watanabe, Yoshihiro TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	121.427C27 NUMBER: US/10/012,896	SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 110 LENGTH: 3410	TTE: UNA ORGANISM: Homo sapiens US-10-012-896-110

Alignment Scores:

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                                                yLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu
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                                                                       llAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro
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                                      13A-113 (1-553) x US-10-012-896-110 (1-3410)
Length:
Matches:
Conservative:
Mismatches:
Indels:
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Similarity:
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                                                                  361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla
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US-09-895-793-110
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RESULT 4

US-09-085-793-110

Sequence 110, Application US/09095793

FUDLICACTION NO. US20020192763A1

GENERAL INFORMATION:
APPLICANT: XU, Jiangchun
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Malooker, Susan L.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Reter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Skeik, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Wonell, John
APPLICANT: Houghton, Raymond L.
APPLICANT: Winals de Bassols, Carlota

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Publication No. US20020193296A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L
APPLICANT: Harlocker, Susan L.
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US-09-895-814-110
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Matches:
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Vinals de Bassols, Carlota
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SOFTWARE: FastSEQ for Windows Version
                                                                                                                                 Skeiky, Yasir A.W.
Hepler, William T.
Henderson, Robert A.
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Ö.
                                               Day, Craig H.
Vedvick, Thomas S
Carter, Darrick
Kalos, Michael D.
Retter, Marc W.
Stolk, John A.
                                                                                                    Li, Samuel X.
Wang, Aijun
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US-09-895-814-110
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Best Local Similarity:
Query Match:
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Pred. No.:
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10 2 9 2 8	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220	NESULUS - 02 - 03 - 03 - 03 - 03 - 03 - 03 - 03
1	AlaalaLeuGlyProThrGlubroalaGluGlyLeuSerAlaProSerLeuSerProHis 240	AB A AB AB AB AB AB AB AB AB AB AB AB AB
1	1 CyscysProcysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260	TITELL TO COUNTY
7	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280	NOCOLE PERCENTIANT NOCOLE BEST COLE
Db 106	1 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 30	NS-09
Oy 28 Db 112	4 AGCTGGATGGCACTCATGACCTTCACGCTGTTTTACACGGATTTCGTGGGCGAGGGCT	Align Pred. Score Perce Best
Qy 30 Db 118	01 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320 	Perce
Oy 32 Db 124	1 ValargMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340 	Query DB:
Qy 34 Db 130	ValMetAspargLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360 	US-09
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Qy 40 Db 148	11 SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly 420 	Db Qy
Oy 42 Db 154	11 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440	Db Qy
Qy 441 Db 1604	1 PheproAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu 460 	Db Qy
Oy 46 Db 166	61 CysGlyAlaSerAlaCysAspValSerValArgValValValGlyGluProThrGluAla 480 	qa vo
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2	ThralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln 540	5 A

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APPLICANT: Reed, Steven G.
APPLICANT: Red, Jiangchun
APPLICANT: AL, Jiangchun
APPLICANT: AL, Jiangchun
APPLICANT: Dillon, Davin C.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.446D1
CURRENT FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 101
SOFTWARRE: FastSEQ for Windows Version 3.0
FILE OID NO 100
343
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Conservative:
Mismatches:
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09-745-288-100
equence 100, Application US/09745288
atent No. US20010018058A1
ENERAL INFORMATION:
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ORGANISM: Homo sapien
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Local Similarity:
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181	201	221	241	261 1064	281 1124	301 1184	321	341	361 1364	381 1424	401	421 1544	441	461 1664	481 1724	501 1784	521

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1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu
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PLICANT: Skelky, Yasir A.W.
PLICANT: Skelky, Yasir A.W.
PLICANT: Hepler, William
TLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
LE REFERENCE: 210121.427C23
RRENT FILING DATE: 2001-01-12
MBER OF SEQ ID NOS: 934
FTWARE: FastSEQ for Windows Version 13.0
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Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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mence 110, Application US/09759143
ent No. US200202248A1
ERAL INFORMATION:
                                                                                                   Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                                                                                                                                               Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Day, Craig H.
Vedvick, Thomas S.
Carter, Darrick
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RGANISM: Homo sapien
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	Qy 501 LeuSerGlnValAlaProSerLeuPhel	Qy 521 ThralaTyrMetValSerAlaAlaGlyl	Qy 541 ValValPheAspLysSerAspLeuAlal	щo	GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C. APPLICANT: Mitcham, Jennifer	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT: APPLICANT:			CURRENT APPLICATION NUMBER: US/09/" CURRENT FILING DATE: 2001-02-09 "NUMBER OF SEQ ID NOS: 943 SOFTWARE: FASLED for Windows Ver:	SO I EO	-780-669-110 ment Scores: No.:	HCH	-09-593-	Oy 1 MerValGinArgLeuTrpValSerArgi 	Oy 21 ValAsnLeuLeuThrPheGlyLeuGluV	Qy 41 ProLeuLeuLeuCluvalGlyValGluC
121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 14	044 GAGCTGGCACTGCTC 141 ThrProLeuGluAla 1014 APPCACHGGAGGCC	161 TyrservaltyralabheMetileSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 18 161 TyrservaltyralabheMetilleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 18 764 TACFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	181 IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 20	201 GlyLeuchthreulePhereuthrCystalaaharhrLeuchaladluglu 22 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	221 AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240	241 CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260 	261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280 	281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300 	301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHiSTyrAspGluGly 320 	321 ValargMetGlySerLeuGlyLeuPheLeuGlnCysalaIleSerLeuValPheSerLeu 340 	341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 3	361 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValThrAla 380 	381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400 	401 SerLeuTyrHisArg 	421 AlaSerSerGluAspSerLeuWetThrSerPheLeuProGlyProLysProGlyAlaPro 440	441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeu 460 	461 CysGlyAlaSerAla 	481 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu 50
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uGluLysPheMetThrMetValLeuGlyIleGly 60. AND METHODS FOR THE THERAPY AND PROSTATE CANCER 3410 553 0 0 0 80-669-110 (1-3410) aLystyrSerala 553 ||||||||||||||| |CAAATACTCAGÇG 1942 Length:
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ò	181	IleAsoTrbAsoThtSerAlaLenAlaProTvrLenGlvThrGlnGlnGlnGlnCvsLenPhe 200	Οy	541
연	824	ATTGACTGGGACACCACTGGCCCCCTACCTGGGCACCAGGAGGAGTGCCTCTTT 883	qq	1904
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Q Dp	321	ValargMetGlySerLeuGlyLeuPheLeuGlnCysalaIleSerLeuValPheSerLeu 340 		ATTOI NAN REC
oy Bb	341	ValMetaspargLeuValGlnargPheGlyThrargalaValTyrLeuAlaSerValAla 360 		REI TELEC TEI
Oy Op	361	AlaPheprovalalaalaGlyalaThrCysLeuSerHisSerValalavalvalthrala 380 		INFORMZ SEQUI LER TYE
ογ	381	SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla 400		STI TOI
qq	1424	TCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGCTCTCCCCTACACACTGGCC 1483		ORIG
oy Op	401	SerLeuTyrHisargGluLysGlnValPheLeuProLysTyrArgGlyAspThrd191yd1y 420 	US-(US-09-030
	•			

ce 110, Application US/09030606
No. US20020081580A1
No. US20020081580A1
LICANT: Xu, Jiangchun
LICANT: Dillon, Davin C.
LE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF PROSTATE CANCER AND METHOD BER OF SEQUENCES: 204
RESPONDENCE ADDRESS: ThralaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGln ArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeu EDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OMPUTER: Patentin Release #1.0, Version #1.30

RENT APPLICATION DATA:

ILING DATE: 25-FEB-1998 DDRESSEE: SEED and BERRY LLP TREET: 6300 Columbia Center, 701 Fifth Avenue IIY: Seattle EFERENCE/DOCKET NUMBER: 210121.428C3 ECOMMUNICATION INFORMATION: ELEPHONE: (206) 622-4900 ELEFAX: (206) 682-6031 MATION FOR SEQ ID NO: 110: UENCE CHARACTERISTICS: LASSIFICATION:
ORNEY/AGENT INFORMATION:
AME: Maki, David J.
EGISTRATION NUMBER: 31,392 SNGTH: 3410 base pairs (PE: nucleic acid Homo sapiens single SCULE TYPE: CDNA linear TRANDEDNESS: OPOLOGY: line 98104 RGANISM: 0-606-110 ΜĀ 0-606-110 TATE: W

Scores

No.: int Similarity: Local Similarity: Match: 593-793A-113 (.y: 1-55	1.44e-259 2861.00 100.00\$ 100.00\$ 100.00\$	Length: Matches: Conservative: Mismatches: Indels: Gaps:	3410 553 0 0 0 0	
4etValGlnArgL	υ – Ε	uTrpValSerArg	euLeuArgHisArgL	ysalaginLeuLeuLeu 	20 343
/alasnLeuLeuTh 		rPheGlyLeuGlu 	ValasnLeuLeuThrPheGlyLeuGluValCysLeualaalaGly11eThrTyrValPr 	lyilethrTyrvalPro 	40 · 403
ProLeuLeuLeuGlı 	_ ~ ~	1ValGlyValGlu 	GluLysPheMetThrM GAGAGTTCATGACCA	roLeuLeuLeuGluValGlyValGluGluLysPhemetThrmetValLeuGlyIleGly 	60 463
ProValLeuGlyLeu 		JValCysValPrc 	roValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHiSTrpArgGl 	erAspHisTrpArgGly 	80 523
ArgTyrGlyArgAr 		gargProPhelle 	ArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlylleLeuLeuSerLe 	lyileLeuLeuSerLeu 	100
PheLeuIleProArc		JAlaGlyTrpLeu 	AlaGlyLeuLeuCysP. 	PheLeuIleProArgalaGlyTrpLeualaGlyLeuLeuCysProAspProArgProLeu 	120 643
SluLeuAlaLeuLeu 	5-0		GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPh 	ysGlyGlnValCysPhe 	140 703
Phr ProLeuGluAlai 	ซี — ซั	LeuLeuSerAsp 	Thr ProLeuglual a Leu Leuserasp Leu Pheargasp proAsp His Cysarggln. 	sphiscysargglnala 	160 763
TyrSerValTyrAlaP 	G — B	heMetileSer TCATGATCAGI	TyrSerValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAl 	lyTyrLeuLeuProAla 	180 823
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AlaAlaLeuGlyProf 	5 - 3	rhrGluProAla 	laalaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHi. 	roSerLeuSerProHis 	240 1003
CysCysProCysArg ¹ 	8 – 8	AlaArgLeuAla 	ysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLe 	laLeuLeuProArgLeu 	260 1063
isGlnLeuCysCys 	vi — €	ArgMetProArg 	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCy. 	neValalaGluLeuCys 	280 1123
SerTrpMetalaLeu 	3~6	MetThrPheThr 	LeuPheTyrThrAspP 	SerTrpMetalaLeumetThrPheThrLeuPheTyrThraspPheValGlyGluGlyLeu 	300 1183
fyrGlnGlyValProA RCCAGGGGGTGCCCA	&=&	rgAlaGluPro GAGCTGAGCCG	GlyThrGlualaarga 	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 	320 1243

340	360	380	14	400	~ ·	15	440	1603	460		1723	1 1	500	9 6	520 1843	540	1903				
ValargwetGlySerLeuGlyLeuPheLeuGlnCysalalleSerLeuValPheSerLeu	1 ValMetaspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla	1 AlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAl	4 ccrirccrereccrececereccararecrereccacarerecereres	1 SeralaAlaLeuThrGlyPheThrPheSerAlaLeuGlhIleLeuProTyrThrLeuAla	4 TCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGC	1 SELENTYTHISARGGARGASCHWALTMELENTOMYSTYFARGELYSPINICTYGYY	1 AlaSerSerGluAspSerLeuMetThrSerPheLeuPröGlyProLysProGlyAlaPro	4 GCTAGCAGTGAGGACGAGCCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGGAGGCTCCC	1 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeu The control of t		1 CysG yAtaSerAtaGysAsyVatSerVatArgVatVatVatVatUGtyGturroffirGtuAfa	,	1 ArgValValProGlyArgGlyIleCysLeuAspLeuAlaileLeuAspSerAlaPheLeu 		1 LeuserGingalAlaProserLeuPheMetGiySerTieValGinLeuserGinserver LeuserGingalAlaroserLeuPheMetGiySerTieVillililililililililililililililililil	1 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPhe		1 ValValPheAspLysSerAspLeuAlaLysTyrSerAl		RESULT 10 US-09-822-827-110 IS-09-822-827-110 Sequence 110, Application US/09822827 Fatent No. US20020081680A1 GENERAL INFORMATION: APPLICANT: XU, Jiangchun TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERRNCE: 210121.534C1 CURRENT APPLICATION NUMBER: US/09/822,827 CURRENT FILING DATE: 2001-03-28 NUMBER OF SEQ ID NOS: 982 SEQ ID NO: 982 SEQ ID NO: 982 LENGTH: 3410 TYPE: DNA ORGANISM: Homo saplen US-09-822-827-110	i Similar 11 Simi
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alAsnLeuLeuThrPheGlyLeuGluV 	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40 	δδ qq	381 Se 1424 TC
roLeuLeuLeuGluValGlyValGluGlu 	ProLeuLeuLeuGluValGlyValGluGluLySPheMetThrMetValLeuGlylleGly 60 	do de	
rovalLeuGlyLeuValCysValProLei 	ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpÅrgGly 80 	Qy Db	421 A1
rgTyrGlyArgArgArgProPheIleTrE 		QY	441
heLeulleProArgAlaGlyTrpLeuAla 	12	QQ Dp	461
luLeuAlaLeuLeuIleLeuGlyValGlyl 	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140 	QQ QQ	481
hrProLeuGluAlaLeuLeuSerAspLeuF 	ThrProLeuGlualaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160 	Qy Db	501 Le 1784 CT
TyrSerValTyralaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 	yG yCysLeuGlyTyrLeuLeuProAla 180 	do do	521
<pre>11eAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCys\(\text{LeuPhe}\) 111111111111111111111111111111111111</pre>	rrLeuGlyThrclnGluGluCysheuPhe 200 	qa	1904
GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 	alAlaAlaThrLeuLeuValAladiuGlu 220 	RESI US-(' SE	RESULT 11 US-09-115-45 ; Sequence 1 ; Patent No.
AlaalaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 	yLeuSerAlaProSerLeuSerProHis 240 		GENERAL IN APPLICANT APPLICANT TITLE OF
CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProÀrgLeu 	rgAsnLeuGlyAlaLeuLeuProArgLeu 260 		TITLE FILE R CURREN
HisGlnLeuCysCysargMetProArgThrLeuArgArgLeuPheValAlaGlu ^l LeuCy; 	euargargleuPhevalalaGlubeuCys 280 		NUMBER O SOFTWARE EQ ID NO LENGTH:
SerTrpMetalaLeuWetThrPheThrLeuPheTyrThraspPheValGlyGludlyLeu 	heTyrThrAspPheValGlyGluGlyLeu 300)-sn	TYPE: DN ORGANISN 3-09-115-45
Tyr61nG1yValProArgAlaGluProClyThrGluAlaArgArgHisTyrAspCluGly 	hrGlualaargArgHisTyraspoluGly 320 	Align Pred. Score Percel	Alignment Sc Pred. No.: Score: Percent Simi
alargMetGlySerLeuGlyLeuPheLeuG 	ValargmetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340 	DB:	ry Match
alMetAspArgLeuValGlnArgPheGly1	ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360)-sn	-09-593-79

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CANT: Xu, Jiangchun
CANT: Dillon, Davin C.
OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF
OF INVENTION: METHODS FOR THEIR USE
REFERENCE: 210121.427C4
NT APPLICATION NUMBER: US/09/115,453B
NT FILING DATE: 1998-07-14
NT FILING DATE: 1998-07-14
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110, Application US/09115453B
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1364	Qy 381 SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGl 	Qy 401 SerLeuTyrHisArgGluLysGlnValPheLeuProLy	Qy 421 AlaSerSerGluAspSerLeuMetThrSerPheLeuPr 	Qy 441 PheProAsnGlyHisValGlyAlaGlyGlySerGlyLe	Qy 461 CysGlyAlaSerAlaCysAspValSerValArgValVa 	Qy 481 ArgValValProGlyArgGlyIleCysLeuAspLeuAl 	Qy 501 LeuSerGlnValAlaProSerLeuPheMetGlySerII	Qy 521 ThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuva	Oy 541 ValValPheAspLysSerAspLeuAlaLysTyrSerAl 	ED (V)	; GENERAL INFORMATION: ; APPLICANT: Xu, Jiangchun ; APPLICANT: Dillon, Davin C. ; APPLICANT: Mitcham, Jennifer L.	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	APPLICANT: Henderson, Robert A. A. APPLICANT: Hural, John APPLICANT: MCNeill, Patricia D. APPLICANT: Houghton, Raymond L.		HAPLICANT: Meagher, Madeleine Joy TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: DIAGNOSIS OF PROSTATE (FILE REFERENCE: 210121.427027 CURRENT APPLICATION NUMBER: US/10/012,896
Oy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20	Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40	Qy 41 ProLeuLeuGluValGluGluGluGluLysPhemetThrMetValLeuGlyIleGly 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	LleuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 	31yargArgArgProPhelleTrpAlaLeuSerLeuGlylleLeuLeuSerLeu 10 	Qy 101 PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120	lleuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe		rvalTyralapheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 	rpasphrSeralaLeualaproTyrLeuGlyThrGlnGluGluCysLeuPhe 	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaalaThrLeuLeuValAlaGluGlu 	ThrGluProA	0y 241 CysCysProCysArgalaargLeuAlaPheArgasnLeuGlyAlaLeuLeuProArgLeu 260	Oy 261 HisGinLeuCysCysrgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280	Oy 281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300	Qy 301 TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320 	<pre>Qy 321 ValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeu 340 </pre>	Oy 341 ValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAla 360

ACAGTGTGCCGTGGTGACAGCT 1423 ilnileLeuProTyrThrLeuAla 400 roglyproLysProglyAlabro 440 alvalGlyGluProThrGluAla 480 lalleLeuAspSerAlaPheLeu 500 FOR THE THERAPY AND ANCER Ala 553 ||| 3CG 1942

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NUMBER OF SOFTWARE: SSO ITWARE: SSO SSOFTWARE: SSO SSOFTWARE: ON CANISM CONTROL OF C	ID NOS: 1011 SEQ for Windows Version 3.0 Sapiens	1: 7.21e-246 Length: 4034 2716.50 Matches: 553 t.y: 70.09% Conservative: 0 arity: 70.09% Mismatches: 0 94.95% Indels: 236 Gaps: 1	.13 (1-553) x US-10-012-896-704 (1-4034)	ValGinargLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 	alCysLeuAlaAlaGlyIleThrTyrValPro 4	SGCCGCAGGCATCACCTATGTGCC	LeuleuGluValGluValGluGluLysPheMetThrMetValLeuGlyTleGly	GlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 8	GGCCTGGTCTGTTCTGTTCTTTTTTTTTTTTTTTTTTTT	GlyArgArgArgArgProPheIleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100	Cuccecceccciicaicaecacia de la contra del la contra del la contra del la contra de la contra de la contra de la contra de la contra del la contra de la contra de la contra de la contra de la contra de la contra del la contra del la contra de la contra de la contra de la contra de la contra del la contra de la contra de la contra del la cont	LIEPTOAIGALAGIYITPLEUALAGIYLEULEULYSPIOASPPIOAIGFIOLU 120 	AlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValcysPhe	gAspProAspHisCysArgGlnAla 16	9	ValTyralaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAla 180 	LeuGlyThrGlnGluGluCy	TGGGACACCAGTGCCCTGGCCCCCTACCTGGGCACCCAGGGGGGGG	euThrieullePheieuThrCysValAlaAlaThrieuLeuValAlacluGlu 22	TCACCCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 94	LeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 24	TGGGCCCCACCGAGCCAGCAGAAGGGCTGTCGGCCCCCTCCTTGTCGCC	ysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260	CGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTG	CysargMetProargThrLeuargargLeuPheValalaGluLeuCys 28	recedentececedecerecedecedecrerregregerere
NUMBER SOFTWAN SOFTWAN SOFTWAN SOFTWAN SEG ID IN TYPE: 1 ORGANI. 1	DF SEQ ID NOS E: FastSEQ fo. 7 704 : 4034 DNA SM: Homo sapi. 396-704	ores: larity: Imilarity	793A-113 (1-5		ValAsnLeuLeuTh	GTCAACCTGCTAAC	LeuLe	ProValLeuGlyLe	CCAGTGCTGGGCCT	gTyrGlyAr 	CGC1A1GGCCGCCG	FIELEULLEFIOAL 	GluLeuAlaLeuLeuIle 	ThrProLeuGluAl	ACTCCACTGGAGGC	yrSerVall 	IleaspTrpAspTh	ATTGACTGGGACAC	lyLet 	SCCTO	laAla	CAGC	CysCysProCysAr	TGCTGTCCATGCCG	HisGlnLeuCysCy	сассадствтветв
	SOF SED LE TY OR	nent No.: : nt S Loca Mat	-09-593			4	4 04	Н	61	80 6	101	581	2 4	14	7	9	81	21	20	88	22	4	241	01	261	61

QY	281	rPheThrLeuPheTyrThrAspPheValGlyGluGlyLe
QQ	21	
Οy	301 1	TyrGlnGlyvalProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 319
qq	1181	ACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATG
Qy	319	319
QQ	1241 4	CAGCCAGCAGAGGCTG
οy	319 -	319
qq	1301	GCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGG 1360
ΟŸ	319 -	319
QΩ	1361 #	ATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCTTGCGGTTTC 1420
Qy	319 -	319
qq	1421 4	AGGAAGGCCTCTGGCTGCTCTAGGAGTCTGAFCAGAGTCGTTGCCCCAGTTTGACAGAAG 1480
ΟŸ	319 -	319
qq	1481	SAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGGATTTCAGAT 1540
: 0y	319 -	319
QQ	1541	CTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCAACGACTTTCCAAATAATCTCA 1600
Οy	319 -	319
ΩD	1601	CCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTT 1660
δλ	319 -	319
QQ	1661	GTGTTCCCTCTCACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACC 1720
δy	319 -	319
QQ	1721 T	TTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTA 1780
δy	319 -	319
QQ	1781	GACTCCCATTGCTAGAGGTAGAAAGGGGAAGGGTGCTGGGGAGCAGGGCTGGTCCACAGC 1840
Οy	319 -	319
qq	1841 2	AGGICTCGTGCAGGTACCTGTGGTTCCGCTTCTCATCTCCCTGAGACTGCTCCGAC 1900
Qy	320 -	325 325 325 325 325 325 325 325 325 325
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Qy	325 I	rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 345
qq	1961	CTCCCTGGTCTTCTCTGGTCATGGACCG
Qy	345 u	uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAl 365
QQ	2021	ATTTGGCCAGTGTGGCAGCTTTCCCTGTGG
οy	65	AlaGlyAlaThrCysLeuSerHisSerValÄlaValValThrAlaSerAlaAlaLeuTh 38
QQ	2081 T	AC 21
Qy	82	r 40
qq	2141	GGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTC

Alignment Scores

580 140 700 820 520 ArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120 ThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnAla 160 760 180 200 880 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys 280 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220 40 9 80 281 ATGGTCCAGAGGCTGTGGGTGAGCCGCCTGCTGCGGCACCGGAAAGCCCCAGCTCTTGCTG ACTCCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 1leAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu---ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 4034 553 0 0 236 1 US-09-593-793A-113 (1-553) x US-09-895-793-704 (1-4034) Conservative: Mismatches: Matches: Indels: Length: Gaps: 7.21e-246 2716.50 70.09% 70.09% 94.95% Percent Similarity: Best Local Similarity: Query Match: 341 101 641 821 881 1001 1061 41 401 61 461 81 581 121 141 701 761 181 201 221 941 241 261 281 1121 1181 161 301 Q

319 310 310	SASPVa SASPVa SASPVa TGATGI TGATGI 111111 11111111111111111111111111111
TGCTCCGAC BMCEG1ySe	APPLICANT: Li, Samuel X. APPLICANT: Wang, Aijun A. APPLICANT: Wang, Aijun T. APPLICANT: Hepher, William T. APPLICANT: Hepher, William T. APPLICANT: Henderson, Robert A. APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Founds de Bassols, Carlota APPLICANT: Fonger, Gary R. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: CHOROSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: CHOROSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: CHOROSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: OFFICE STATES OF WINGER: US/09/895,814 CURRENT FILING DATE: 2001-06-29 NUMBER OF SEQ ID NOS: 990 SEQ ID NO 704 TYPE: DAA TYPE: DAA TYPE: DAA Alignment Scores: CSCORES: 7.21e-246 Alignment Scores: 7.21e-246 Alignment Scores: 7.21e-246 Alignment Scores: 7.0.094 Mismiatches: 236 Query Match: 94.954 Indels: 1 US-09-593-793A-113 (1-553) x US-09-895-814-704 (1-4034)

505	ArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl	485 yA:	ΟŊ
2440	GTGATGTCTCCGTACGTGTGGTGGTGAGCCCACCGAGGCCAGGGTG	381 C	Dp 3
485	CysAspValSerValArgValValValOlyGluProThrGluAlaArgValValProGl	465 a	Οy
2380		321 C	Dp 3
465	31ySerGlyLeuLeuProProProP	445 s	δŷ
23		26	27 Dp 3
445	AGGIGITCCTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGT GCThrSerPheLeuProGlyProLysProGlyAlaProPheProAsn	425	90 Å
7	gGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs	405	
2200	GGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACAGACTGGCCTCCCTC	2141 C	Dp 2
405	GlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr	385 r	δλ
		081 1	Db 2
385	ThrCysLeuSerHisSerValAlaValValThrAlaSerAla	365 a	δλ
208(uvallinii	021	DP 2
0	3GGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGC	61	Db 1
345	rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe	325 r	Qy
1960	CCTTCCCTCCCAGGCTCTGTCTGATGGCCCCTCTCCCTCTGCAGGCGTTCGGATGGGCAG	901 C	Db 1
325	GlyvalArgMetGlyS	320 -	QY
1900	rggitccgcctici	841 A	Db 1
319		319 -	QY
1840	GACTCCCATTGCTAGAGGGTAGAAGGGGAAGGGTGCTGGGGAGCAGGGCTGGTCCACAGC	781 G	Db 1
319		319 -	δy
1780	TTCCTCTGCCTTCAGCAAGGGGGGGTTGCCCACATTCTCTGTGAGGGTCAGTGGAAGAACCTA	721 T	Db 1
319		319 -	δλ
172(CCTCTCACCCGCCTGTCCTCACAGCTGAGACTC	661 G	Db 1
319		319 -	Qy
1660	SCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAA	601 C	Db 1
319		319 -	οy
1600	GGTTCCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCC	541 C	Db 1
319		319 -	Qy
154(TTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGC	481 G	Db 1
319		319 -	Qy
148(GTCGT	421	Db 1
319		319 -	Οy
1420	TGGACCCCATCTGCATACACGCCTTCTCATGGGTGTGGAACATCTCTGCTTGCGGTTTC	361 A	Dp 1

Ş	DD 461 CCAGTGCTGGGCCTGG	Qy 81 ArgTyrGlyArgArgAr 	Qy 101 PheLeulleproArgAl 	Oy 121 GluLeuAlaLeuLeuI.	Qy 141 ThrProLeuGlualaLe 	Qy 161 TyrServalTyrAlaPl 	Qy 181 IleAspTrpAspThrs(Qy 201 GlyLeuLeuThrLeuI)	Qy 221 AlaAlaLeuGlyProTl 	Qy 241 CysCysProCysArgAl 	Qy 261 HisGlnLeuCysCysAv 	Qy 281 SerTrpMetalaLeuMetalaLeumetalaLe	Qy 301 TyrGlnGlyValProAl	319	Db 1241 AAGGCCTTGGCAGCCAG	319	Db 1301 GCTGTGTCTGGGCTGG	7	319	DD 1421 AGGAAGGCCTCTGGCTC	H	Qy 319	Db 1541 CTGCCTGGTTCCAGCCC
COCHID COCHIDANO CHICAMINA CHICAMINA CHICAMINA COCHIDA		<pre>Qy 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa 525 LITHITHITHITHITHITHITHITHITHITHITHITHITHI</pre>	Oy 525 ISeralaalaGlyLeuGlyLeuValalaIleTyrPhealaThrGlnValValPheaspLy 545 	Qy 545 sSerAspLeuAlaLysTyrSerAla 553 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	RESULT 15 US-09-759-143-704 ; Sequence 704, Application US/09759143	; FATENE NO. USZUOZUOZZZ4BAI ; GENERAL INFORMATION; APPLICANT: Xu, Jiangchun ; APPLICANT: Dillon, Davin C.	APPLICANT: MICCORN, Jennier L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqui APPLICANT: Henderson, Robert A.	APPLICANT: Fanger, Gary APPLICANT: Retter, Marc W. APPLICANT: Stolk, John A.	APPLICANT: Day, Craig H. APPLICANT: Vedvick, Thomas S. APPLICANT: Carter, Darrick APPLICANT: Li, Samuel	APPLICANT: Wang, Aljun APPLICANT: ASPLICANT: ASPLICANT: APPLICANT: Hepler, William TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	FILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REPRENCE: 210121.42723 ; CURRENT APPLICATION NUMBER: 05/09/759,143 ; CURRENT FILING DATE: 2001-01-12	NUMBER OF SEQ ID NOS: 934 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 704 LENGTH: 4034	; TYPE: DNA ; ORGANISM: Homo sapiens US-09-759-143-704	Length:	Score: 2140.50 Marches: 553 Percent Similarity: 70.09% Conservative: 0 Best Local Similarity: 70.09% Mismatches: 0	94.95% Indels: 10 Gaps:	US-09-593-793A-113 (1-553) x US-09-759-143-704 (1-4034)	Qy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeu 20 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII		Db 341 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCGAGGCATCACCTATGTGCCG 400	Oy 41 ProLeuLeuGluValGlyValGluGluLysPhemetThrMetValLeuGly1leGly 60	401 CCICIGCTGCTGCTGGGGGTAGAGGAGAAGTTCATGACCATGGTGCTGGTGGTGGTGGTGGT	<pre>QY</pre>

qq	461	CCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTAGGCTCAGCCCAGTGACCACTGGCGTGGA 520
ò		
5 A	521	CGCTATGGCCGCCGCCGCCCTTCATCGGCCATCCTTGGGCATCCTGGAGCCTC 580
Qy	101	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu 120
qа	581	rcccageceere
Qy	7	yGlnValCysPhe 1
qq	641	CCAGGTGTGCTTC 7
Οy		ThrProLeuGlualaLeuLeuSerAspLeuPhaArgAspProAspHisCysArgGlnAla 160
qq	701	CCACTGGAGGCCCTGCTCTCTGACCTCTTCCGGGACCCGGACCACTGTCGCCAGGCC 7
Qy	161	VGlyCysLeuGlyTyrLeuLeuProAla 1
qq	761	TGTCTATGCCTTCATGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTG
Qγ	181	IleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluGluCysLeuPhe 200
QQ	821	SACTGGGACACCAGTGCCCTGGCCCCTACCTGGGCACCCAGGAGGAGTGCCTTTT B
Οy	201	GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGlu 220
qq	881	GCCTGCTCACCTCATCTTCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAG 940
οy	221	AlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHis 240
qq	941	GCAGCGCTGGGCCCCACCGAGCCAGCAGAGGGCTGTCGGCCCCCTCCTTGTCGCCCCAC 1000
Qy	241	CysCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 260
q	1001	TGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCCTGCTTCCCCGGCTG 1060
δλ	261	HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPhevAlAlaGluLeuCys 280
q	1061	CACCAGCTGTGCTGCCGCATGCCCCGCACCTGCGCCGCTTTCGTGGCTGAGCTGTGC 1120
Οÿ	281	SerTrpWetAlaLeuMetThrPheThrLeuPheTyrThraspPheValGlyGlyLeu 300
QQ	1121	AGCTGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTCGTGGGCCGAGGGCCTG 1180
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 319
qa	1181	TACCAGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGT 1240
Qy	319	319
qq	1241	AAGGCCTTGGCAGCCAGCAGGCTGGTGTGGGAGCCGCCCACCAGAGACGACACTCGGG 1300
Qy	319	319
qΩ	1301	GCTGTGTCTGGGCTGGTGCTCTCTCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGG 1360
Qγ	319	319
qa	1361	ATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCTTGCGGTTTC 1420
Qy	319	319
qq	1421	AGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAG 1480
QY	319	319
qq	1481	GAAAGGCGGAGCTTATTCAAAGTCTAGAGGAGTGGAGGAGTTAAGGCTGGATTTCAGAT 1540
Οy	319	319
qq	1541	CTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGGTCCCCCAACGACTTTCCAAATAATCTCA 1600

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Db 1601 CCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTT	CGICITGAAGCCIAIGGCCAGCIGICITI 1660	; Patent No. US200
Ογ 319	319	; GENERAL INFORMAT; APPLICANT: Xu,
Db 1661 GTGTTCCCTCTCACCGGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACC	TGAGACTCCCAGGAAACCTTCAGACTACC 1720	APPLICANT: APPLICANT:
ογ 319	319	
Db 1721 TTCCTCTGCCTTCAGCAAGGGGGGGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTA	CATTCTCTGAGGGTCAGTGGAAGAACCTA 1780	APPLICANT: APPLICANT:
ογ 319	319	APPLICANT:
Db 1781 GACTCCCATTGCTAGAGGTAGAAAGGGGAAGGGTGCTGGGGGAGCAGGCTGGTCCACAGC	GGTGCTGGGGAGGCTGGTCCACAGC 1840	
Фу 319	319	APPLICANT: APPLICANT:
Db 1841 AGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGACTGCTCCGAC	CCTTCTCATCTCCCTGAGACTGCTCCGAC 1900	
Qy 320		APPLICANT: SKE ; APPLICANT: Hep ; APPLICANT: Hep
	TCICCCICIECAGGCGITCGGGTGGGCAG 1900 LeuvalpheserLeuvalMetAspArdLe 345	APPLICANT: R APPLICANT: R TITLE OF INVE
1961		; TITLE OF INVEN; FILE REFERENCE
Oy 345 uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAl 	LeualaSerValalaalaPheProValal 365	CURRENT APPLICA CURRENT FILING NUMBER OF SEQ I SOFTWARE Fast
365		∠ 4 4:
2081		; ORGANISM: HOMO US-09-780-669-704
OY 385 FG19PEThEPRESETALELEGGILLEGEPFOTYTHILEGHULASETLEGHT9H18AT DD 2141 GGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACCTGCCCTCTCTACCACG	ProTyrThrLeuAlaSerLeuTyrHisAr 405 	Alignment Scores Pred. No.:
Qy 405 gGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs	GlyaspThrGlyGlyalaSerSerGluas 425 	Score: Percent Similarity Best Local Similar Query Match:
Oy 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi	LysProGlyAlaProPheProAsnGlyHi 445	DB: IIS-09-593-793A-11
Db 2261 CAGCCTGATGACCAGCTTCCTGCCAGGCCCT	AAGCCTGGAGCTCCCTTAATGGACA 2320	
Qy 445 sValGlyAlaGlyGlySerGlyLeuLeuProProProProProPalaLeuCysGlyAlaSerAl IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ProProProAlaLeuCysGlyAlaSerAl 465 	OY I MEVAIGI Db 281 ATGTCCA
		Oy 21 ValAsnLe
485		2y 41 ProLeuLe
Db 2441 CCGGGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCOV No. 505 aProSerLeuphaMatGlySerTleUalGlnIanscarGlySerValmhralamyrMatVa	GATAGTGCCTTCCTGCTGCTCCCAGGTGGC 2500	61
2501		461
		Qy 81 ArgTyrGl Db 521.CGCTATGG
Oy 545 SSETASPLEUALALYSTYTSETALA 553	TACITIGCIACACAGGIAGIAITIGACAA 2020	Qy 101 PheLeuII
Db 2621 GAGCGACTIGGCCAATACTCAGCG 2645		101

460 lyArgArgArgProPhelleTrpAlaLeuSerLeuGlyIleLeuLeuSerLeu 100 121 GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPhe 140 09 Skeiky, Yasir A.W.
Skeiky, Yasir A.W.
Hural, Yasir A.W.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
VENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND VENTION: DIAGNOSIS OF PROSTATE CANCER
NCE: 210121.427C24
LICATION NUMBER: US/09/780.669
LIGATION NUMBER: US/09/780.669
LING DATE: 2001.02-09 4034 553 0 0 236 1 3 (1-553) x US-09-780-669-704 (1-4034) Matches: Conservative: Mismatches: Indels: Length: LSEQ for Windows Version 3.0 Gaps: pplication US/09780669 020051977A1 lang, Yuqui lenderson, Robert A. Galos, Michael D. Garger, Gary R. Getter, Marc W. Stolk, John A. Bay, Craig H. Gedvick, Thomas S. Garter, Darrick , Jiangchun 11on, Davin C. tcham, Jennifer L. rlocker, Susan L. 7.21e-246 2716.50 70.09% 70.09% 94.95% o sapiens y: rity: TION:

Db 1721 TTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGTCAGTGGAAGAACCTA 1780 Qy 319	319 31 1841 AGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCCTTCTCATCTCCCTGAGACTGCTCCGAC 19	0	5 rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLe 34: 		Oy 365 aAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuTh 385	rGlyPheThrPheSeralaLeuGlnIleLeubroTyrThrLeualaSerLeuTyrHisAr 	5 gGluLysGlnValPheLeuProLysTyrArgĠlyAspThrGlyGlyAlaSerSerGluAs 42 	Qy 425 pSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHi 445	Qy 445 sValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCysGlyAlaSerAl 465	Qy 465 aCysAspValSerValArgValValQlyĠluProThrGluAlaArgValValProGl 485	485 yArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl 5	Db 2441 CCGGGGCATCTGCCTGGACCTCGCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGC 2500 Qy 505 aProSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThralaTyrMetVa 525		Qy 525 ISerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLy 545	Qy 545 sSerAspLeuAlaLysTyrSerAla 553	ZOZI GAGUGAUTIGGUCAAATAUTCAGUG ZO4	KESUL: 105-09-827-704 ; Sequence 704, Application US/09822827 ; Patent No. US20020081680A1 ; Patent No. US20020081680A1	; APPLICANT: Xu, Jiangchun ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER ; FILE REFERENCE: 210121.534C1 ; CURRENT APPLICATION NUMBER: US/09/822,827 ; CIRDEDENT FITING DAMP:	CURRENT FILING DATE: ZUUT-U3-ZB
	oAla 1 TGCC 8	Qy 181 IleaspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPhe 200 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 201 GlyLeuLeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlacluGlu 220	roHis 24	241 CyscysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeu 111111111111111111111111111111111111	261 HisGlnLeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCys	lyLeu 30 SGCTG 11	1u	319 3319 3319	Db 1241 AAGGCCTTGGCAGCAGCAGCTGGTGTGGGAGCCGCCCACAGAGACGACACCTCGGG 1300 Qy 319 319	Db 1301 GCTGTGTGTGTGGTGCCTCTCCATCCTGGCCCCGACTTCTCTGTCAGGAAAGTGGGG 1360 Qy 319 319	1361 ATGGACCCCATCTGCATACACGGCTTCTCATGGGTGTGGAACATCTCTGCTTGCGGTTTC 14	Oy 319 319 Db 1421 AGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAG 1480	319		Db 1541 CTGCCTGGTTCCAGCCGCAGTGTGCCCTCTCCCCCAACGACTTTCCAAATAATCTCA 1600	Qy 319 319 Db 1601 CCAGCGCCTTCCAGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTT 1660	319	OY 319 ***********************************	

	3.4 4.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9.0 9		aGlnLeuLeuLeu 20 	LeThrTyrValPro 40 	LeuGlyIleGly 60 	HistrpArgGly 80 	/lleLeuLeuSerLeu 100 	pProArgProLeu 120 rcccAGGCCCTG 640	yGlnValCysPhe 140 	scysArgGlnAla 160 	yrLeuLeuProAla 180 	uGluCysLeuPhe 200 	uValalaGluGlu 220 	erLeuSerProHis 240 	laLeuLeuProArgLeu 260 	AlAlaGluLeuCys 280
sion 3.0	Length: 403 Matches: 555 Conservative: 0 Mismatches: 0 Indels: 236	22-827-704 (1-4034)	gLeuLeuargHisargLysalaG 	uValCysLeuAlaAlaGlyIl 	luGluLysPheMetThrMetVal 	LeuLeuGlySerAlaSer 	eTrpAlaLeuSerLeuGly 	rpLeuAlaGlyLeuLeuCysProAsp 	1G1yLeuLeuAspPheCysG1, 	ppLeuPheArgAspProAspHisCysArgGln 	sSerLeuGlyGlyCysLeuGlyTy 	aProTyrLeuGlyThrGlnGluGlu 	uThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuV. 	aGluGlyLeuSerAlaProS 	rgLeuAlaPheArgAsnLeuGlyAlaLe 	JThrLeuArgArgLeuPheV
SEQ ID NOS: 982 FastSEQ for Windows Ver 704 4034 41: Homo sapiens 77-704	cores: 7.21e-246 2716.50 ilarity: 70.098 Similarity: 70.098 i 10	93A-113 (1-553) x US-09-8	MetValGlnArgLeuTrpValSerArg 	ValAsnLeuLeuThrPheGlyLeuGluValCy 	obeuLeuLeuGluValGlyValG 	oValLeuGlyLeuValCysValP 	rgTyrGlyArgArgArgProPhell(PheLeulleProArgAlaGlyTrpLe 	luLeuAlaLeuLeuIleLeuGlyVa` 	ThrProLeuGluAlaLeuLeuSerAs 	yrSerValTyrAlaPheMetileSe 	leAspTrpAspThrSerAlaLeuAla 	lyLeuLeuThrLeuIlePheLeuTh 	laalaLeuGlyProThrGluProAla 	ysCysProCysArgAlaArgLeuAl 	HisGlnLeuCysCysArgMetProArg
NUMBER OF SOFTWARE: ESO ID NO 7(EDIGH: 40 TYPE: DNA ORGANISM: 09-822-827	nment S NO.: e: ent Sim Local	9-593-7	1 M 281 A	21 V. 1 341 G	41 Pro	- H	81 AU 	101 P) 581 T	121 G 641 G	141 TJ 1 701 A	161 T	181 I 1 821 A	201 G	221 A 941 G	241 C	261 H
; SE; SE	Align Pred Score Perce Best Query DB:	us-0	Oy Dp	Qy Db	Oy Dp	Oy Db	Oy Dp	Qy	Oy Db	Oy Db	Qy Db	Qy Db	Qy Dp	Oy Dp	Qy Db	Oy Dp

Οy	281	SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu 300
qa	1121	ICGATGGCACTCATGACCTTCACGCTTTTTACACGGATTTCGTGGGCGAGGGCT
Qy	301	TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGlu 319
qa	1181	ACCAGGGCGTGCCCAGAGCTGAGCCGGGCACCGAGGCCCGGAGACATGATGATGATGATGATGATGATGATGATGATGATGATGA
Qy	319	319
Db	1241	
Qy	319	319
qa	1301	GCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGCCCCGACTTCTCTCTGTCAGAAAGTGGGG 1360
Qy	319	319
qq	1361	AFGGACCCCCATCTGCATACACGCCTTCTCATGGGTGTGGAACATCTCTGCTTGCGGTTTC 1420
Qy	319	319
qa	1421	AGGAAGGCCTCTGGCTGTTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAG 1480
Qy	319	319
qa	1481	GAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGGCTGGATTTCAGAT 1540
QY	319	319
qq	1541	CIGCCIGGTICCAGCCGCAGIGIGCCCCTCTGCTCCCCCAAACGACTTTCCAAATAATCTCA 1600
Qy	319	319
qa	1601	CCAGCCCCTTCCAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCCAGCTGTCTTT 1660
QY	319	319
qq	1661	GTGTTCCCTCTCACCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACC 1720
Qy	319	319
qq	1721	CCTCTGCCTTCAGCAAGGGCGTTGCCCACATTCTCTGAGGGTCAGT
Qy	319	319
qa	1781	TGCTGG
Qy	319	319
qa	1841	
Qy	320	GlyvalArgMetGlySe 325
qq	1901	GCAGGCGTTCGGATGGGCA
Qy	325	rLeuGlyLeuPheLeuGlnCysAlaIleSerLeuValpheSerLeuValMetAspArgLe 345
qa	1961	SGGCTGTTCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGG
δy	345	uValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAl 365
qa	2021	SCAGCGATTCGGCACTCGAGTCTATTTGGCCAGTGTGGCCAGCTTTCCCTGT
QY	365	aalaGlyalaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuTh 385
qq	2081	cerreceacarecrereceacagrerecerrefracacrireaece
Qy	385	rGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisAr 405
Op	2141	STTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTC

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993 CCCAGGAAGAGGGGCCCCTGTGAGGATTGCAĠGCTCTGGAGTCACACTGCTTGTTGAAAC 1052
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                                                                                                                                                  453 ACTACATCCTCCTTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 512
                                                                                                                                                                                                                                                                                                    CCTCTGCCCTGGGAGCTGCTTGGAGGGAGGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 572
                                                                                                                                                                                                                                                                                                                                               692
                                                                                                                                                                                                                                                                                                                                                                                                                                  693 AAAIGCICCIAACCITIGGCIAGCCCITITATAATIIAIAGCGAITATCICATITAAIGC 752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu------
          4894
551
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                                                                                   US-09-593-793A-113 (1-553) x US-10-012-896-702 (1-4894)
                              Conservative:
Mismatches:
Indels:
          Length:
Matches:
          5.33e-229
2538.50
51.11%
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                               Percent Similarity:
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Alignment Scores:
Pred. No.:
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           No.:
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q	1173 AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC 1232
Οy	75
ф	1233 TICTCACGGAGCTIGGITCCCCTICCCCTTGCCCTTTACTIGTCCCAGCCATTGACTCAT 1292
οy	ProLeuLe
qq	CATTGGT
Oy Dp	72 GIySeralaSerAspHisTrpargGlyArgTyrGlyArgArgArgProPheileTrpAla 91
Qy Dp	92 LeuserLeuglyIleLeuLeuserLeuPheLeuIleProArgAlaglyTrpLeuAlagly 111
Oy Dp	112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeulleLeuGlyvalGlyLeu 131
Oy Dp	LeuaspPheCysGlyGlnValCysPheThrProLeuGlualaLeuLeuSerAspLeuPhe 151
Qy Db	152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Qy Db	172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
Oy Dp	192 LeuglyThrGlnGluGluCysLeuPheGlyLeuLhrLeuIlePheLeuThrCysVal 211
Qy	212 AlaalaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly 231
Oy Db	232 LeuseralaProserLeuserProHiscysCysProCysArgalaargLeualaPhearg 251
Qy	252 AsnLeuglyalaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Qy Dp	272 ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291
Oy Dp	292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311
y dy	319
ò	9
QQ	3 AGCCGCCCACCACAGACACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGC 21
οy	. 319
QQ	
δ	319
g	2253 GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC 2312

Oy	y 319	319
QQ	2313 AGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAG	2372
Qy	319	319
qq	o 2373 TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCT	2432
Qy	319	319
QQ	2433 CCCCCAACGACTTTCCAAATCTCACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCG	2492
δy	319	319
qq	2493 TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGCCTGTCCTCACAGCTG	2552
ΟŸ	319	319
QQ	2553 AGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGGGGGGGTTGCCCACA	2612
δλ	319	319
qq	2613 TTCTCTGAGGGTCAGTGGAAGGAACCTAGACTCCCATTGCTAGAGGGTAGAAAGGGGAAGGG	2672
Οy	319	319
QΩ	2673 TGCTGGGGAGCAGGGCTGGTCCACAGAGGTCTCGTGGAGCAGGTACCTGTGGTTCCGCC	2732
Qy	319	319
QQ	2733 TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCAGGCTCTGTCTG	2792
Qy	320GlyvalArgMetGlySerLeuGlyLeuPheLeuGlnCysAlalleSer	336
qq	2793 TCCCTCTGCAGGGGTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCCATCTC	2852
٥y	336 uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe	356
QQ	2853 GETCTTCTCTCTGGTCATGGACCGGCTGGTGCGAGCGATTCGGCACTCGAGCAGTCTATT	2912
Qy	/ 356 ualaSerValAlaAlaPheProValAlaAlaGlyAla†hrCysLeuSerHisSerValAl	376
QO	2913 GCCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGG	2972
Qy	/ 376 aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr	396
qq	2973 CGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGAI	3032
QY	/ 396 oTyrThrLeuAlaSerLeuTyrHiSArgGluLysGlnValPheLeuProLysTyrArgGl	416
QQ	3033 CTACACACACGGCCTCCCTCTACCACCGGGGGAGCAGGTGTTCCTGCCCCAAATACCGA	3092
δλ	416 yAspThrGlyGlyAlaSerGluAspSerLeuMetThrSerPheLeuProGlyProLy	436
q _Q	3093 GGACACTGGGGGGTGCTAGCAGTGAGGAGCCTGATGACCAGCTTCCTGCCAGGCCCT	3152
Qy	436 sProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr	456
qq	3153 GCCTGGAGCTCCCTTCCCTAATGGACACGTGGGTGTTGGAGGCAGTGGCCTGCTCCCACC	3212
δy	456 oProProAlaLeuCysGlyAlaSerAlaCysAspvalSerValArgValValValGlyGl	476
QQ	3213 TCCACCGGGTCTGGGGGGCCTCTGCTGTTTTTTTTTTTT	3272
Qy	476 uProThrGluAlaArgValValProGlyArgGly1leCysLeuAspLeuAla1leLeuAs	496
qq	3273 GCCACCGAGGCCAGGGTGGTTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGA	3332
Οy	496 pSerAlaPheLeuLeuSerGlnValAlaProSerLeupheMetGlySerIleValGlnLe	16
qq	3333 TAGIGCCITCCIGCIGICCCAGGIGGCCCCATCCCIGITIAIGGGCICCAIIGICCAGCI	3392

516 uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy	6y	57
UD 3555 CAUCLAGICIGICACIONITATIGETOTCIGCCACAGOCCIGGETCIGGICACATITA 3452 OV 536 FDAGADAMHTCHVAIVAIVAIDHGAGATTGGAARATGAANISTAGTAAGAANIS 553	qa	513 CC1
34.53	Qy	57
411.7 19	qa	573 GG
89 en	QY	57
; Publication No. US20020192763A1 ; GENERAL INFORMATION:	qq	633 CCC
: APPLICANT: Xu, Jiangchun	QY	57
Mitcham, Jenni Harlocker Sus	qa —	693 AA
: Jiang, Yuqiu : Kalos Michael D	ογ	57
Retter,	qa	753 TT
	QY	57
Carter, Darrick	q a	813 TT
	٥٧	57
; APPLICANT: Applicant Ann. Applicant Handeren Robert A	qa —	873 GG1
Hural, John	Qy	57
; APPLICANT: Houghton, Raymond L. : APPLICANT: Houghton, Raymond L. : APPLICANT: Vinale de Bassols Carlota	qa	933 GAT
	Oy	22
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	qa))))
	QY	57
29	qa	1053 GCI
SOFTWARE: FastSED for Windows Version 3.0	Qy	57
LENGTH: 4894	q _Q	1113 ATG
; ORCANISM: Homo sapiens US-09-895-703-702	Qy	57
Alianment Scores:	q _Q	1173 AAT
	Qy	22
t Similarity: 51.11% Conservative: Ocal Similarity: 51.11% Mismatches:	qa	1233 TTC
88.73% Indels: 9 Gaps:	49	58
US-09-593-793A-113 (1-553) x US-09-895-793-702 (1-4894)	옵 	
Oy 1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20	δ .	72
Db 274 ATGGTCCAGAGGCTGTGGGTGAGCCCTGCTGCGGCACCGGAAAGCCCAGCTCTTGCTG 333	on 6	
Oy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTy†ValPro 40	<u>д</u>	32 Leu 1413 CTG
334 GTCAACCTGCTAACCTTTGGCCTGGAGGTGTTTTGGCCGCAGGCATCACCTATGTGCCG	ζO	112 Lev
Oy 41 ProLeuLeuCluValGlyValGluGluLysPheMetThrMetValLeu 57 57	qq	1473 CTG
57	Qy	132 Lev
453 ACTACATCCTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA	qa 	1533 CTC

ΟŊ	57	25 57
QQ :	513 (CCTCTGCCCTGGGAGCTGCTTGGAGGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 572
Qy	57	57
qq	573 (GGAGGGTGACCCTGGGCTGAGGGGGCCACACCCAAGAGAAAGAA
QY	57	25
Dp	633 (CCCCAGTCACCTCTGGATCCCTGGTCCTGCACAGAGCCTGGTCATAGGAGACACTGGAG 692
δλ	57	
qq	693 1	AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC 752
ΟY	57	25
Dp	753 1	TTACAACCACCATTTGAGGTGATCCATTTTACAGAGAAGGAAG
Qy	57	57
pp	813 7	TTAGGTAAGTCTTAGCCAAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 872
Qy	57	57
Dp	873 (GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 932
Qy	57	57
Op	933 (SATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCCTCACC 992
Qy	57	57
qq	993 (CCCAGGAAGAGGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 1052
Qy	57	25
Dp	1053 (GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTCTTAGTTGCTCC 1112
Qy	57	57
QQ	1113	ATGCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1172
Qy	. 22	25
QΩ	1173 /	AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC 1232
Qy	. 73	25
QQ	1233 7	ITCTCACGGAGCTIGGTTCCCCTTCCCCTTGCCCTTTACTTGTCCCAGCCATTGACTCAT 1292
Qy	. 85	
qq	1293 #	STCCCGCTCCT
δλ	72 (GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91
qq	1353 (CTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGC
οy	92 1	LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
qq	1413 (STCCTTGGGCATCCTGCTGGTCTTTCTCATCCCAAGGGCCGGCTGGCT
δ	112	31
ΩQ	1473 (-1
οy	132	heThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
D D	1533 (TGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGTGAC

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172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191 	Qy 3.
2 LeuGlyThrGlnGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211 [Qy 3
AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly 231	Oy 3
1//3 GCAGCCACACTGCTGGTGGCTGAGGAGGCAGGGCTGGGCCCCCACCGAGCCAGCAGAGGG 1832 232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251	
	DD 291
252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271 	02 OD 2
ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291	Qy 30
.953 CGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTT 2012	Qy
TACACGGATTTCGTGGGCGAGGGCTGTACCAGGGCGTGCCCAGAGCTGAGGCCCGGGCACC	30c qa
312 GlualaArgArgHisTyrAspGlu	Oy 4 Db 31
	oy
AGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCCTCCTCCATCCTGGC	Db 321
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2193 CCCGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCCATCTGCATACACGGCTTCTCATGG 2252	00 OV
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2253 GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC 2312	
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2373 TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGT 2432	Db 34
319	RESULT US-09-8
2433 CCCCCAACGACTTTCCAAATAATCTCACCAGCGCTTCCAGCTCCAGGCGTCCTAGAAGCG 2492	
319 319	; GENERA; APPLI
493 TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTTCCCTCTCACCCGCCTGTCCTCACAGCTG 2552	APPLI APPLI
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553 AGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACA 2612	APPLI
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2613 TICTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGG 2672	

7	319	2792	336	356 2912	376	396 3032	416 3092	436	456 3212	476 3272	496 3332	516 3392	536 3452		
TGCTGGGGAGCAGGCTGGTCCACAGCAGGTCTCGTGCAGGTACCTGTGGTTCCGCC	6	3 TTCTCATCTCCCTGAGACTGCTCCGACCTTCCCTCCCAGGCTCTGTCTG	0GlyvalArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe	WetaspargLeuValGlnargPheGlyThrargalaValTyrLe 	ervalAl 	euGlnIleLeuPr TGCAGATCCTGCC	6 oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGl 	6 yASPThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy	6 sProGlyAlaProPheProAsnGlyHisValGlyAlad lyGlySerGlyLeuLeuProPr	6 oProProAlaLeuCysGlyAlaSerAlaCysAspVal\$erValArgValValValGlyGl	6 uProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAs	b pSerAlaPheLeuLeuSerGlnValAlaProSerLeupheMetGlySerIleValGlnLe	6 uSerGInSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy	6 rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553 	ESULT 20 S-09-895-814-702 S-09-895-814-702 Sequence 702, Application US/09895814 Publication No. US20020193296A1 GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Mitchan, Davin C. APPLICANT: Mitchan, Dannifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Jiang, Yuqiu APPLICANT: Kalos, Michael D. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Stolk, John A. APPLICANT: Carter, Davrick APPLICANT: Carter, Davrick APPLICANT: Li, Samuel X.
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qq	873	36
Qy	57	57
qq	933	AAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGT
Οy	57	57
qq	993	AGAGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCA
Qy	57	25
qq	1053	CTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTCT
Qy	57	25
QQ	1113	GCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTT
Qy	57	25
qq	1173	AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC 1232
Qy	57	25
qq	1233	TTCTCACGGAGCTTGGTTCCCCTTCCCCTTTACTTGTCCCAGCCATTGACTCAT 1292
Qy	58	GlyIleGlyDroValLeuGlyLeuvalCysValProLeuLeu 71
qq	1293	TTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTA 1
Qγ	72	/SerAlaSerASpHisTrpArgGlyArgTyrGlyArgArgArgProPhelleTrpAl
qq	1353	GCTATGCCGCCGCCGCCCTTCATCTG
Qy	92	JeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
qq	1413	STCCTTGGGCATCCTGCTGAGCCTCTTCTCATCCCAAGGGCCGGCTGGCT
Oγ	112	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuLeuGlyValGlyVeu 131
qq	1473	screreccesarcccadeccccreaacrecaccrearccreaecereaecr
Qy	132	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
qq	1533	SGACTICTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTCAGCTCTTC 1
Qγ	152	ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
qq	1593	SGACCCGGACCACTGTCGCCAGGCCTACTCTGTTGTTCATGATCAGTCTTGGG 16
QY	172	GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
qa	1653	TGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCTAC 1
Qy	192	LeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
QQ	1713	SCACCCAGGAGGAGGCCTCTTTTGGCCTGCTCTCTCTTTTTTTT
Qγ	212	AlaThrLeuLeuValAlaGluGluAlaAjaLeuGlyProThrGluProAlaGluGl
qq	1773	HELLINITIE HELLINITIE
Qy	232	LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251
qq	1833	STCGGCCCCCTCTTGTCGCCCCCACTGTCTTCCGGGCCCGCCTTGGCTTTCCG
Οy	252	AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu 271
Dp	1893	CTGGGCGCCCTGCTTCCCCGGCTGCTGCTGCTGCCGCATGCCCGCACCTG 1
Qy	272	ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 291

<u>,</u>	1	MetvalGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20	0
9	4/7	AIGGICCAGAGGIGIGAGCCGCCIGCIGCGGCACCGGAAAGCCCAGCICTIGCIG	3.3
<u>></u> 4	334	ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGly1leThrTytValPro 4	0
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<u>></u> -	57	25	7
q	453	ACTACATCCTCCTTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 51	12
λ·	57	55	7
ą	513	CCTCTGCCCTGGGAGGTGCTTGGAGGGAGAGGTGGTCTGCTGGGAAGGCATTGGTGGGCA 57	72
Δī	57	57	7
ą	573	GGAGGGTGACCCTGGGCTGAGGGGGCACACCAAGAGAAGAAGAAGAATACCAAGGACATA 63:	32
<u> </u>	57		7
ڡۣ	633	CCCCAGTCACCTCTGGATCCCTGGTCCTGCAGAGCCTGGCTCATAGGAGACACTGGAG 69.	92
<u>~</u>	57	57	7
۵	693	AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC 75	52
٧.	57	25	7
۾	753	TTACAACCACATTTGAGGTGATCCATTTTACAGAAGGAAG	12
¥	57	57	7
٥	813	TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAG	72
<u>≻</u> ,	57		7
ą	873	GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 9	32
<u>⊁</u>	57	57	7
ā	933	GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCCTCACC 95	92
λ	57	25	7
ā	993	CCCAGGAAGAGGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 10	052
<u>≻</u>	57	25	7
Q	1053	GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTCTTAGTTGCTCC 11	112
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۾	1113	ATGCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 11	172
^	57	25	7
۵	1173	AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC 12	232
<u>~</u>	57	25	7
۾	1233	TTCTCACGGAGCTTGGTTCCCCTTCCCCTTGCCCTTTACTTGTCCCAGCCATTGACTCAT 12	292
≯ 1	28	GlylleGlyProValLeuGlyLeuValCysValProLeu 71	1
Q	1293	ACTACTTCCCTTCTTGCAGGGATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTA 1	352

qq	1353 GGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGCCCTTCATCTGGGCA 1412
Qy	2 LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 111
qq	TGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCT
Qγ	12 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeulleLeuGlyValGlyLeu 131
QQ	3 CTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCTG 15
Qy	32 LeuAspPheCysGlyGlaValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
QQ	3GACTTCTGTGGCCAGGTGTGCTTCACTCGAGGCCCTGCTCTCTGACCTCTTC 15
Qy	152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
qq	SGACCCGGACCACTGTCGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGG
Qy	172 GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
Dp	GCTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCTAC 17
Qy	192 LeuGlyThrGlnGluGluCysLeuPheGlyLeuThrLeuIlePheLeuThrCysVal 211
qq	SCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGT
Qy	212 AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly 231
QQ	SCCACACTECTEGTEGCTGAGGAGGCAGCGCTGGGCCCCACCGAGCCAGGAAGG
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δλ	272 ArgArgLeuPheValAlaGluLeuCysSerTrpWetAlaLeuWetThrPheThrLeuPhe 291
qq	CGGCTCTTCGTGGCTGTGCTGTGCTGGGTGGCTCTTTTCACGCTGTT
Qy	yrThraspPheValGlyGluGlyLeuTyrGlnGlyValProArgal.
qa	CACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGC
Qy	lualaargargHisTyraspGlu
qq	GGCCCGGAGACACTATGATGAAGGTAAG
6y :	319 319
qq	2133 AGCCGCCCACCAGAGACGACACTCGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGC 2192
Οy	319 319
qa	2193 CCCGACTTCTCTCTCTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2252
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qq	2253 GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC 2312
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qq	2313 AGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGCGGAGCTTATTCAAAGTCTAGAGGGAG 2372
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TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTG 2552
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AGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACA 2612
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GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlalleSerLe 336
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aValValThralaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGln11eLeuPr 396
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yaspihrdlyglyalasersergluaspserLeuwetthrserPheLeuProGlyproLy 436
SProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr 456
OProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGl 476
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PSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516
uSerGInSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAla11eTy 536
rPhealaThrGlnValValPheaspLysSerAspLeualaLysTyrSerAla 553

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513 CCTCTGCCCTGGGAGCTGCTTGGAGGGAGGGTGTCTGCTGGGAAGGCATTGCTGGGCA 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      633 CCCCAGTCACCTCTGGATCCCTGGTCCTGCAGAGCCTGGCTCATAGGAGACACTGGAG 692
                                                                                                                                                                                                                                                       APPLICANT: Warg, Allun APPLICANT: Warg, Allun APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
APPLICANT: Hepler, William
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS OF PROSTATE CANCER
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
TITLE OF INVENTION: UNDABER: US/09/780,669
CURRENT APPLICATION NUMBER: US/09/780,669
CURRENT FILING DATE: 2001-02-09
NUMBER OF SEQ ID NOS: 943
SEQ ID NO 702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   453 ACTACATCCTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA
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equence 702, Application US/09780669 atent No. US20020051977A1
                                             Xu, Jiangchun
Dillon, Davin C.
Mitcham, Jennifer L.
Harlocker, Susan L.
                                                                                                       Jiang, Yuqui
Henderson, Robert A.
Kalos, Michael D.
Fanger, Gary R.
Retter, Marc W.
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Day, Craig H.
Vedvick, Thomas S.
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t Local Similarity:
                                 ENERAL INFORMATION:
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693	3 AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC 752
57	7
753	3 TTACAACCACCATTTGAGGTGATCCATTTTACAGAAGGAAG
57	7
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57	
873	3 GGTCTCCCAGCCGGAGGTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 932
57	
933	3 GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCTCACC 992
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993	3 CCCAGGAAGAGGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 1052
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1053	3 GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTCTTAGTTGCTCC 1112
57	7 57
1113	3 ATGCCTCAGTTTGTCCATCTGAAAATGGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1172
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1233	3 TTCTCACGGAGCTTGGCTTCCCCTTGCCCTTTACTTGTCCCAGCCATTGACTCAT 1292
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1293	
72	2 GlySeralaSerAspHisTrpArgGlyArgTyrGlyArgArgArgArgProPheIleTrpAla 91
92	2 LeuSerLeuGlylleLeuLeuSerLeuPheLeulleProArgAlaGlyTrpLeuÄlaGly 111
112	2 LeuLeuCysFroAspProArgProLeuGluLeuAlaLeuLeuTleLeuGlyValGlyLeu 131
132 1533	2 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
152 1593	2 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
172 1653	2 GlyGysLeuGlyTyrLeuLeuProAlaileAspTrpAspThrSerAlaLeuAlaproTyr 191
192 1713	2 LeuGlythrdingludlucysLeuPheGlyLeuLeuThrLeuIlePheLeuThr/cysVal 211
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356	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe	336	ζ
2852	TCCCTCTGCAGGCGTTCGGATGGGCAGCCTGGGGGCTGTTCCTGCAGTGCGCCATCT	2793	q
336	GlyvalArgMetGlySerLeuGlyLeuPheLeuClnCysAlaIleSer	320	ΣŽ
2792	TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG	2733	qo
319		319	Σλ
2732	TGCTGGGGAGCAGGGCTGGTCCACAGCAGGTCTTCGTGCAGCAGGTACCTGTGGTTCCGCC	2673	Q
319		319	Σÿ
2672	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGG	2613	QQ
319		319	Σy
2612	AGACTCCCAGGAAACCTTCAGACTACCTTCC	2553	q
319		319	ΣŽ
2552	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGT	2493	qq
319		319	λχ
2492	CCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCG	2433	qq
319		319	Σλ
2432	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCT	2373	q
319		319	ΣŸ
2372	AGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAG	2313	qq
319		319	λχ
2312	GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC	2253	qq
319		319	λ
2252	CCCGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG	2193	q
319		319	δŏ
2192	AGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGC	2133	g
319		319	δy
2132	GAGGCCCGGAGACACTATGATGAAG	2073	q
319		312	δ
311 2072	TyrthraspPheValGlyGluGlyLeuTyrGlnGlyValProArgalaGluProGlyThr 	292 2013	Oy Ob
2012	CGCCGGCTCTTCGTGGCTGTGCTGTGCTGGGTGGCACTCATGACTTCACG	1953	QQ
291	ArgargLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheTh	272	ōλ
271 1952	AsnLeuGlyAlaLeuLeuProArgLeuHis(252 1893	Qy Db
251 1892	LeuSerAlaProSerLeuSerProHisCy 	232	QY
	Adantantireureuranadatuanuanadareuranykronnolukrondatuany 		D O
231	AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGl	212	οy

qq	2853	GGTCTTCTCTG				2912	q a
Οŷ	356		AlaPheProValAl	aAlaGlyAlaThrCys	sLeuSerHisSerValAl	376	Oy
qq	2913		AGCTTTCCCTGTGGC	TGCCGGTGCCACATGC	GGCCAGTGAGCATTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCCACAGTGTGGC	2972	qa
Ωy	376		SerAlaAlaLeuTh	rGlyPheThrPheSe	aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr	396	οy
QQ	2973		TCAGCCGCCCTCAC	CGGGTTCACCTTCTC	AGCCCTGCAGATCCTGCC	3032	qa
QY	396		aSerLeuTyrHisAr	gGluLysGlnValPhe	eLeuProLysTyrArgGl	416	QY
qq	3033		TCCCTCTACCACCG	GGAGAAGCAGGTGTT	CTACACACTGGCCTCCCTCTACCACCGGGGGGGGGGGTTCCTGCCCAAATACCGGG	3092	qa .
Qy	416		AlaSerSerGluAs	pSerLeuMetThrSer	yAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy	436	٥y
Q O	3093		rgctagcagtgagga	CAGCCTGATGACCAGO	CTTCCTGCCAGGCCCTAA	3152	ପ୍ର
ογ	436		OPheProAsnGlyHi	sValGlyAlaGlyGl	sProGlyAlaProPheProAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProPr	456	Qy
QΩ	3153		CTTCCCTAATGGACA	CGTGGGTGYTGGAGG	CAGTGGCCTGCTCCCACC	3212	qu
Οy	456		CysGlyAlaSerAl	aCysAspValSerVal	OProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValGlyGl	476	QY
QQ	3213		receesecrerec	CTGTGATGTCTCCGT	ACGTGTGGTGGTGGTGA	3272	qa
ογ	476		ArgValValProGl	yArgGly1leCysLe	uAspLeuAlalleLeuAs	496	Qy
QQ	3273		AGGGTGGTTCCGGG	CCGGGGCATCTGCCTC	GCCCACGGAGGCCAGGGTCCGGGCCGGGGCATCTGCCTGGACCTCGCCATCCTGGA	3332	qq
Οy	496		LeuSerGlnValAl	aProSerLeuPheMet	pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe	516	Oy
QΩ	3333		SCTGTCCCAGGTGGC	CCCATCCCTGTTTATC	GGGCTCCATTGTCCAGCT	3392	qa
Qy	516		ThrAlaTyrMetVa	SerAlaAlaGlyLe	uSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTy	536	QY
qa	3393	CAGCCAGTCTGTC	CACTGCCTATATGGT	GICTGCCGCAGGCCTC	GGGTCTGGTCGCCATTTA	3452	qa
ΟŸ	536		NalValPheAspLy	rPheAlaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla	sTyrSerAla 553		Qy
qa	3453		GGTAGTATTGACAA	GAGCGACTTGGCCAAA	ATACTCAGCG 3504		qa
RES	SULT 23	000-600-					QY
S	equence	e 702, Applica	Sequence 702, Application US/098228	127			qa
	ENERAL	GENERAL INFORMATION:	LOSOMI				Qy
	TITLE (OF INVENTION:	COMPOSITIONS A	FOR	THE THERAPY AND		qa
	FILE RI	EFERENCE: 2101	121.534C1	PROSTATE CANCER			Qy
	CURREN	T FILING DATE:	NUMBER: US/U9/ : 2001-03-28	822,827			qa
	NUMBER SOFTWAI	OF SEQ ID NOS RE: FastSEQ fo	<pre>; NUMBER OF SEQ ID NOS: 982 ; SOFTWARE: FastSEQ for Windows Version 3.0</pre>	ion 3.0			Qy
S	EQ ID L	NO 702 H: 4894					qa
- C	ORGANISM	. Homo sapi	rens				Qy
20 2	0.9-0.22						qa
Pre	Pred. No.:	. :	5.33e-229	Length:	4894		Qy
Per	cent Si	ercent Similarity:	51.118	Conservative:			qa
One:	ry Mato	4	94.115 88.73% 10		526 526		Qy
; ;		;	10	caps:	•		qa
- 80	545	-/93A-113 (1-5	78-60-S0 X (FC	2-82/-/02 (1-489)	94)		Qy

1 MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu

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993 CCCAGGAAGAGGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 1052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1113 ATGCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1173 AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1233 TTCTCAGGAGCTTGGTTCCCCTTCCCCTTGCCCTTTACTTGTCCCAGCCATTGACTCAT 1292
                                                                453 ACTACATCCTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 512
                                                                                                                                                                                                                                                                                                                                                                             513 CCTCTGCCCTGGGAGCTGCTTGGAGGGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    573 GGAGGGTGACCCTGGGCTGAGGGGGCACACCAAGAGAAGAAGAAGAATACCAAGGACATA 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         633 CCCCAGTCACCTCTGGATCCCTGGTCCTGCACAGAGCCTGGTCATAGGAGACACTGGAG 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693 AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTÄTAGCGATTATCTCATTTAATGC 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     753 TTACAACCACCATTTGAGGTGATCCATTTTACAGAGGAAGCAGGAGGAGCTTTTAAGAGG 812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               873 GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGGTGGACTCCTGACTCTGCA 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       933 GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAA¢CATTGTGTGACAACCCCTCACC 992
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Thu Feb 20 11:12:04 2003

SCCGCCCTTCATCTGGGCA 1412	galaglyrrpLeualagly 111 	uLeuIleLeuGlyValGlyLeu 131 	IGluAlaLeuLeuSerAspLeuPhe 151 	TyralaPhemetIleSerLeuGly 171 		Cysval 211	ProThrGluProAlaGluGly 231 GCCCACCGAGCAGAGGG 1832	ArgAlaArgLeuAlaPheArg 251 	ArgMetProArgThrLeu 277	 eThrLeuPhe 291 	GlyValProArgAlaGluPróGlyThr 311 	319 CCAGCAGAGGCTGGTGGG 2132	319	TGGTGCCTCTCCATCCTGGC 2192	319	GCATACACGGCTTCTCATGG 2252	319	GCTGCTCTAGGAGTCTGATC 2312	319	TATTCAAAGTCTAGAGGGAG 2372		GCCGCAGTGTGCCCTTGCT 2432	319	CTCAGGCGTCCTAGAAGCG 2492
GGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCC	LeuSerLeuGly1leLeuLeuSerLeuPheLeu1leProArg/ 	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuL 	LeuAspPheCysGlyGlnValCysPheThrProLeuGluA 	ArgAspProAspHisCysArgGlnAlaTyrSerValTyrA 	GlyCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAla 	euGly TGGGC	AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyP 	LeuSeralaproSerLeuSerProHisCysCysProCysA 	ProArgLeuHisGlnLeuCys 	euPheValAlaGluLeuCysSerTrpMetAl 	TyrThraspPheValGlyGluGlyLeuTyrGlnGlyValP 	GlualaargargHisTyraspGluGlualaargargargargargargargargaggccttGGCAG		AGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGC		CCCGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCATCT		GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTG		AGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCT		TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCA		CCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAG
1353	92	112	132	152 1593	172	6 4	212	232	252	272 1953	292	312	319	2133	319	2193	319	2253	319	2313	319	2373	319	2433
qq	Oy Dp	o o	oy Db	Qy	oy Dp	oy Op	Oy Dp	Qy Db	Q Q	Qy	Qy	Oy Dp	οy	QQ	οy	ф	Οy	qq	Οy	QQ	δý	Dp	Qy	qq

Οy	319	316
qq	2493	GTT.
Qy	319	319
QQ	2553	GACTCCCAGGAAACCTTCAGACTACCTTCCTCCCTTCAGCAAGGGGCGTTGCCCA
Οy	319	319
qq	2613	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGG 2672
Οy	319	319
qq	2673	CGTGCAGCAGGTACCTGTGGTTCCG
Qy	319	319
qq	2733	TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG
Οy		GlyvalArgMetGlySerLeuGlyLeuPheLeuGlnCysAlalleSerLe 33
Op	2793	rgcaggcgttcggatgggcagcctrggggctgttcctgcagtgcgccatctcc
oy D	336	uValpheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
ò	2	ServalalaalapheprovalalaalaalagivalamhrCvsLenSerHisServalAl 37
g q	, A	0
οy	7	6
qq	2973	STGGTGACAGCTTCAGCCGCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 30
Oy Db	396	OTYTThrLeuAlaSerLeuTyrHiSArgGluLysGlnValPheLeuProLysTyrArgGl 416
Qy Db	416	yAspThrGlyGlyAlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLy 436
0y	36	labroPheproAsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuPr
Db	3153	GCCTGGAGCTCCCTTCCCTAATGGACACGTGGGGGTGTTGGAGGCAGTGGCCTGCTCCCACC 3212
Qy	456	OPTOProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValValValGlyGl 476
δy	476	roThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuA
qq	3273	GCCTGGACCTCGCCATCCTGGA
δy	496	pSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGlnLe 516
QQ	3333	AGTGCCTTCCTGCTGTCCCAGGTGGCCCCATCCTTTATGGCCTCCATTGTCCAG
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oy Dp	536 3453	rPhealaThrGlnValValPheAspLysSerAspLeuAlaLysTyrSerAla 553
RESU US-1 ; Se ; Pu	SULT 24 -10-012- Sequence Publicat	: 896-705 : 705, Application US/10012896 : .ion No. US20020183251A1

b 524 CCCAGTCACTCTGGATCCCTGGTCTGCACAGAGCTCATAGGAGACACTGGAG 583	57	584 AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC	57	b 644 TTACAACCACCATTTGAGGTGATCCATTTTACAGAGGAGGAGGGAG	y s7 57	d 704 TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763	y 57 57	b 764 GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 823	y S7 57	b 824 GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCCTCACC 883	у 57 57	b 884 CCCAGGAAGAGGGCCCCTGTGAGGATTGCAGGCTCTGAGACACTGCTTGTTGAAAC 943	y 57 57	b 944 GCTGCCTCTTACCCTCCTAGGTCTGCGCCTTTGAATAAGTATCACTTMTTAGTTGCTCC 1003	у 57	b 1004 ATGCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1063	у 57	b 1064 AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC 1123	y s7 57	b 1124 TTCTCACGGAGCTTGGTTCCCCTTCCCCTTTACTTGTCCCAGCCATTGACTCAT 1183	58	1184 ACTACTTCCCTTCTTGCAGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCTA	y 72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgArgArgProPheIleTrpAla 91	12.44 GGC.LCAGCCAG.1GACCAC.1GGCG.1GGACGC.1A1.CGGCCAC.CGCCCCC.1.CA.1C.14GGCCA.	1304 CTGTCCTTGGCCATCCTGCTGAGCCTCTTTCTCATCCGAAGGCCGGCTGGCT	y 112 LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuCleueLleuGlyValGiyLeu 131	1364 crecreseccedarecerageceergaaderedeeredereareergageerg	132 LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe	1424 CTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCTGCTCTCTGACCTCTTC	y 152 ArgAspProAspHisCysArgGinAlaTyrSerValTyrAlaPheMetileSerLeuGly 171	1404 COGGGGCCCGGGGCGCGGGGGGGGGGGGGGGGGGGGGG	15.4 Organization	192 LeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal
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ပ္	; APPLICANT: Dillon, Davin C. ; APPLICANT: Mitcham, Jennifer L.	: Harlocker, Susan I : Jiang, Yuqiu		Stolk, John A. Day, Craig H.	. Cart	APFLICANT: Ul, Samuel A. ; APPLICANT: Wang, Aljin ; ADPITONM: Choit, worth a		; APPLICANT: Hural, John ; APPLICANT: MANAGIL Datricia D	Houghton, Raymond I	; APPLICANT: Vinais de Bassols, Carlota ; APPLICANT: Proy, Teresa ; APPLICANT: Programme Program	; AFFILCANN: ranger, vary k.	OF INVENTION:	; IIILE REFERENCE: 210121.427C27	CURRENT APPLICATION NUMBER: US/10/01Z, 896 CURRENT FILING DATE: 2001-12-10	; NOMBER OF SEQ ID NOS: 1011 ; SOFTHARE: FastSEQ for Windows Version 3.0	; SEQ 1D NO 705 ; LENGTH: 6976	; Organism: Organisms re-no-na-na-na-na-na-na-na-na-na-na-na-na-na-	Alianment Coorse	Allyliment Scoles: 1.16e-191 Length: 6976 Score 2144 On Matches: 651	larity: 30.48% Conservative: imilarity: 30.48% Mismatches:	74.94% Indels: 9 Gaps:	US-09-593-793A-113 (1-553) x US-10-012-896-705 (1-6976)	Oy 1 MetValGlnargLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20	Db 165 ATGGTCCAGAGGCTGTGGGTGAGCCTGCTGCTGCGCACACCCGGAAAGCCCAGCTCTTGCTG 224	Oy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 40	41 ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeu	285 CCTCTGCTGCTGGAGTGGGGGTAGAGGTAGAGTTCATGACCATGGTGCT-GGGTGAGTC	Qy 57 57	Db 344 ACTACATCCTCCTTCCTTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 403	Qy 57 57	Db 404 CCTCTGCCCTGGGAGCTGCTTGGAGGGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 463	Oy 57 57	Db 464 GGAGGGTGACCCTGGGCTGAGGGGCCACCAAGAGAAGAAGAGAATACCAAGGACATA 523 Qy 57

qq	1604	CTGGGGAGCCAGGAGTGCCTTTTGGGCTGCTCACTTCATCTTCACTTCACCTG	1663
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g	1784		1843
δý	272		291
QQ	1844	GGCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTTT	1903
οχ	292		311
qq	1904	TACACGGATTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCCAGAGCCTGAGCCGGGCCCC	1963
δý	312	GlualaargargHisTyrAspGlu	319
g	1964		2023
ζ	319		319
q	2024	AGCCGCCCACAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCCTCCCATCCTGGC	2083
ά	319		319
g	2084	CCCGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG	2143
λ	319		319
q	2144	GTGTGGAACATCTCTGCGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC	2203
χ̈	319		319
q	2204	AGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAÖAGGGAG	2263
λ	319		319
q	2264	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCÇTCTGCT	2323
λ	319		319
q	2324	CCCCCAACGACTTTCCAAAATCTCACCAGCGCCTTCCAGGTCAGGGGTCCTAGAAGCG	2383
ά	319		319
qc	2384	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACGCCGCCTGTCCTCACAGCTG	2443
ζ	319		319
q	2444	AGACTCCCAGGAAACCTTCAGACTACCTTCCTTCAGCAAGGGGCGTTGCCCACA	2503
λ̈	319		319
q	2504	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGGTAGAAGGGGAAGGG	2563
ζ	319		319
q	2564	TGCTGGGGAGCAGGCTGGTCCACAGAGGTCTCGTGCAGGTACCTGTGGTTCCGCC	2623
ķ	319		319
qo	2624	TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG	2683
λ	32	GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaileSerLe	36
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δy dg	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356
0	35	1A1 376
q	0	11 3C 28
Οy	376	ω-
οqα	2864	CCTG
Qγ	396	oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal
qq	2924	TCCC
Οy	409	608 408
οg	2983	AGTCAGGGTGGGAGGGGTGTGTTTTGGGAGGCCAACTAGCTCAGAACCTGGTAT 3042
οy	409	409
Dp	3043	CTGGCAAGCAACTTTGGAGAATGCTTCTTTGAATCAGAGAAGAAGCTTATCCTAGCCCCA 3102
Qy	409	409
qq	3103	GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT
Qγ	409	608
Dp	3163	TCAGGACTGTGTAGCACTTGAATGGATGATTGCAGGAAATGCAAAATACGATAGTGGGAA 3222
Qy	409	409
qq	3223	TCCCGAAGGGTCAGGCCAGGAGGCCTAGGCTTCTAGGCTGGTTGTTCTATGGAGAGG 3282
Οy	409	409
qq	3283	CAGGCCCTGAATCAGATGACCCCTGGGCCCATTCAGCCTCAGCAGAGGGGAGTGGGAATG 3342
Qy	409	608 408
qq	3343	GTCCAGCCTTAGCAACACCTTTCTTCAGGGGGGGCAGCAACCTGACTTAGCCTGTATCCTAC 3402
Qy	409	607
QQ	3403	TCTGGTCTCTGAGATGGGGCAGGCTCCTTCCTACCCCCTTTCTTT
Qy	409	608
qq	3463	TITCIGICIAATICCCTITICTTITCTGCATCCCTCCTTTGCCTCCTTCCCTTTCTCT 3522
Οy	409	608
qq	3523	TCCCCTTCCCCTTCCCCTGTGGCAGATATCTGAGCTTGACACCTGACCCACTCACT
Qy	409	604
Op	3583	CACTGTGTAAGTTGTGGGGACCTCCTTCTTGGTTGGCCCTACACTAACCAGCCCCTCCAG 3642
Qy	409	607
qq	3643	GGGCCCCTTTCCTTGGGAAGCCACCTAACCCAGGTAGTGTGGTCATCCTTGTCCCCTCCA 3702
Qy	409	608
QQ	3703	CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCCTTGAGGGGCATGAAGTTGG 3762
Οy	409	409
qq	3763	GGTGTCCCAAGGGAGGAGGAGATGCAGGACTGCTCTCATAGAGCTCTCAGACTGTAGGGA 3822

; APPLI ; TITLE	; APPLICANT: Fanger, Gary R. TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSTS OF DESCRIPTE CANCED	qa	80
FILE	REFERENCE: 10.10.1. STANDOLD OF FNOSTRIE CANCEN NT APPLICATION NUMBER: US/09/895, 793	ΟŊ	
CURRE		QQ	ð
SOFTW	ARE: FastSEQ for Windows Version 3.0	Qy	
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) ORGA	Orania Managarians -0.9.503.73.704.	Qy	
o co co		qq	10
Pred. No.:	cores:	QY	
Percent	ilarity: 30.48 Conservative: 0	qq	11
DB:	ct Similaticy: 50.40% mismacones: 2 tch: 74.94% mismacones: 2 tch: 9 Gans: 3	٥y	
US-09-593	-793A-113 (1-553) x US-09-895-793-705 (1-6976	QQ	11(
		Qy	•
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ı	Vallasnienschappest vienschutzeschappest vilombenvivalore	Qy	•
2	GTCAACCTGCTAACCTTTGGCCTGGAGGTGTGTTTGGCCGCAGGCATCACCTATGTGCCG	QQ	13(
0y 4		ΟY	ä
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Db 344	ACTACATCCTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGGACA	qα	14.
		Qy	ä
4	CCTCTGCCCTGGGAGCTGCTTGGAGGGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA	QQ	148
Qy 57		Qy	H
Db 464	GGAGGGTGACCCTGGGCTGAGGGGGCACACCAAGAGAAAAAAAA	qq	154
0y 57	7	Οy	ij
Db 524	4 CCCCAGTCACCTCTGGATCCCTGGTCCTGCAGAGCCTGGCTCATAGGAGACACTGGAG 583	qa	16(
Qy 57		Ολ	7
Db 584	4 AAATGCTCCTAACCTTTGGCTAGGCCTTTTATAATTTATAGGGATTATCTCATTTAATGC 643	q Q :	166
Qy 57	7	δi	, ,
Db 644	4 TTACAACCACCATTTGAGGTGATCCATTTTACAGAAGGAAG	an :	77
Qy 57	7	δo	7
Db 704	4 TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763	a d	178
Qy 57	7	à à	7
Db 764	4 GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 823	α i	T A
0у 57	7	ਤੇ ਫ਼	701
Db 824	4 GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCCTCACC 883	3 8	2 2
Qy 57	7	Š	ก

qq	884 CCC	CAGGAAGAGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 943
οy	57	57
QQ	944 GCT	GCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTMTTAGTTGCTCC 1003
Oy	57	25
qq	1004 ATG	GCCTCAGTTTGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA 1063
Οy	57	22
qq	1064 AAT	TTACAGCATCCCTGTGAAGACGTAGCACAĞTGTCGAGTACGGAATGTTATTTCCATCC 1123
δy	57	25
qq	1124 TTC	CTCACGGAGCTTGGTTCCCCTTCCCCTTTACTTGTCCCAGCCATTGACTCAT 1183
δý	58	
qq	1184 ACT	ACTICCCITCTIGCAGGCATIGGTCCAGGGCTGGGCCTGGTCTGTGTCCCGCTCCT
Qγ	72 G1y	ySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla 91
Dp	. ტ	CAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGCCG
QY	92 LeuSe	ISELLEUGLYILELEULEUSELLEUPHELEUILEPROARGALAGLYTFPLEUALAGLY 111
ΩD	1304 CTG	CCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCCAAGGGCCGGCTGGCT
δy	112 Leu	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu 131
qq	1364 CTG	TGCCCGGATCCCAGGCCCCTGGAGCTGGCACTGCTCATCCTGGGCGTGGGGCT
λŏ	m (pphecysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe 151
g	24	ACTICTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGTGACCTCTTTC 14
Qy	'n	spProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly 171
Op Op	1484 CGG	ACCCGGACCACTGTCGCCAGGCCTACTÇTGTCTATGCCTTCATGATCAGTCTTGG
Qy	172 Gly 	CysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyr 191
Вр	1544 GGC	TGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCT
οy	192 Leu	uGlyThrGlnGluGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal 211
QQ	1604 CTG	scacccaggagagagctrangectaccccccaccarcraccraccracca
οy	212 Ala	aThrLeuLeuValAlaGluGluAlaA aLeuGlyProThrGluPr
Op	1664 GCAG	scacacrecregrescreases de consecue de cons
οy	232 Leus	erAlaProSerLeuSerProHisCysCys
Ор	1724 CTG	ceeccccrccrrerceccccacrecrercarecceecccecrreecrrrece
οy	252 Asn	euCysCysArgMetPr
QQ	1784 AAC	TGGCGCCCTGCTTCCCCGGCTGCACCTGTGCTGCCGCATGCCCCGCACCCT
δy	272 Arg	ArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrF
qq	1844 CGC	CGGCTCTTCGTGGCTGTGCAGCTGGATGGCACTCATGACCTTCACGCTGTT
δy	292 Tyr	ThraspPheValGlyGluGlyLeuTyrGlnGlyValProArgAla
QQ	1904 TAC	<u>acggatttcgtgggcgagggctgtaccagggcgtgcccagagctgagccgggc</u>
δy	312 Glu 	AlaArgArgHisTyrAspGlu319

pp	1964	GAGGCCCGGAGACACTATGATGAAGGTAAGGCCTTGGCAGCCAGC	2023
ογ	319		319
QQ	2024	AGCCGCCCACAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGC	2083
οy	319		319
QQ	2084	CCCGACTTCTCTGTCAGGAAAGTGGGGGATGGACCCCCATCTGCATACACGGCTTCTCATGG	2143
οy	319		319
QQ	2144	GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC	2203
Οý	319		319
QQ	2204	AGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAG	2263
οy	319		319
qq	2264	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCT	2323
οy	319		319
QQ	2324	CCCCCAACGACTTTCCAAATAATCTCACCAGCGCTTCCAGCTCAGGGGTCCTAGAAGCG	2383
Οy	319		319
QQ	2384	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGCCTGTCCTCACAGCTG	2443
٥y	319		319
qq	2444	AGACTCCCAGGAAACCTTCAGACTACCTTCCTGCCTTCAGCAAGGGGCGTTGCCCACA	2503
οy	319		319
QQ	2504	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGGTAGAAAGGGGAAGGG	2563
ογ	319		319
QQ	2564	TGCTGGGGAGCAGGCTGGTCCACAGAGGTCTCGTGCAGGAGGTACCTGTGGTTCCGCC	2623
Qy	319		319
ор	2624	TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG	2683
οy	320	GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe	336
qq	2684		2743
οy	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe	356
q	2744	GGTCTTCTCTCTGGTCATGGACCGGCTGGTGCAGCGATTCGGCACTCGAGCAGTCTATTT	2803
οy	356	ualaSerValalaAlaPheProValAlaAlaGlyAlaThrCySLeuSerHisSerValAl	376
qq	2804	GCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCCATGCCTGTCCCACAGTGTGGC	2863
οy	376	aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr	396
qq	2864	CGTGGTGACAGCTTCAGCCCCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC	2923
ογ	396	oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal	409
QQ	2924	CTACACACTGGCCTCCCTCTACCACCGGGAGAGCAGGT-ACTCATTGGCCAGTGGGTGG	2982
٥y	409		409
qq	2983	AGTCAGGGTGGGAGGGGTGGGTTTTTGGGAGGCCAACTAGCTCAGAACCTGGTAT	3042
οy	409		409
QQ	3043	CTGGCAAGCAACTTTGGAGAATGCTTCTTTGAATCAGAGAAGAAGCTTATCCTAGCCCCA	3102

Qy	409		409
qq	3103 GGGCCAGA	 GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT	 TTCTGGGAATGACTTCCTGGGG 3162
Qγ	409		409
QQ	3163 TCAGGACT	TCAGGACTGTGTAGCACTTGAATGGATGATTGCAGGAAATGCAAAATACGATAGTGGGAA	ATGCAAAATACGATAGTGGGAA 3222
οy	409		409
qq	3223 TCCCGAAG	TCCCGAAGGGTCAGGCCAGGAGCCCTAGGCTTCTAGGCTGGTTGTTCTATGGAGAGG	GGCTGGTTGTTGGAGAGG 3282
QY	409		408
QQ	3283 CAGGGCGC	CAGGGCGCTGAATCAGATGACCCCTGGGCCATTCAGCCTCAGGAGAGGGGAGTGGGAATG	TCAGCAGACGGGAGTGGGAATG 3342
QY	409		409
qq	3343 GTCCAGCC	GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC	CCTGACTTAGCCTGTATCCTAC 3402
QY	409		409
Dp	3403 TCTGGTCT	TCTGGTCTCTGAGATGGGGCAGGCTCCTTCCTACCCCC	TTTCTTTCTGGCTTATTTTTCT 3462
Qγ	409		607 408
QQ	3463 TTTCTGTC	TTTCTGTCTAATTCCCTTTTCTTTTCCTGCATCCCTCCTTTGCCTTCCTT	TTGCCTCCTTCCCTTTCTCCT 3522
QY	409		607
qq	3523 TCCCCTTC	TCCCCTTCCCCTTCCCCTGTGGCAGATATCTGAGCTTGACACCTGACCCACTCACT	ACACCTGACCCACTCACTTGGG 3582
δλ	409		408
qq	3583 CACTGTGT	CACTGTGTAAGTTGTGGGGACCTCCTTCTTGGTTGGCCCTTACATAACCAGCCCCTCCAG	CTACACTAACCAGCCCCTCCAG 3642
ΟŸ	409		604 406
QQ	3643 GGGCCCCT	GGGCCCCTTTCCTTGGGAAGCCACCTAACCCAGGTAGTGTGGTCATCCTTGTCCCTCCA	STGGTCATCCTTGTCCCCTCCA 3702
Qγ	409		408
QQ	3703 CTGACCTC	CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCCTTGAGGGGGCATGAAGTTGG	SCCTTGAGGGCCATGAAGTTGG 3762
δλ	409		408
q	3763 GGTGTCCC	GGTGTCCCAAGGGAGGAGGAGATGCAGGACTGCTCTCATAGAGCTCTCAGACTGTAGGGA	PAGAGCTCTCAGACTGTAGGGA 3822
Qy	409		607 408
qq	3823 AGACCTGC	AGACCTGCCCCTGCGTCTCGTAGCACTTGAGGAGAGGA	GTAGGTAAGTTCGTAGCTGAGA 3882
0λ	409		409
qq	3883 GGCTGGTT	GGCTGGTTAACTGAGTAGGTAGCTGCAGGGGTGAGAGGT	PATGGAGGGAGGGCTAAGGT 3942
Οy	409		408
qq	3943 TTTGGTTG	TTTGGTTGGGGGAGCCTGGTCCCTGAGACCCCTGTTAGCCCACTGATAACCTTCTTCAGC	CCCACTGATAACCTTCTTCAGC 4002
δλ	409		607 408
qq	4003 CTTCACTC	CTTCACTCTTCTGCTTGCCTGGGGGGGCAGGGGGCT	GGCATCAGCGGCCAGGCCTGA 4062
Οy	409		409
QQ	4063 GTATGTGC	GTATGTGCTGTCGTGCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGAGC	MATCTTCTCCAGATGGAGGAGC 4122
ΟY	409		409
QQ	4123 ATGTCTGT	atgtctgtcctcggaccactccagactccaacctcagcggacattcctggggtggcaggc	GACATTCCTGGGGTGGCAGGC 4182

133 AGGREGATE CONTRICTED CONT	•		0000
423 CAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	qq	AGGGAGGAGAAGTCCTGGGAGGCCCCTTCCTAACAGCAGCTGATGGCAGACTTGGCACTG	•
1313 CAGGCTGGTCGTTGGTTTGGCCTGGTGGTGGCTGGCGTGGCTTGC 100 101	οy		400
409 CONTROLLED CONTROL	QQ	CACGCTGTCTGCCTGTTCCCTTTGCCCACTTGTTGAGCTGCATGGTGAGCCGTGGGCTTCC	5323
1303 CTGGTGTCAGGTTTGAGGTTTGAGGTTTGAGGTTCCCAAGGCTCTGG AACT 199 190 191	οy		4 80
409 109	QQ	CTGGTGTCAGGTTTGAGCTCTGCCATGGCTCCCACCTCGCAAATGCAGCCAACTC	7383
4353 TICTGGCATGGGGCANTGTTGGCATTGTCCTTAAATAGGAGCTCTGG 4122 409 5553 4423 GCCATCAAGGGCAGGGATGGTGGACTGACTGACTCAATTCAAA 4182 09 5553 4433 GCCAGGAAGGAAGGCATGAGGGGGGGGGGGGGGGGGGGG	οy		000
409 409	qq	TTCTGGCATGGGGACAATGTTGGATAAGACCTGGCCTTGTCCTTAAATAGGAGGCTCTGG	0443
4123 GCCATCAAGGGCATGGGGATGGTGGACCAGTCACTCAAGTCAGA 4482 452 465 489 494 499 499 499 499 499 499 499 499	δý		526
483 CACCAGGAMGGAACTCCACCACACCTCGGGGGGGGGGGGG	QQ	GCCATCAAGGGCAGGGTTGGGGGGATGGTGGTCGACCAGTCACTCTGATCTAAGTCAGA	5000
1483 CHECKOGROMOGNACTORIONACTIVECOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCOCO	ΟŊ		546 rAspLeuAlaLysTyrSerAla 553
454 AGAGGGACATTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCCCCAAGGCTGGGGGACA 6602 Sequence 715, AGACGGACATTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCC	qq	CAGCAGGAAGGAAGTGAGAAGCCTTCAACATTAGCACAGGTGGGGGTGGGGGGGG	DD 3303 CGACIIGGCCAAAIACICAGCG 3304
4543 AGAGGGACATTCCTCCTGCTTGCTGCTCGCCCAAGGCCCCAAGGCCCCCCCC	δγ		NESULT 20 US-09-895-814-705
409 APPLICANT 101100. Day in C.	qq		; Sequence 705, Application US/05033014; Publication No. US/0020193296A1
4693 AGGGGGCTACCTACTACGGGCCCCAACACACACACACACA	Οy		; General Information: ; Applicant: Yu. Jiangchun
409 APPLICANT ALTHOUGH APPLICANT ALTHOUGH ALTHOUGH APPLICANT ALTHOUGH ALTHOUGH APPLICANT ALTHOUGH ALTHOUGH APPLICANT ALTHOUGH APPLICANT ALTHOUGH APPLICANT ALTHOUGH APPLICANT APPLICAN	QQ	AGGGAGCTCATGGCAGGGCAGCTACCCTAGTGGCATCTGGGACCCCCAGAGAGGCAGAGGT	APPLICANT: DILLON, DAVIN C. APPLICANT: MItcham, Jennifer L.
463 TCTCTCCACCGGGCATGGGGCGCAGGAGGAGGAGAGAGAG	ογ		APPLICANT: Harlocker, Susan L. , APPLICANT: Jiang Yuqiu
409 APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT Hoteler COLUMN APPLICANT COLUMN APPLICANT Hoteler COLUMN APPLICANT COLUMN APPLICANT Hoteler COLUMN APPLICANT COLUMN	qq	TCTCTGCACCGGGCAATGAGGATTTCCAGATGTCGGAGTGGAGGCAGGC	APPLICANT: Raios, Michael D.
4723 GTTAGGGGGGGTTTGGGGCTTTGGGTTTTGTTCCTC 4782 APPLICANT: Carter, Darrick APPLICANT: GTTGTTCCTGGGGGTTTTGGTTCCTTGGGG 4842 APPLICANT: GTTGTTCCTTGGGGTTTTGGTTCTTTGGTGGG 4842 APPLICANT: GTTGTTCCTTGGGGTTTGGGGTTTTGGTTGGGG 4842 APPLICANT: GTTGTTCCTTGGGGTTTGGGGTTTGGGGGGGGGGGGG	δy		APPLICANT: SCOLK, John A.
409	QQ	GTTAGGAGAGCCTGCGTGGGGGTTTGGGCCATCAGGGGCCCTGCCTTTGGCTTTTGTTCCTC	APPLICANT: VEGATICK, INCHINGS 5.
4783 TOTACTOTGCATCTTACATTCCCCTGTGTCTTTCCTTACCTTGCAG 4842 APPLICANT SMALLAN 4843 CTCTCTTCTCTCATCCACCTTGTCTTTCCTTACCTTGCAG 4842 APPLICANT Henderson, Robert A. 4843 CTCTCTTCTCTCTCTCTTACTTGCTTCTTCTTAGAGGCT 4902 APPLICANT Henderson, Robert A. 4843 CTCTCTTCTCTCTCTCTCTTAGAGTTTGTCTTCTTCTTCTTAGAGGCT 4902 APPLICANT Henderson, Robert A. 4843 CTCTCTTCTCTCTCTCTTAGAGTTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTC	δλ		
489	QQ	TGTTCTGTGCATCTCTTACCACCGTCTTCATTCCCCCTGTGTCTTTTCCTTACCTTGGAG	
4843 CTCTGTTCTCTGATCTGTGTCTCCTTACCTGTTACCTGTTACTAAGAGGCT 4902 APPLICANT: Winslate de Bassols, Carlota 409	οy		
409	g	CTCTGTTCTCTCTGATCTGTGATATTGAGTTTGTCTGCCTCTTACCTGTTCTAAGAGGCT	Houghton, Raymond L.
4903 AGAGGAGCCTAGACTTCGCCCCCCCCCTTCCCCC 4962 TITLE OF INVENTION: COMPOSTIONS AND METHODS FOR THE TITLE OF INVENTION: COMPOSTIONS OF PROSTATE CANCER. 409	٥y		APPLICANT: VINGLS de Bassols, Calloca ; APPLICANT: FOY, Freesa
409	Q	903 AGAGGAGACCTAGACTTCTGGGTTCACATTTGTCCCCGCCCTACCCCGTTACCCTTCTCC	; AFFILCANI: Fallgel, GG17 N.; TITLE OF TWOMING COMPOSITIONS AND METHODS FOR T
CURRENT APPLICATION NUMBER: 02/09/893,014	οy		FILTE OF INVENTION: DIAGNOSIS OF PROSIME CANCER; FILE REFERENCE: 201011.427026
SEQ ID NO 705 SEQ ID NO 70	Op	CACTCCTGAGGAAGGGTCCTGGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCCT	CURRENT APPLICATION NUMBER: US/09/893,814
SO23 GCTCCTGATTCTCATGAAGTCCCTGGGATGGAGGATGCAGGGTCTGTTCTCACA 5082 1 LENGTH: 6976 1 TYPE: DNA 1 ORGANISM: Homo sapiens 1	Οý		SOFTWARE: FastSEQ for Windows Version 3.0
TYPE: DNA Homo sapiens TYPE: DNA	qq	GCTCCTGATTCTCATGAAGTCCCATTGCCCCTGGGATGGAGGGCAAGGGTCTGTTCTCACA	; SEQ ID NO 705 ; LENGTH: 6976
410	٥y		ORGANISM: Homo s
410PheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSe 426	QO	GCTGGGGTGGTGCCAGTGCTGGGTACACACCTGTCCTCTTCCCCTTTTCTTCACCCCTCT 514	ν .
SCCTTAGGTGTTCTCCCCAAATACCGAGGGCACTGTGTGTTTTTTTT	οy	PheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSe	Scores: 1.16e-191
426 rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisva 446 1111111111111111111111111111111111	qa	GCCTTAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAC	30.48% Conservativ
US-09-593-793A-113 (1-553)	۶۵ و	rLeuwetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 	74.94% Indels: 9 Gaps:
	3 8	CC1641GACCAGCT1CC1GCCCAGGGCCCC1GGAGCCTCCC11CCC1AA1GGACACGT	(1-553)

Thu Feb 20 11:12:04 2003

319		319	0y
~	GAGTTAAGGCTGGATTTCAGATCTGCCTGG	2264	QQ
319		319	QY
2263	CGTTGCCCCAGTTTGACAGAAGGAAAGGCG	2204	qq
319		319	Qy
2203	GTGTGGAACATCTCTGCTTTGCGGTTTCAGGAAGGCCTCTGGCTGTAGGAGTCTGATC 25	2144	Dp
319		319	Qy
	CGACTTCTCTGTCAGGAAAGTGGGGGATGGACCC	2084	QQ
319		319	Qy
2083	AGCCGCCCACCAGAGACGACACTCGGGGCTGTGTGTGGGCTGGTGCCTCTCCATCCTGGC	2024	qa
319		319	Qy
0	AGGCCCGGAGACACTATGATGAAGGTAAGGCCTT	1964	QQ
319	GluAlaArgArgHisTyrAspGlu	312	Oy
0			Db
311	TyrThrAspPheValGlyGluGlyLeuTyrGlnGl	292	Qy
ת ס	CGCCGGCTCTTCGTGCTGTGCTGTGCAGCTGTGCAT	1844	A 6
	AACCIGGGGGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCATGCCCCGCACCC	ထိ	QQ Q
	AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysAr		Qy
1783	CCCCTCCTTGTCGCCCCACTGCTGTCCATGCCGGG	1724	Db
251	LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheAr	232	QY
1723	GCAGCCACACTGCTGGTGGCTG	ý.	୍ ପ୍ର
5 5		,	3 8
211	LeuGlyThrGlnGluGluCySLeuPheGlyLeuLhrLeull 	1604	λo d
1603	GGCTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCAGTGCCCTGGCCCCCT	4	qa ,
191	GlyCysLeuGlyTyrLeuLeuProAlalleAspTrpAs	172	ΟY
1543	CGGGACCCGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCTTGG		Dβ
171	gaspproaspHisCysArgGlnalaTyrSerValTyralaPheMetIleSerLe	152	QY
1483	CIGGACTTCTGIGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGACTTTC	1424	qa
151	LeuAspPheCysG1yG1nValCysPheThrProLeuG1uAlaLeuLeuSerAspLeuPh	132	ΟY
1423	CTGCTGTGCCCGGATCCCAGGCCCCTGGAGCTGCTCATCCTGGGCGTGGGCTG	1364	qu
131	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLe	112	QY
1363	CTGTCCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCAAGGGCCGGCTGGCT	1304	qq
	LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGl	92	QY
1303		1244	ΩD

ð	2324	CCCCCAACGACTTTCCAAATAATCTCACCAGCGCCTTCCAGGTCTCAGGAGGG 2383	
<u>*</u>	319	319	
ą	2384	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTTCCCTCTCACCGCCTGTCCTCACAGCTG 2443	
<u>~</u>	319	319	
ą	2444	AGACTCCCAGGAAACCTTCAGACTACCTTCCTGCCTTCAGCAAGGGGGGTTTGCCCACA 2503	
λ	319	319	
ą	2504	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGG 2563	
λ	319	319	
ą	2564	TGCTGGGGAGCAGGGCTGGTCCACAGCAGGTCTCGTGCAGGAGGTACCTGTGGTTCCGCC 2623	
<u>~</u>	319	319	
ą	2624	TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG	
λ	320	GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 336	
ą	2684		
<u>ک</u> ج	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356 	
3	ì		
<u>ک</u> ۾	356	ualaSerValalaalaPheproValalaalaGlyalaThrCysLeuSerHisSerValal 376 	
~	376		
, <u>a</u>	2864		
ζ	396		
ą	2924		
<u>~</u>	409	408	
ð	2983	AGTCAGGGTGGGAGGGGTGGTCTTGTGGGAGGCCAACTAGCTCAGAACCTGGTAT 3042	
<u>γ</u>	409	608	
ð	3043	CTGGCAAGCAACTTTGGAGAATGCTTCTTTGAATCAGAGAAGAAGGTTATCCTÄGGCCCCA 3102	
λ	409	409	
Q	3103	GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT	
λ	409	408	
q	3163	TCAGGACTGTGTAGCACTTGAATGGATGATTGCAGGAAATGCAAAATACGATAGTGGGAA 3222	
χ̈	409	408	
q	3223	TCCCGAAGGGTCAGGCCAGCAGGAGCCCTAGGCTTCTAGGGTTGTTCTATGGAGAGG 3282	
ζ	409	608	
ą	3283	CAGGGCGCTGAATCAGATGACCCCTGGGCCATTCAGCCTCAGCAGACGGGAGTGGGAATG 3342	
λ	409	408	
Q	3343	GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402	
χ	409	409	
ð	3403	TCTGGTCTCTGAGATGGGGCAGCTCCTTCCTACCCCCTTTCTTGTGGCTTATTTTCT 3462	

454	CAGCAGGAAGGAAGTGAGAAGCCTTCAACAȚAAGCACAGGCTGGGGGTGGGGGGGGGG		4483	qq
409			409	δy
448	GCCATCAAGGGCAGGGGTTGGGGGGGATGGTGGTCGACCAGTCACTCTGATCTAAGTCAGA		4423	DЪ
409			409	ò
442	TTCTGGCATGGGGACAATGTTGGATAAGACCTGGCCTTGTCCTTAAATAGGAGGCTCTGG		4363	ОÞ
409			409	٥y
436	CTGGTGTCAGGTTTGAGCTCTGCCATGGCTCCCACCTCGCAAATGCAGCCAACTC		4303	ДQ
409			409	δy
430	CACGCTGTCTGCCTGTTCCTTTGCCCACTTGTTGAGCTGCATGGTGAGCCGTGGGCTTCC	-	4243	Dp
409			409	Qy
424	AGGGAGGAGAAGTCCTGGGAGGCCCCTTCCTAACAGCAGCTGATGGCAGACTTGGCACTG		4183	Op
409			409	Qy
418	ATGTCTGTCCTCGGACCACTCCAGACTCCAACCTCAGCGGACATTCCTGGGGTGGCAGGC	-	4123	QQ
409			409	Qγ
412	GTATGTGCTGTCGTGCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCCAGATGGAGGAGC		4063	Dp
408			409	οy
4062	CTTCACTCTTCTGCTTGCCTGGGGCTGGGGGGGTGGCATCAGCGGCCAGGCCTGA		4003	qq
409			409	Qγ
400	TTTGGTTGGGGGAGCCTGGTCCCTGAGACCCCTGTTAGCCCCACTGATAACCTTCTTCAGC		3943	QQ
409			409	δy
394	GGG†GAGAGGTATGGAGGGGAGGGGCTAAGGT	GGCTGGTTAACTGAGTAGGTAGCTGCAGGGGTGAGAGGTATGGAGGGGAGGGGCT	3883	Dp
409			409	δ
388	AGACCTGCCCCTGCGTCTCGTAGCACTTGAGGAGAGGAG		3823	Dp
409			408	Qγ
3823	GGTGTCCCAAGGGAGGAGGAGGATGCAGGACTGCTCTATAGAGCTCTCAGACTGTAGGGA		3763	Dp
409			409	ΟY
376	CTGACCTCACTGAGCTACAAACCTGGGTGGTGGACTCTGCCTTGAGGGGGCATGAAGTTGG		3703	pp
409			409	Qγ
370	GGGCCCCTTTCCTTGGGAAGCCACCTAACCCAGGTAGTGTGGGTCATCCTTGTCCCTCCA		3643	pp
409			409	Qγ
364	CACTGTGTAAGTTGTGGGGACCTCCTTCTTGGTTGGCCCTACACTAACCAGCCCCTCCAG	_	3583	qq
409			409	Οy
358	TCCCCTTCCCCTTCCCCTGTGGCAGATATCTGAGCTTGACACCTGACCCACTCACT		3523	QQ
409			409	οy
352	TITCIGICIAATICCCITITCTITICCIGCAȚCCCICCTITGCCICCTICCCITICCCC		3463	QQ
409			409	Ωy

qq	584 AAAT	AATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC	643
οy	57		57
Dp	644 TTAC	TACAACCACCATTTGAGGTGATCCATTTTACAGAGGAAGGA	703
οy	57		57
QQ	704 TTAG	TAGGTAAGTCTTAGCCAAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA	763
٥y	57		57
QQ	764 GGTC	GTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGAGTCTCTGCA	823
٥y	57		57
QQ	824 GATA	AAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGTG	883
٥y	57		57
QQ	884 CCCA	CCCAGGAAGAGGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC	943
ογ	57		57
Ω	944 GCTG	i CTAGGTCTGCGCCTTTGAATAAGTATCACTTMTTAGTTGC	1003
οý	57		57
g	1004 ATGC	CTCAGTITGTCCATCTGAAAATGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA	1063
γo	57		57
q	1064 AATT		1123
Οy	57		57
QQ	1124 TTCT	TTCTCACGGAGCTTGGCTTCCCCTTGCCCTTTACTTGTCCCAGCCATGACTCAT	1183
٥y	28		71
QQ	1184 ACTA0	CTTCCCTTCTTGCAGGCATTGGTCCAGTGCTGGGCCTGGTCTGTTGTTGTTGTTGTTGTTGTTGTT	1243
δý	72 GlySe	eralaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla	91
Dp	1244 GGCT	*** AGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCCCCGCCCTTCATCTGGGCCCCCCCC	1303
Qy Dp	92 Leuse 1111 1304 CTGT(erLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly 	111 1363
οy	112 Leul	ieuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeu	131
QQ	1364 CTGC		7
οy	132 LeuAs	spPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe	151
q	1424 CTGG	CTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGTGTTTTC	1483
cy Op	152 ArgAs 184 CGGG	AspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSe ^l reuGly 	171
è	172 GlyCr	vs[.eng]vTvr[.en].enDrcA]aT]eAsnTrnAsnThrSerA]af.enA]aDrcTvr	_
임	. 4	GGTGCCTGGGCTACCTCCTGCCTGCTTTTTTTTTTTTTT	9
οy	192 LeuG	LeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal	211
q	1604 CTGG	GCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCTCATTCTTCCTCACTGCTGCTG	1663
ογ	212 AlaA	AlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly	231

В	1664	GCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGCTGGGCCCCCACCGAGCCAGCAGAAGGG 1	723
ΟŊ	232	LeuSerAlaProSerLeuSerProHisCysCysArgAlaArgLeuAlaPheArg 2	151
ΩD	1724	GGCCCCCTCCTTGTCGCCCCCACTGCTGTCCATGCCGGGCCCGCTTGGCTTTCCGG 1	1783
Οy	252	LeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu	271
QQ	1784	AACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCGATGCCCCGCACCTG 1	1843
ΟŊ	272	ArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe 2	163
QQ	1844	cerescreascreaceresarescacrearsaccreacererr	903
ΟŊ	292	TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 3	111
QQ	1904	CTGTACCAGGGCGTGCCCAGAGCTGAGCCGGGCACC 1	.963
Οy	312	lualaargargHisTyrAspGlu3	119
qq	1964		023
Οy	319		119
qq	2024	AGCCGCCCACCAGAGACGACACTCGGGGCTGTGTGTGGGCTGGTGCCTCTCCATCCTGGC 20	083
Οy	319	3:	119
pp	2084	CCCGACTTCTCTGTCAGGAAAGTGGGGATGGACCCCATCTGCATACACGGCTTCTCATGG 2	143
οy	319	· · · · · · · · · · · · · · · · · · ·	119
qq	2144	GGCCTCTGGCTGCTCTAGGAGTCTGATC 2	203
δλ	319	3	119
qq	2204	AGAGTCGTTGCCCCCAGTTTGACAGAAGGAAAGGCGGAGCTTATTCAAAGTCTAGAGGGAG 2	263
οy	319	3:	119
qq	2264	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTCTGCT 2	323
Qy	319	3:	19
qq	2324 (CCCCCAACGACTITCCAAATAATCTCACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCG 2:	383
Qy	319	3.	19
qq	2384	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTG 24	443
Οy	319	3:	19
qq	2444	AGACTCCCAGGAAACCTTCAGACTACCTTCCTCCTTCAGCAAGGGGCGTTGCCCACA 2	503
Οy	319	3.	19
qq	2504	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGGTAGAAAGGGGAAGGG 29	563
Qy	319	3:	119
qq	2564	TGCTGGGGAGCAGGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCC 2	623
Qy	319	.E	119
qq	2624	CCCTCCCAGGCTCTGTCTGATGGCCCCTC 2	683
Qy	320	lyvalArgMetGlySerLeuGlyLeuPheLeuGlnCysAlaIleSerLe 3	36
qq	2684	searesecasceresecretrecrecastecearerecer 2	7
ŏŏ i	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 39	95
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		02	409
38 3	356 uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuScrHisSerValAl 376 	qa	3883 GGCTGGTTAACTGAGTAGGTAGCTGCAGGGGTGAGAGGTATGGAGGGGGGGG
~	aValValThralaSorAlaAlaConThrGlvDhoThrDhoSorAlaIonGlvIloIonDr	Qy	409
28		qq	TITGGTTGGGGGAGCCTGGTCCCTGAGACCCCTGTTAGCCCCACTGATAACCTTCTTCAGC
m		Oy Dp	409
29	2924 CTACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGT-ACTCATTGGCCAGTGGGTGG 2982	^O	
4		qq	4063 GTATGTGCTGTCCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGAGC 4122
29	AGTCAGGGTGGGGGGGGGTCTGGGTTTTTGGGAGGCCAACTAGCTCAGAACCTGGTAT	δλ	
4 6		qa	4123 ATGTCTGTCCTCGGACCACTCCAGACTCCAACCTCAGCGGACATTCCTGGGGTGGCAGGC 4182
<u>ک</u> ۲	3043 CIGGCAAGCAACTITGGAGAATGCTTCTTTGAATCAGAGAAGAAGAAGCTTATCCTAGCCCCA 3102	0y	409
31	GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT	qa	4183 AGGGAGGAGAAGTCCTGGGAGGCCCCTTCCTAACAGCAGCTGATGGCAGACTTGGCACTG 4242
4		Qy	409
31	3163 TCAGGACTGTGTAGCACTTGAATGGATGGATTGCAGGAAATGCAAAATACGATAGTGGGAA 3222	qa	4243 CACGCTGTCTCCTTTTGCCCACTTGTTGAGCTGCTGGTGAGCCGTGGGCTTCC 4302
4		δλ	409
32	3223 TCCCGAAGGGTCAGGCCAGCAGGAGCCCTAGGCTTCTAGGCTGGTTGTTCTATGGAGAGG 3282	qa —	CTGGTGTCAGGTTTGAGCTCTGCCATGGCTCCCACCTCGCAAATGCAGCCAACTCAACTC
4	604 408	Qy	
3283	33 CAGGCCGCTGAATCAGATGACCCCTGGGCCATTCAGCCTCAGCAGAGGGGAGTGGGAATG 3342	qa .	TTCTGGCATGGGGACAATGTTGGATAAGACCTGGCCTTGTCCTTAAATAGGAGGCTCTGG
4	608	ΟŊ	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3343	13 GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402	qa	GCCATCAAGGGCAGGGGTTGGGGGGATGGTGGTCGACCACTCACT
4	607	Qy	
3403	3 TCTGGTCTCTGAGATGGGGCAGGCTCCTTCCTACCCCCTTTCTTT	ସ୍ପ -	CAGCAGGAAGGAAGTGAGAAGCCTTCAACATTAGCACÁGCTGGGGGAGGTGGGGA
409	60	δδ.	
3463	3 TITCIGICIAAIICCCIITICIITICCIGCAICCCICCIITGCCICCTICCCIIICTCCT 3522	Dp —	AGAGGACATTCCTCCTGCTTGGGGTCTACTGGATTCTCCCTGCCCCAAGGCTGGGGACA
409	609 609	Oy	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3523	3 TCCCCTTCCCCTGTGGCAGATATCTGAGCTTGACACCTGACCACTTGGG 3582	a ::	4603 AGGGAGCTCATGGCAGGGCAGCTACCCTAGTGGCATCTGGGGACCCCAGAGAGCAGAGCT 4662
409	60 408	ζ. ζ	
3583	3 CACTGTGTAAGTTGTGGGGGACCTCCTTCTTGGTTGGCCCTACACTAACCAGCCCCTCCAG 3642	gg (TOTOTIGCACCGGGCAATGAGGATTTCCAGATGTCGGAGGGGAGG
409	60 61	Š	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3643	3 GGGCCCCTTTCCTTGGGAAGCCACCTAACCCAGGTAGTGTGGTCATCCTTGTCCCTCCA 3702	qa —	GTTAGGAGAGCCTGCGTGGGGTTTGGGCCATCAGGGGCCCTGCCTTGGCTTTTGTTCCTC
409	607	Qy	409
3703	CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCCTTGAGGGGGCATGAAGTTGG	qu	4783 TGTTCTGTGCGATCTCTTACCACCGTCTTCATTCCCCCTGTGTGTTTTCCTTACCTTGGAG 4842
408		Qy	409
3763	GGTGTCCCAAGGGAGAGAGAGACAGGACTCTCATAGAGCTTCTCAGA	qq	4843 CTCTGTTCTCTCTGATCTGTGATATTGAGTTTGTCTGCCTCTTACCTGTTCTAAGAGGCT 4902
409		δλ	409
3823	ではいい かいかい かいかい かいかん かいかい かいかい かいかい かいかい か	qa	4903 AGAGGAGACCTAGACTTCTGGGTTCACATTTGTCCCCGCCCTACCCCGTTACCCTTCTCC 4962
ġ	23 AGALCIGCCCIGCGICICGIAGCACIIGAGGAGGAGIAGGIAAGIICGIAGCIGAGA 3882	l oy	607

NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastSEQ for Windows Version 13.0
SEQ ID NO 705
LENGTH: 6976

TYPE: DNA

CACTCCTGAGGAAGGGTCCTGGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCTC	409	GCTCCTGATTCTCATGAAGTCCCATTGCCCCTGGGATGGAGGCAAGGGTCTGTTCTCACA 5082	409	GCTGGGGTGGTGCCAGTGCTGGGTACACACCTGTCCTTTTCCTTTCTTCACCCCTCT 5142	PheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSe 426		rLeumetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446		GlyalaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAlaCy 466 	SASPValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486		gGlylleCysLeuAspLeuAlalleLeuAspSerAlaPheLeuLeuSerGlnVålAlaPr 506 		ATCCCTGTTTATGGGGTCCATTGTCAGCTCAGCCAGTCTCTCACTGCTTATATATGGGGTCTC	ralaalaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLySSe 546 	rAspLeualalysTyrSerala 553	RESULT 28 1Sequence 705, Application US/09780669 1Sequence 705, Application US/09780669 1Setent No. US20020051977A1 1Sequence 705, Application US/09780669 1Setent No. US20020051977A1 1Sequence 705, Application US/09780669 1Septicant: Xu, Jiangchun C. 1Septicant: Mitcham, Janinifer L. 1Septicant: Handcoker, Susan L. 1Septicant: Handcoker, Susan L. 1Septicant: Handcoker, Godel D. 1Septicant: Reteer, Marc W. 1Septicant: Stolk, John A. 1Septicant: Stolk, John A. 1Septicant: Vedvick, Thomas S. 1Septicant: Vedvick, Thomas S. 1Septicant: Wang Aijun A. 1Septicant: Hepler, William 1Septicant Hepler, William 1Septicant Hepler, William 1Septicant Hepler, William 1Septicant Hepler, William 1Septicant Hepler, William 1Septicant Heple
4963	409	5023	409	5083	410	5143	426 I	5203	446 J 5263 C	466 8	5323 1	486 g	5.06		526 r	546 I	SULT 28 -09-780-66 Sequence O Pactent No. 7 GENERAL IN APPLICANT A
QQ	δ	qq	οy	qq	δy	qq	οy	QQ	Qy Dp	δý	QQ	9 0 0	ò	90	Qy Db	Oy Dp	RESULT OS -09 - Seque

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944 GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTMTTAGTTGCTCC 1003
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                                                                                                                                                                                                                                                                                                                                                                                                                524 CCCCAGTCACCTCTGGATCCCTGGTCCTGCACAGAGCCTGGCTCATAGGAGACACTGGAG 583
                                                                                                                                                                                                                                                                                                                                                                                                                                                        643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 884 CCCAGGAAGAGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC 943
                                                                                                                                                                                                                                                                                    344 ACTACATCCTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGACAGGAGTA 403
                                                                                                                                                                                                                                                                                                                              404 CCTCTGCCCTGGGAGCTGCTTGGAGGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 463
                                                                                                                                                                                                                                                                                                                                                                      464 GGAGGGTGACCCTGGGCTGAGGGGGCACACCAAGAAGAAGAAGAAGAATACCAAGGACATA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          704 TTAGGTAAGTCTTAGCCAAAGCCAAATAGCAGCTGAACAGTAGAGCTGGGACTCCATCAA 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   764 GGTCTCCCAGCCGGAGCTTGCTCCTACCCCTAGGACAAGGGGTGGACTCCTGACTCTGCA 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATAAATTCTACAAAAGCCACAGAAGGCAAGTAGTAACCATTGTGTGACAACCCCTCACC 883
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                                                                                                                                    584 AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAAATGC
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                                        6976
551
0
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1257
3
                                                                                                                 US-09-593-793A-113 (1-553) x US-09-780-669-705 (1-6976)
                                       Length:
Matches:
Conservative:
Mismatches:
Indels:
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2144.00
30.48%
30.48%
74.94%
; ORGANISM: Homo sapiens
US-09-780-669-705
                                                         Percent Similarity:
Best Local Similarity:
Query Match:
                              Alignment Scores:
Pred. No.:
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δλ	57	57	
Db 1	004 ATGCCTCAGTTTGTCCATCTGAAAATGGGGGGCATCTGTAATGCCTGTGTTATGAGGAGTA	1063	
Qy	57	57	
Db 1	064 AATTACAGCATCCCTGTGAAGACGTAGCACAGTGTCGAGTACGGAATGTTATTTCCATCC	1123	
οy		57	
Db 1	124 TTCTCACGGAGCTTGGTTCCCCTTGCCCTTTACTTGTCCCAGCCATTGACTCAT	1183	
,	TO S	·	
a a	184 ACTACTICCCTTCTTGCAGGCATTGGTCCAGTGCTGGGCCTGGTCTGTGTCCCGCTCCT	1243	
70 4	72 GlySerAlaSerAspHisTrpArgGlyArgTyrGlyArgArgArgProPheIleTrpAla		
4	244	ה ה ה	
	30.	1363	
^	LCysProAspProArdProLeuGluLeuAlaLeuLeulleLeuGlyValGlyLe		
1		4	
ογ	132 LeuaspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe	151	
Dp 1		1483	
ολ	152 ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMet11eSerLeuGly	171	
Dp 1	cesaccacificsccassccracicistcratscritarisar	1543	
ογ	172 GlyCysLeuGlyTyrLeuLeuProAla11eAspTrpAspThrSerAlaLeuAlaProTyr	191	
Db 1	544 GGCTGCCTGGGCTACCTCCTGCCTTGACTGGGACACCAGTGCCCTGGCCCCCT	1603	
οy	192 LeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal	211	
Dp 1(604 CIGGGCACCCAGGAGGAGGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGC	1663	
 λα	212 AlaalaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGly	231	
Dp 1(664 G	1723	
. Yo	232 LeuSerAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg	251	
Db 1.	724 CTGTCGGCCCCCTCCTTGTCGCCCCCCCCCCGCTGCCGGCCCGCTTGGCTTTCCGG	1783	
: Āā	252 AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCysArgMetProArgThrLeu	271	
Ob 17	784 AACCIGGGCGCCCIGCTICCCCGGCTGCACCGGTGTGCTGCCCGCATGCCCCGCACCTG	1843	
. Yo	272 ArgargLeuPheValalaGluLeuCysSerTrpMetAlaLeuMetThrPheThrLeuPhe	291	
Db 11	844 CGCCGGCTCTTCGTGGCTGTGCTGTGCTGTGTGTTTTTTT	1903	
ογ	292 TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr	311	
Db 1	SAGCCGGG	1963	
λo	312 GlualaArgArgHisTyrAspGlu	319	
Dp 1	964 GAGGCCCGGAGACACTATGAT	2023	
λo	319	319	
. q ₀	024 AGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCTGGC	2083	

ΟŻ	319	319	ن
qq	2084	CCCGACTICICIGICAGGAAAGIGGGGAIGGACCCCATCIGCAIACACGGCIICICAIGG 214	43
Qy	319	319	6
qq	2144	GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGGCTGCTCTAGGAGTCTGATC 220	:03
QY	319	319	6
qq	2204	agagtcgttgccccagtttgacagaaggaaagccgaa <mark>c</mark> cttattcaaagtctagagggag 226	993
Qy	319	319	٥.
Ωp	2264	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCCTCTGCT 232	123
QY	319	319	6
QΩ	2324	CCCCCAACGACTITCCAAATATCTCACCAGCGCCTTCCAGCTCAGGCGTCCTAGAAGCG 238	883
QY	319	319	61
qo	2384	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCCGCCTGTCCTCACAGCTG 244	143
QY	319	319	6]
qa	2444	AGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGGGGGGTTGCCCACA 250	503
Οy	319	319	61
qq	2504	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGG 256	993
QY	319	319	6
qq	2564	TGCTGGGGAGCAGGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCC 262	523
QY	319	319	6
QQ	2624	TTCTCATCTCCCTGAGACTGCTCCGACCTTCCCTCCCAGGCTCTGTCTG	583
Qy	320	33	98
qq	2684	TCCCTCTGCAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCATCTCCCT 274	743
δλ	336	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaValTyrLe 356	99
qq	2744	:TCTGGTCATGGACCGGCTGGTGCGCGATTCGCCACTCGAGCAGTCTATT 2	803
Qy	356	uAlaSerValAlaAlaPheProValAlaAlaGlyAlaThrCysLeuSerHisSerValAl 376	9
qq	2804	28	363
δλ	376	ValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr 39	96
QQ	2864	29	323
Óγ	396	oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal409	6(
qq	2924	CIACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGGT-ACTCATTGGCCAGTGGGTGG 298	982
QY	409	408	60
QQ	2983	AGTCAGGGTGGGAGGGGTGGTCTGGGTTTTTGGGAGGCCCAACTAGCTCAGAACCTGGTAT 304	42
QY	408	408	6
Dp	3043	CTGGCAAGCAACTTTGGAGAATGCTTCTTTGAATCAGAGAAGAAGCTTATCCTAGCCCCA 310	0.5
ΟŊ	409	409	6(
QQ	3103	GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT	.62
QY	408	409	6

105 TCAGGACTGTTAAGCACTTGAATGGATGATTGCAGGAAATGCAAAATACGATAGTGGGAA 409 1223 TCCCGAAGGGTCAGGCCAGCAGGACCCTTAGGCTGTTGTTCTATGGAGAGG 409 1324 CCCGGAAGGGTCAGCCCAGGACCCTTAGGCTGTTGTTCTATGGAGAGG 409 1325 CCCGTTAGCAACACCTTTCTTCTAGGCTGTTGTTGTTGTTGTTCTTTCT

qq	4243	CACGCTGTCTGCCTGTTGCCCACTTGTTGAGCTGCATGGTGAGCCGTGGGTTTCC 4302
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3	2	
ΟŊ	409	607
qq	4363	TTCTGGCATGGGGACAATGTTGGATAAGACCTGGCCTTGTCCTTAAATAGGAGGCTCTGG 4422
Qy	409	409
qq	4423	GCCATCAAGGGCAGGGGTTGGGGGGGATGGTGGTCGACCAGTCACTCTGATCTAAGTCAGA 4482
ΟŊ	409	608
QQ	4483	CAGCAGGAAGGAAGTGAGAAGCCTTCAACATTAGCACAGCTGGGGGTGGGGGAGGTGGGA 4542
ΟŊ	409	409
qq	4543	AGAGGGACATICCICCIGCITGGGGICIACIGGAITCICCCTGCCCCAAGGCTGGGGACA 4602
ΟŊ	409	409
qq	4603	AGGGAGCTCATGGCAGGCCAGCTACCTAGTGGCATCTGGGACCCCAGAGAGGCAGAGCT 4662
Oy	409	609
qq	4663	CCAGAT
Οy	409	608
QQ	4723	GTTAGGAGGCCTGCGTGGGGTTTGGGCCCATCAGGGGCCCTGCCTTGGCTTTTGTTCCTC 4782
Qy	409	409
QQ	4783	TGTTCTGTGCATCTCTTACCACCGTCTTCATTCCCCCTGTGTCTTTTCCTTACCTTGGAG 4842
Qy	409	409
qq	4843	CTCTGTTCTCTGTGATCTGTGATATTGAGTTTGTCTGCCTCTTACCTGTTCTAAGAGGCT 4902
QY	409	409
qq	4903	CACATTTG
QY	409	409
qq	4963	CACTCCTGAGGAAGGGTCCTGGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCTC
Qy	409	608
QQ	5023	GCTCCTGATTCTCATGAAGTCCCCATTGCCCCTGGGATGGAGGCAAGGGTCTGTTCTCACA 5082
Qy	409	409
QC	5083	GCTGGGGTGCCAGTGCTGGGTACACACCTGTCCTCTTCCCCTTTTCTTCACCCCTCT 5142
ΟY	410	PheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSe 426
QQ	5143	CTGCCCAAATACCGAGGGACACTGGAGGTGCTAGCAGTGAGGAC
Qy	426	MetThrSerPheLeuProGlyProLysP
qq	5203	AGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCTTATGGACAC
Qy	44	OProAlaLeuCysGlyAlaSerAlaCy 466
qq	5263	GGTGCTGGAGGCAGTGGCCTGCTCCCACCTĊCACCGGGCTTTGCGGGGCCTCTGCCTG 53
Qy	466	sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486

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Š	400 gcty11ecySpeuAspreuAstrebeuAspserAtaPhebeubeusercinVatAtaPr 500	ζ		•
q	5383 GGGCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGTGGCCCC 5442	qq	584 AAAIGCICCIAACCI	
οy	506 oSerLeuPheMetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526	Qy	57	
QQ	5443 ATCCCTGTTTATGGGCTCCATGTCCAGCTCAGCCAGTCTGTCATGCTTTTTTTT	QQ	644 TTACAACCACCATT	
δý	526 rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe 546	Qy	57	•
q	5503 TGCCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAG 5562	qa	704 TTAGGTAAGTCTTAC	9
οy	546 rAspLeuAlaLysTyrSerAla 553	QY	57	•
Ob		qa	764 GGTCTCCCAGCCGG	~
RESULT	29	Qy	57	,
us-u	Sequence 705, Application US/09822827	qa	824 GATAAATTCTACAA	~4.
GE .	Patent NO. USZUUZUUBIBBUAI GENERALI INFORMATION:	Qy	57	,
	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND	qq	884 CCCAGGAAGAGGGG	0
	TILE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER LES REFERENCE: 210/21/534(2): 50/2003 000	QY	57	
	WREEL FILLION NUMBER: US/US/OZZ,0Z/	qq	944 GCTGCCTCTTACCCJ	
 	NOMBER OF SEC ID NOS: 982 SOFTWARE: FastSEQ for Windows Version 3.0	Qy	57	•
 A	SEQ ID NO /05 LENGTH: 6976	QQ	1004 ATGCCTCAGTTTGTC	_
!	TYPE: DNA CONTROL HOMO Sapiens	Qy	57	•
0-50	1-822-821-705	Db	1064 AATTACAGCATCCCJ	_
Pred	ent Scores: No.: 1.16e-191 Length:	QY	57	
Score: Percen	2144.00 30.48%	qq	1124 TTCTCACGGAGCTTC	9
Best Quer	Mismatches: Indels:	Qy	88	
	. : : : : : : : : : : : : : : : : : : :	qa	1184 ACTACTTCCCTTCT	
0.50	(1-553) X US-US-822-82/-/US (1-69/6)	Qy	72 GlySerAlaSerAs	ъ.
ž ž	MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 	qq	1244 GGCTCAGCCAGTGA	_ 0
<u>a</u> ,	ATGSTCCAGAGGCTGTGGGGGCCCTGCTGCGGGAAAGCCCAGCTCTTGCTG	Qy	92 LeuSerLeuGlyIle	Ψ.
λα d	21 ValAssiLeuleuThrPheGlyLeuGluValCysEeuAlaAlaGlyIleThrTyrValPro 40 	QQ	1304 CTGTCCTTGGGCAT	
2	Dvo[out out out utal [utal of utal of utal of utal of utal outal	QY	112 LeuLeuCysProAs	
h 수		qО	1364 CTGCTGTGCCCGGA	
δý		Οy		
g	344 ACTACATCCTTCCTTCCTGTTCCAGATACATGCCACCTGGCATGTGGGGACAGGAGTA 403	qq	1424 CTGGACTTCTGTGG	$\overline{}$
γo	57 57	Οy		v2 —
ą	404 CCTCTGCCCTGGGAGCTGCTTGGAGGGGAGAGGTGGTCTGCTGGGAAGGCATTGCTGGGCA 463	qq	1484 CGGGACCCGGACCA	_
οy	25	οy	172 GlyCysLeuGlyTyr 	
q	464 GGAGGGTGACCCTGGGCTGAGGGGGCACACCAAGAGAAAGAA	qq		· ·
λα	57 57	ΟŽ		
_ q	CCCCAGTCACCTCTGGATCCCTGGTCCTGCACAGACCTGGCTCATAGGAGACACTGGAG	q0 : .	r i	\sim

QY	57		22
qq	584 /	AAATGCTCCTAACCTTTGGCTAGCCCTTTTATAATTTATAGCGATTATCTCATTTAATGC	643
δλ	57		27
QQ	644	TTACAACCACCATTTGAGGTGATCCATTTTACAGAGAAGGAAG	703
δy	27		57
qq	704	AATAGCAGCTGAACAGTAGAGCTGGGAC	763
QY	27		57
qq	764 (STCTCCCAGCCGGAGCTTGCTCCTACC	823
οy	22		57
Dp	824 (TCTACAAAAGCCACA	883
Qy	23		57
QQ	884 (CCCAGGAAGAGGGCCCCTGTGAGGATTGCAGGCTCTGGAGTCACACTGCTTGTTGAAAC	943
δλ	57		57
qq	944 (GCTGCCTCTTACCCTCCCTAGGTCTGCGCCTTTGAATAAGTATCACTTMTTAGTTGCTCC	1003
Oy	22		23
QO	1004	atgcctcagtttgtccatctgaaaatgggggcatctgt <mark>a</mark> atgcctgtgttatgagggta	1063
Οy	23		22
Dp	1064	aattacagcatccctgtgaagacgtagcacagtgtcgagtacggaatgttatttccatcc	1123
οy	22		22
qq	1124	TTCTCACGGAGCTTGGTTCCCCTTCCCCTTTACTTGTCCCAGCCATTGACTCAT	1183
Οy	28	GlyIleGlyProValLeuGlyLeuValCysValProLeuLeu	71
qq	1184	GGTCCAGTGCTGGCCTGGTCTGTGTCCC	1243
Qy	72 (GlySerAlaSerASpHisTrpArgGlyArgTyrGlyArgArgArgProPhelleTrpAla	91
qq	1244 (rcadecadraccacredestesadecrarescescesecerricarereses	1303
ΟŸ	92	LeuSerLeuGlyIleLeuLeuSerLeuPheLeuIleProArgAlaGlyTrpLeuAlaGly	111
Ор	1304 (cerressearcescreteascererretearceaassescescreserase	1363
ΟŸ	112	LeuLeuCysProAspProArgProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyVeu	131
QQ	1364 (CTGGAGCTGCACTGCTCATCCTGGGCGTGG	1423
Oy	132	LeuAspPheCysGlyGlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeuPhe	151
QQ	1424 (CTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGCTCTGACCTCTTTC	1483
ΟŸ	152 /	ArgAspProAspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGly	171
QQ	1484 (SACCOGGACCACTGTCGCCAGGCCTACTCTGTCTATGCCTTCATGATCAGTCT	1543
οy	172 (yCysLeuGlyTyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAla	191
qq	1544 (ccrescoraccoccrescorateacressacacacacaccocrescocc	1603
ΟŸ	192	LeuGlyThrGlnGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysVal	211
qg :	1604 (GCACCCAGGAGGGCCTCTTTGGCCTGCTCACCTCATCTTCCTCACCTGCGT	1663

Qy Dp	212 /	AlaalaThrLeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaĠluGly 231 	
Οy	232 1	IAlaProSerLeuSerProHisCysCysProCysArgAlaArgLeuAlaPheArg 251	
QQ	1724	CTGTCGCCCCCTCCTTGTTGTTGTTGTCCATGCCGGCCCCCTTGCCTTTCCGG 1783	
ζ O	252 /	AsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCySCysArgMetProArgThrLeu 271 	
ογ	272	e 291	
QQ	1844 (
۶۵ و	292	TyrThrAspPheValGlyGluGlyLeuTyrGlnGlyValProArgAlaGluProGlyThr 311 	
3 6	* 6	1990 TO TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TO THE TOTAL TOTAL TO THE TOTAL TO	
දු දු	312 0	GluAlaArgArgHisTyrAspGlu	
ογ	319	916	
QQ	2024	AGCCGCCCACCAGAGACGACACTCGGGGCTGTGTCTGGGCTGGTGCCTCTCCATCCTGGC 2083	
οy	319	319	
Ор	2084 (CCCGACTICICIGICAGGAAAGIGGGGAIGGACCCCAICIGCAIACACGGCIICTCAIGG 2143	
ογ	319	319	
qq	2144 (GTGTGGAACATCTCTGCTTGCGGTTTCAGGAAGGCCTCTGGCTGCTCTAGGAGTCTGATC 2203	
οχ	319	319	
q	2204 #	agagtcgttgccccagtttgacagaaggaaaggcggagcttaftcaaagtctagagggag 2263	
δ	319	319	
Q Q	2264 1	TGGAGGAGTTAAGGCTGGATTTCAGATCTGCCTGGTTCCAGCCGCAGTGTGCCCTTGCT 2323	
οy	319	319	
qq	2324 (CCCCCAACGACTITCCAAATAATCTCACCAGCGCCTTCCAGCTCAGGCGTCCTÄGAAGCG 2383	
ογ	319 -	319	
e G	2384 1	TCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCTCTCACCGCCTGTCCTCACAGGTG 2443	
δy	319	319	
Q	2444 7	AGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGCCTTCAGCAAGGGGCGTTGCCCACA 2503	
δy	319	319	
q	2504 1	TTCTCTGAGGGTCAGTGGAAGAACCTAGACTCCCATTGCTAGAGGTAGAAAGGGGAAGGG 2563	
ά	319	319	
g	2564 1	TGCTGGGGAGCAGGCTGGTCCACAGCAGGTCTCGTGCAGCAGGTACCTGTGGTTCCGCC 2623	
δ	319 -	319	
q	2624 T	TTCTCATCTCCCTGAGACTGCTCCGACCCTTCCCTCCCAGGCTCTGTCTG	
λά	320	GlyValArgMetGlySerLeuGlyLeuPheLeuGlnCysAlalleSerLe 336	
g	84	CCTCTGCAGGCGTTCGGATGGGCAGCCTGGGGCTGTTCCTGCAGTGCGCCCATC	
δλ	336 1	uValPheSerLeuValMetAspArgLeuValGlnArgPheGlyThrArgAlaVa¦lTyrLe 356	

qq ::	2744	
Οy	356	ualaSerValalaalaPheProValalaalaGlyalaThrCysLeuSerHisSerValal 376
QQ	2804	GCCCAGTGTGGCAGTTTCCCTGTGCCTGCCGGTGCCACTGCCTGTCCCACAGTGTGGC 2863
Oy	37	avalvalthralaseralaalaufenthrglyphethrPheSeralaLeuGln11eLeupr 396
qa	2864	CGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACCTTCTCAGCCCTGCAGATCCTGCC 2923
ογ	396	oTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnVal
qq	2924	CTACACACTGGCCTCCCTCTACCACCGGGAGAAGCAGGT-ACTCATTGGCCAGTGGGTGG 2982
Qy	409	608
qq	2983	AGTCAGGGTGGGGGGGGTGGTTTTTGGGAGGCCAACTAGCTCAGAACCTGGTAT 3042
Qy	409	409
qa	3043	CTGGCAAGCAACTTTGGAGAATGCTTCTTTGAATCAGAGAAGAAGCTTATCCTAGCCCCA 3102
Qy	409	608
qa	3103	GGGCCAGAGGCTTGGGCTGCAGAACAGTGTAGATTAGAT
Qy	409	409
qa	3163	TCAGGACTGTGTAGCACTTGAATGGATGATTGCAGGAAATGCAAAATACGATAGTGGGAA 3222
Qy	409	608
οp	3223	TCCCGAAGGGTCAGGCCAGCAGGAGCCCTAGGCTTCTAGGCTGGTTGTTCTATGGAGAGG 3282
Qy	409	607
qa	3283	CAGGGCGCTGAATCAGATGACCCCTGGGCCATTCAGCCTCAGCAGACGGGAGTGGGAATG 3342
Qy	409	409
qq	3343	GTCCAGCCTTAGCAACACCTTTCTTCAGGGAGCAGCAACCTGACTTAGCCTGTATCCTAC 3402
QY	409	409
qq	3403	TCTGGTCTCTGAGATGGGGCAGGCTCCTTCCTACCCCTTTCTTT
ΟŊ	409	607
qq	3463	TITCIGICIAATICCCTTITCTTTTCCTGCATCCCTCCTTTGCCTCCTTCCCTTTCTCCT 3522
οy	409	409
Dp	3523	TCCCCTTCCCCTTCCCCTGTGGCAGATATCTGAGCTTGACACCTGACCCACTCACT
QY	409	409
qq	3583	CACTGTGTAAGTTGTGGGGACCTCCTTCTTGGTTGGCCCTACACTAACCAGCCCCTCCAG 3642
QY	409	409
qq	3643	GGGCCCCTTTCCTTGGGAAGCCACCTAACCCAGGTAGTGTGGTCATCCTTGTCCCCTCCA 3702
QY	409	409
qq	3703	CTGACCTCACTGAGCTACAAACCTGGGTGCTGGACTCTGCCTTGAGGGGCATGAAGTTGG 3762
οy	409	409
qq	3763	GGTGTCCCAAGGGAGAGAGATGCAGGACTGCTCTCATAGAGCTCTCAGACTGTAGGGA 3822
Qy	409	607

qq	3823	AGACCTGCCCTGCGTCTCGTAGCACTTGAGGAGAGGAGTAGGTAAGTTCGTAGCTGAGA 3882		,	
ò	409	607	Qy		
QQ	3883	GGCTGGTTAACTGAGTAGGTAGCTGCAGGGTGAGAGGTATGGAGGGAG	QQ .		CACTCCTGAG
οÿ	409	408	λo i		
QQ	3943	TTTGGTTGGGGGAGCCTGGTCCCTGAGACCCCTGTTAGCCCACTGATAACCTTCTTCAGC 4002	QQ (GCTCCTGATI
δχ	409	607	Š)
qq	4003	CTTCACTCTTCTGCTTGCCTGGGGGGGGGGGGGGGCTGGCATCAGCGGCCAGGCCTGA 4062	ga i		GCTGGGGTGG
οy	409	408	Š		
qq	4063	GPATGTGTGTCGTGCCAGGGAACGTTCTGGGGCTAGCCATCTTCTCCAGATGGAGGAGC 4122	gg (GCCTTAGGTG
ολ	409	608	δò		rLeumetThr
qq	4123	ATGICIGICCICGGACCACICCAGACICCAACCICAGCGGACAITCCIGGGGIGGCAGGC 4182	a :		CCTGATGACC
οy	409	409	à î		1617A1a617
QQ	4183	AGGGAGAGAAGTCCTGGGAGGCCCCTTCCTAACAGCAGCTGATGGCAGACTTGGCACTG 4242	g ë		GGGTGCTGGA
ò	409	408	δo i		SASPVALSER
QQ	4243	CACGCTGTCTGCCTGTTCCTTTGCCCACTTGTTGAGCTGCATGGTGAGCCGTGGGCTTCC 4302	gr '		or crec
Qy	409	409	δo i		gGlyIleCys
qq	4303	CTGGTGTCAGGTTTGAGCTCTGCCATGCGCTCCCACCTCGCAAATGCAGCCAACTCAACTC 4362	gg (GGGCATCTGC
δλ	409	408	Å 7		OSerLeuPhe
QO	4363	TTCTGGCATGGGGACAATGTTGGATAAGACCTGGCCTTGTCCTTAAATAGGAGGCTCTGG 4422	gg (CTGTT
Οy	409	608	λo		rAlaAlaGly
QQ	4423	GCCATCAAGGGCAGGGGTTGGGGGGGATGGTGGTCGACTCAGTCTGATCTAAGTCAGA 4482	gg ;		GCAGGC
οy	409	608	Š Š		rAspLeuAla
qq	4483	CAGCAGGAAGGAAGTGAGAAGCCTTCAACATTAGCACAGGTGGGGGCTGGGGGGGG	an :	מספס בפשר	775511
Qy	409	608	RESUI US-1	RESULT 30 US-10-012-896-703	703
Op	4543	AGAGGGACATTCCTCCTGCTTGGGGTCTACTGGATTCTCCCTGCCCCAAGGCTGGGGACA 4602	Se	Sequence 703, Application No.	, Appl No. US
οy	409	409		i	Xu, Ji
QQ	4603	AGGGAGCTCATGGCAGGCAGCTACCCTAGTGGCATCTGGGACCCCCAGAGAGGCAGAGCT 4662	.		Mitch
Qy	409	408		APPLICANT:	Jiang
qa	4663	TCTCTGCACCGGGCAATGAGGATTTCCAGATGTCGGAGGGCAGGCA		APPLICANT:	Rette
Οy	409	409		APPLICANT:	Day,
qq	4723	GTTAGGAGAGCCTGCGTGGGGTTTGGGCCCATCAGGGGCCCTGGCCTTTTGTTCCTC 4782		APPLICANT:	Carte
Qγ	409	409		APPLICANT:	Wang,
qq	4783	TGTTCTGTGCATCTCTTACCACCGTCTTCATTCCCCTGTGTCTTTTCCTTACCTTGGAG 4842	.	PPLICANT:	Heple
٥y	409	409		APPLICANT:	Hural Hural
qq	4843	CTCTGTTCTCTCTGATCTGTGATATTGAGTTTGTCTGCCTCTTACCTGTTCTAAGAGGCT 4902		APPLICANT:	Hough
οy	409	408		APPLICANT:	Foy,
QQ	4903	AGAGGAGACCTAGACTTCTGGGTTCACATTTGTCCCGGCCCTACCCGTTACCCTTCTCC 4962	₹ ₹	APPLICANT:	Wanta

	40x	80*
	Db 4963	CACTCCTGAGGAAGGGTCCTGGTTAGACTTGGACCAAGTAGGGTCTCCATCTTCTCTCTT 5022
	Qy 409	409
_	Db 5023	GCTCCTGATTCTCATGAAGTCCCATTGCCCCTGGGATGGAGGCAAGGGTCTGTTCTCACA 5082
	Qy 409	409
Nati	Db 5083	GCTGGGGTGCCAGTGCTGGGTACACACCTGTCCTTTCCTTTTCTTCACCCCTCT 5142
	Qy 410	PheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSe 426
1	Db 5143	GCCTTAGGTGTTCCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACGAG 5202
	Qy 426	rLeuMetThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVa 446
1	Db 5203	CCTGATGACCAGCTTCCTGCCAGGCCCTAAGCCTGCAGCTCCCTTCCCTAATGGACACGT 5262
	4 4	GlyAlaGlyGlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAlaCy 466
	Db 5263	GGGTGCTGGAGGGAGTGGCCTGCTCCACCCGCGCCTCTGCGGGGCCTCTGCCTG 5322
	Oy 466	sAspValSerValArgValValValGlyGluProThrGluAlaArgValValProGlyAr 486
	Db 5323	TGATGTCTCCGTACGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTTCCGGGCCG 5382
	oy 486	gGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaPr 506
1	Db 5383	GGGCATCTGCCTGGACCTCGCCATCCTGGATGCCTTCCTGCTGTCCCAGTGGCCCC 5442
	Qy 506	OSerLeuPheMetGlySerlleValGlnLeuSerGlnSerValThrAlaTyrMetValSe 526
1	Db 5443	ATCCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCTATATGGTGTC 5502
	2y 526	rAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLysSe 546
	Db 5503	TECCGCAGGCCTGGGTCTGGTCTTTACTTTGCTACACAGGTAGTATTTGACAAGAG 5562
	Oy 546	rAspLeuAlaLysTyrSerAla 553
	Db 5563	CGACTIGGCCAAATACTCAGCG 5584
	RESULT 30 US-10-012-896 SEQUENCE 70 SEQUENCE 70 GENERAL INF APPLICANT: APPLIC	CTTGGCCAAATACTCAGCG 558. -703 No. US20020183251A1 No. US20020183251A1 ORMATION: Xu, Jiangchun C. Mitcham, Davin C. Mitcham, Jennifer L. Harlocker, Susan L. Jiang, Yuqiu Kalos, Michael D. Retter, Marc W. Stelk, John A. Day, Craig H. Vedvick, Thomas S. Carter, Darrick Li, Samuel X. Wang, Aijun Skelky, Yasir A.W. Hepler, William T. Henderson, Robert A. Hural, John McNeill, Patricia D. Hural, John McNeill, Patricia D. Hunghton, Raymond L. Vinals de Bassols, Car Froy, Teresa Fanger, Gary R. Wantanabe, Yoshihiro

Madeleine Joy COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNNOSIS OF PROSTATE CANCER 11.4270/012,896 2001-12-10 1011 Windows Version 3.0	3.6e-171 Length: 2904 1920.50 Matches: 390 77.23% Conservative: 0 77.23% Indels: 115 67.13% Gaps: 1	3) x US-10-012-896-703 (1-2904)	ValTyralaPheMetileSerLeuGlyGlyCysLeuGlyTyrLeuLeuBroalalleasp 182 	rpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluGluCysLeuPheGlyLeu 202 	LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAla 222 	LeuglyProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHiscysCys 242 	ProcysargalaargLeualaPheargAsnLeuGlyalaLeuLeuProargLe ^U HisGln 262 	LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282 	MetalaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeüTyrGln 302 	GLyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGl ^j Val 321 	321	GAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGAAAGGCGG 539	321	TATTCAAAGTCTAGAGGGAGTGGAGGTTAAAGGCTGGATTTCAGATCTGCCTGGT 599	321	CCAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATATCTCACCAGCGCCT 659	321	CAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCAGCTGTCTTTGTGTTCCCT 719	321
Meagher, M VVENTION: CO VVENTION: D SINCE: 210121 SINCE: 210121 SINCE DATE: EE ID NOS: RESEQ for 13 MastSEQ for 13 13 104	Scores: 3.6e 1920 milarity: 77.2 Similarity: 77.1 h: 9	-793A-113 (1-553) x	ValTyrAlaPheMetileSe: 	TrpAspThrSerAlaLeuAla 	LeuThrLeuIlePheLeuTh: 	LeuGlyProThrGluProAla	ProCysArgAlaArgLeuAla 	LeuCysCysArgMetProArg	MetalaLeumetThrPheTh: 	GlyvalProArgAlaGluPro GlyvalProArgAlaGluPro		TCTGGCTGCTCTAGGAGTCTGATCAGAGTC		AGCTTATTCAAAGTCTAGAG		TCCAGCCGCAGTGTGCCCTC		TCCAGCTCAGGCGTCCTAGA	
APPLICANT: TITLE OF IN TITLE OF IN FILE REFERE CURRENT APPL CURRENT FIL NUMBER OF S SOFTWARE: E SEQ ID NO 70 LENGTH: 29 TYPE: DNA ORGANISM: US-10-012-896	Alignment Pred. No.: Score: Percent Si Best Local Query Matc	US-09-593	Oy 163 Db 1	Qy 183 Db 61	Qy 203 Db 121	Qy 223 Db 181	Qy 243 Db 241	Oy 263 Db 301	Oy 283 Db 361	Qy 303 Db 421	0y 321	Db 480	Qy 321	Db 540	Qy 321	DD 600	0у 321	099 qa	Qy 321

CTGC 779	yreu 328	SCTG 839	Arg 348 	Ala 368 GCC 959	Thr 388	Gln 408 CAG 1079	Met 428 ATG 1139	.GlyAla 448 GGTGCT 1199	spval 468 ATGTC 1259	yile 488 CATC 1319	erLeu 508 CCCTG 1379	aAla 528 CGCA 1439	pLeu 548 CTTG 1499		
ACTACCTTCCT	ArgMetGlySerLeuGl	SCAGCCTGGG	rgLeuValGlnArg 	alalaalagl 	aAlaLeuThrGlyPheThr cGCCCTCACCGGGTTCACC	isargGluLy. 	luAspSerLe AGGACAGCCT	isval 	CysA TGTG	61yArgG1 	laProS	cvalserAl	pLysSerAs 		
AAACCTTCAGA	ArgMetG	CTTCGGATGG	ValMetAspArgI 	ervålalaalapheprovalalaalaglyala 	SeralaalaL 	PheSerAlaLeuGlnIleLeuProTyrThrLeualaSerLeuTyrHisArgGluLysGln 	alPheLeuproLysTyrArgGlyAspThrG ^l yGlyAlaSerSerGluAspSerLeuMet 	ProPheProAsnGlyF 	CysGlyAlaSerAla 	aArgvalvalPro 	teuteuSerGlnValA 	ValThrAlaTyrMet	valvalPheAsi GTAGTATTTGA(
GACTCCCAGG		CTTCAGCAAGGGGGGTTGCCCACATTCTCTGAGGGGGTT	alleSerLeuValPheSerLeuValMel 	aServalAla 	SServalAlavalvalThrAlaSerAl 	rThrLeuAla CACACTGGCC	pThrGlyGly 	oglyalaPro 	OProAlaLeuCys	Threjual	AlaPhe 	erglnserval 	eAlaThrGlnVa 	-	2793
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0 CTCAC		0 CTTCAG	9 PheLeu 0 TTCCTG	9 PheGly TTCGGC	9 Thrcys ACATGO	9 Pheses 	9 ValPhe GTGTTC	9 ThrserF 0 ACCAGCT	9 GlyGly 0 GGAGGC	9 Serva] 0 TCCGTA	9 CysLeu 0 TGCCTG	9 PheMet(0 TTTATG	9 GlyLeuC 0 GGCCTGC	9 AlaLysTy 	1 2 3 3 - 70 3 -
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                                                               CCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTACCTTCCTCTGC 779
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; APPLICANT: Kalos, Michael D. ; APPLICANT: Retter, Marc W. ; APPLICANT: Stolk, John A. ; APPLICANT: Day, Craig H. ; APPLICANT: Vedvick, Thomas S. ; APPLICANT: Carter, Darrick	APPLICANT: Hang, Aijun APPLICANT: Wang, Aijun APPLICANT: Skeiky, Yasir A.W. APPLICANT: Hepler, William T. APPLICANT: Henderson, Robert A. APPLICANT: Hural, John APPLICANT: Hural, John APPLICANT: Horeit, Patricia D.	APPLICANT: Vinals de Bassols, Carlota APPLICANT: Vinals de Bassols, Carlota APPLICANT: Foy, Teresa APPLICANT: Foy, Teresa TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.47C26 CURRENT APPLICATION NUMBER: US/09/895,814 CURRENT FILING DATE: 2001-06-29 NUMBER OF SEO ID NOS: 990	E: FastSEQ for Windows Version 3.0 o 703 i 2904 sin Homo sapiens SM: Homo sapiens SCores:		163 ValtyralaphemetileSerLeuGlyGlyCysLeuGlyTyrLeuLeuProaláileasp 	Oy 203 LeuThrLeuilePheteuThrCysValAlaAlaThrLeuieuValAlaGluGluAlaAla 222	241 CCATGCGGGCCCGTTGCGGAACCTGGGCGCCTGCTTCCCGGCTGCACAG 253 LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTTP	Qy 303 GlyvalProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGlyVal 321

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Qy	321	321
qq	720	CTCACAGCTGAGACTCCGA
Qy	322	
qq	780	ACATTCTCTGAGGGGTTCGGATGGGCAGCCTGGG
Qy	329	PheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuValGlnArg 348
Dp	840	TCCTGCAGTGCGCCATCTCCCTGGTCTTCTCTGGTCATGGACCGGCTGGTGCAGGG 89
Qy	349	PheGlyThrargalaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla 368
qq	006	CGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTTCCCTGTGGCTGCCGGTGCC 95
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Qy	509	SerGlnSerValThrAlaTyrMetValSerAlaAla 5
QQ	1380	SGCTCCATTGTCCAGCTCAGCTCTCACTGCCTATATGGTGTCTGCCGCA 14
δλ	529 (PheAspLysSerAspLeu 54
qq	1440 (SCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGGGACTT
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APPLICANT KALOS, MICHAEL D.
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Mitcham, Jennifer L.
Harlocker, Susan L.
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APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Henderson, Robert A.
APPLICANT: Henderson, Robert A.
APPLICANT: Ralos, Michael D.
APPLICANT: Ratlos, Michael D.
APPLICANT: Retter, Marc W.
APPLICANT: Rotter, Marc W.
APPLICANT: Day, Craig H.
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APPLICANT: Hepler, William
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                                                    Sequence 703, Application US/09780669 Patent No. US20020051977A1
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Best Local Similarity:
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MetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeuTyrGln
                                                 PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln
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                                                                                                                                                                                                                                                                                                                                                                   PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaGlyAla
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                                                                                                                                480 TCTGGCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAGGCGG
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Db 1440		qa	540 AGC1
Qy 549	AlaLysTyrSerAla 553	Qy	321
Db 1500		qq	600 TCC
RESULT 3	5-827-703	Qy	321
Sequent Sequent	2 27 73 25 703. Application US/09822827	qq	660 TCC
GENERA	NO. DESCONDENDED. INFORMATION:	Ωy	321
TITLE	TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND THIR OF INVENTION.	qa	720 CTC#
FILE	REFERENCE: 210151534C1 TO STATE AND THE CANCER THE ADDITION NITHERED TO TO A CONCERN NITHERED TO TO A CONCERN NITHERED TO TO TO TO TO A CONCERN NITHERED TO TO TO TO TO TO TO TO TO TO TO TO TO	Qy	322
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SOFTW.	NOTE SELVITORIES: 302 ARE: FastSEQ for Windows Version 3.0	Qy	329 Phei
LENG	MO 703 FH: 2904	qa	840 TTC
ORGA	UNIX. Homo sapiens	Qγ	349 Phe
alignment a		qa	900 TTC
Pred. No.:	3.6e-171 Length:	Qy	369 Thr
Percent	tive: 0	qa	960 ACA
Query Mai	67.13% Indels:	Qγ	389 Phes
US-00-593	-793A-113 (1-553) x HS-N9-822-	qq	1020 TTC
}		Qy	409 Vale
UY 163 Db 1	3 VAITYTALAFNEMECIIESELLESELLESTINGIYCISLEUGIYTYFLEULEUFTOATAILAASD 182 	qq	1180 GTG1
18	TroasonhrseralatenalabronvrtenglymhrglnglnGuctenbbeglyten	δδ	429 Thrs
		Ωp	1140 ACC
Qy 203	LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAla	ΟŊ	449 GlyG
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Qy 223		δλ	Ser
Db 181	. CTGGGCCCCACCGAGCCAGAAGGCTGTCGGCCCCTCCTTGTCGCCCCACTGCTGT 240	QD :	
	ProCysargalaArgLeuAlaPheargAsnLeuGlyAlaLeuLeuProArgLeuHisGln	g d	489 CYSI
	CCATGCCGGGCCCGCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAG	QY	509 Phe
Qy 263	LeuCysCysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrp 282 	Ωp	1111 1380 TTT
	CIGIGCIGCCGCALGCCCCCCCCCCCCCCCCCCCCCCCCC	QY	529 GlyI
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Db 480) TCTGCCTGCTCTAGGAGTCTGATCAGAGTCGTTGCCCCAGTTTGACAGAAAGGAAAGGCGG 539	Pul E	lication FRAL INF
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qa	540	CTTATTCAAAGTCTAGAGGGAGTGGAGGAGTTAAGG	тстесстеет	599
Qy	321	1 1 1		321
qa	009	CAGCCGCAGTGTGCCCTCTGCTCCCCCAACGACTTTCCAAATAA	ACCAGCGCCT	659
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qq	099	CAGCTCAGGCGTCCTAGAAGCGTCTTGAAGCCTATGGCCCAGCTGTCT	STGTTC	719
QY	321		:	321
qq	720	CACCCGCCTGTCCTCACAGCTGAGACTCCCAGGAAACCTTCAGACTA	CTTCCTCTGC	779
Qy	322	ArgmetC	31ySerLeuGlyLeu	328
q	780	TCAGCAAGGGGCGTTGCCCACATTCTCTGAGGGCGTTCGGATG	-5	839
Qy	329	3lnCysAlaIleSerLeuValPheSerLeuValMetAsp	GlnAr	348
qa	840	RGCAGTGCCCATCTCCCTGGTCTTC	CAG	æ
Qy	349	PheGlyThrArgAlaValTyrLeuAlaSerValAlaAlaPheProValAlaAlaC	aAlaGlyAla	36
qq	006	GAGCAGTCTATTGGCCAGTGTGGCAGCTTTCCCT	GTGC	95
Qy	369	ThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThrGlyPheThr	rGlyPheThr	388
qq	960	CTGTCCCACAGTGTGCCGTGTGACAGCTT	CGGGTTCACC	10
δy	389	PheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGln	gGluLysGln	408
qq	1020	Trereascerseasarcerseceracacacascersecreses	GGAGAAGCAG	10
Qy	409	ValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMet	pSerLeuMet	42
qq	1080	rctgcccaataccgagggacactggaggtg	CAGCCTGATG	11
Qy	429	ThrSerPheLeuProGlyProLysProGlyAlaProPheProAsnGlyHisVal	sValGlyAla	4
ΩD	1140	SCTTCCTGCCAGGCCTAAGCCTGGAGCTCCC	cerecerecr	11
Qy	4	GlyGlySerGlyLeuLeuProProProProAlaLeuCySGlyAlaSerAlaCys	aCysAspVal	468
qq	1200	SCAGTGGCCTGCTCCCACCTCCACCGCGCTCTGGGGGCCT		12
Qγ	469	ServalArgvalvalValGlyGluProThrGluAlaArgvalvalProGly	yArgGlylle	48
qq	1260	CCGTACGTGGTGGTGGGTGAGCCCACCGAGGCCAGGGTGGTTCCG	2000	13
Qy	489	CysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAl	aProSerLeu	50
Dβ	1320	GCCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTCCCAGGT	CCATCC	13
Qy	209	PhemetGlySerIleValGlnLeuSerGlnSerValThrAlaTyrMetVa	lSerAlaAla	528
QΩ	1380	ATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCATATATAT	srcreccec	14
Qy	529	eTyrPheAla1	sSerAspLeu	548
QQ	1440	GCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTGAC	SAGCGAC	H
Qy	549	SerAla 553		
qa	ō	CCAAATACTCAGCG		
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         APPLICANT: Mitchen, Jennifer L.
APPLICANT: Mitchen, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Kalos, Wichel D.
APPLICANT: Kalos, Wichel D.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Vedvick, Thomas S.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Skeiky, Yasir A W.
APPLICANT: Wang, Aljun
APPLICANT: William T.
APPLICANT: Hepler, William T.
APPLICANT: Henderson, Robert A.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: World: Yoshihiro
APPLICANT: Wangher, Gary R.
APPLICANT: Wangher, Madeleine Joy
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
APPLICANT: Wangher, Madeleine Joy
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.427C27
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 1011
SOFFWARR: FestsEQ for Windows Version 3.0
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Dillon, Davin C.
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u	Db 799		TCAGTCTTGGGGGCTC	sceredecracerecre	creccarreacregeac	828
0 0	Oy 185 Db 859		.eualaProTyrLeuG] 	lythrGlnGluGluCysI 	ThrSeralaLeuAlaProTyrLeuGlyThrGlnGluClysLeuPheGlyLeuLeuThr 	204
0 0	Oy 205		.euThrCysValAlaAl 	laThrLeuLeuValAlaC 	LeullePheLeuThrCysValAlaAlaThrLeucuValAlaGluGluAlaAlaLeuGly	224
			roAlaGluGlyLeuSe	erAlaProSerLeuSerF	ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys	244
_ (CAGCAGAAGGGCTGTC	GGCCCCCTCCTTGTCGC	CCCACTGCTGTCCATGC	1038
с д	Oy 245 Db 1039		.eualaPheargasnLe 	euGlyAlaLeuLeuProP 	ArgalaargLeualaPheargasnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 	264 1098
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	Db 1099		CCCGCACCCTGCGCCC	THE COCCECCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	TGTGCAGCTGGATGGCA	1158
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4 U N U	Alignment Pred. No. Score: Percent S	Alignment Scores: Pred. No.: Score: Percent Similarity:	4.58e-123 1403.50 97.45%	Length: Matches: Conservative:	1203 267 0	

Retter, Marc W.

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                                    US-09-593-793A-113 (1-553) x US-09-895-793-851 (1-1203)
Mismatches:
Indels:
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Harlocker, Susan L.
Jiang, Yuqiu
Kalos, Michael D.
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97.45%
49.06%
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Best Local Similarity:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
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Mismatches:
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Matches:
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CURRENT APPLICATION NUMBER: US/09/895,814
CURRENT FILING DATE: 2001.06-29
NUMBER OF SEQ ID NOS: 990
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                       Henderson, Robert A.
Hural, John
McNeill, Patricia D.
Houghton, Raymond L.
Vinals de Bassols, Carlota
Foy, Teresa
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1403.50
97.45%
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Skeiky, Yasir A.W.
Hepler, William T.
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Day, Craig H.
Vedvick, Thomas
Carter, Darrick
                                        Li, Samuel X.
                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
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Best Local Similarity:
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Db 439 GAAGTGGGGTAGAGGAGAAGTTCATGACCAȚGGTGCTGGCCATTGGTCCAGTGCTGGGC 498 Qy 65 LeuValCysValProLeuLeuGlySerAlaSetAspHisTrpArgGlyArgTyrGlyArg 84	1 9	Oy 105 ArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeuGluLeuAlaLeu 124	Qy 125 LeuileLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThrProLeuGlu 144	Qy 145 AlaLeuLeuSerAspLeuPheArgAspProAspHisCysargGlnAlaTyrSerValTyr 164	Qy 165 AlaPheMetileSerLeuGlyGlyCysLeuG [†] yTyrLeuLeuProAlaIleAspTrpAsp 184 	Oy 185 ThrSeralaLeuAlaProTyrLeuGlyThrGlnGluGluGluCysLeuPheGlyLeuLeuThr 204	Qy 205 LeullePheLeuThrCysValAlaAlaThrLeuLeuValAlaGluGluAlaAlaLeuGly 224	Qy 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCysProCys 244	Qy 245 ArgalaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCys 264	Oy 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284	Oy 285 LeuMetThrPheThrLeuPheTyrThrAspPheValGlyGlu 298	RESULT 40 US-09-780-669-851 ; Sequence 851, Application US/09780669 ; Patent No. US20020051977A1 ; GENERAL INFORMATION:	APPLICANT: D1110n, Davin C. APPLICANT: Mitcham, Jonnifer L. APPLICANT: Harlocker, Susan L. APPLICANT: Henderson, Robert A. APPLICANT: Kalos, Michael D. APPLICANT: Fanger, Gary R. APPLICANT: Retter, Marc W.	; APPLICANT: Stolk, John A. ; APPLICANT: Day, Craig H. ; APPLICANT: Vedvick, Thomas S. ; APPLICANT: Carter, Darrick ; APPLICANT: Li, Samuel ; APPLICANT: Anny, Aljun ; APPLICANT: Skeikv, Vasir A W.	
bb 859 ACCAGTGCCCTGCCCCTACCTGGCCACGAGGAGGAGTGCCTCTTTGGCCTGCTCACC 918 Qy 205 LeuIlePheLeuThrCysValAlaalaThrLeuLeuValAlaGluGluAlaAlaLeuGly 224	<pre>Qy 225 ProThrGluProAlaGluGlyLeuSerAlaProSerLeuSerProHisCysCySProCys 244</pre>	Qy 245 ArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGldLeuCys 264	Qy 265 CysArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAla 284	Oy 285 LeuWetThrPheThrLeuPheTyrThraspPheValGlyGlu 298	RESULT 39 US-09-759-143-851 ; Sequence 851, Application US/09759143	GENERAL INFORMATION: APPLICANT: Xu, Jiangchun APPLICANT: Dillon, Davin C.	; APPLICANT: Mitcham, Jennifer L. ; APPLICANT: Harlocker, Susan L. ; APPLICANT: Jiang, Yuqui ; APPLICANT: Henderson, Robert A.	,. , <u>.</u> . ,		CANT: Wang	FILE FOR INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.47C23 CURRENT APPLICATION NUMBER: US/09/759,143 CURRENT FILING DATE: 2001-01-12	SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 851 LENGTH: 1203 TYPE: DATE OSFORMATION: ORGANISM: Homo sapiens US-09-759-143-851	Alignment Scores: Pred. No.: Score: Score: 1403.50 Matches: Percent Similarity: 97.45\$ Mismatches: Ouery Match: 1203 Matches: 267 Monservative: Mismatches: 10 Gaps: 110	US-09-593-793A-113 (1-553) x US-09-759-143-851 (1-1203) Qy 30 ValCysLeuAlaAlaGly	<pre>Qy 45 GluValGlyValGluLysPheMetThrMetValLeuGlyIleGlyProValLeuGly 64 </pre>

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                                                                                                                    Length:
Matches:
Conservative:
                 AND METHODS FOR PROSTATE CANCER
                                                                                                                                         Mismatches:
Indels:
APPLICANT: McNeill, Patricia D.
APPLICANT: Houghton, Raymond L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CAI
FILE REFERENCE: 210121.427C24
CURRENT APPLICATION NUMBER: US/09/780,669
NUMBER OF SEQ ID NOS: 943
SOFTWARE: FastsEQ for Windows Version 3.0
SED ID NO 851
LENGTH: 1203
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1403.50
97.45%
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                                                                                       ; ORGANISM: Homo sapiens
US-09-780-669-851
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Best Local Similarity:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210.12.534C1
CURRENT APPLICATION NUMBER: US/09/822,827
CURRENT APPLICATION NUMBER: US/09/822,827
NUMBER OF SEQ ID NOS: 982
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Mang, Aljun APPLICANT: Skeky, Yasir A.W. APPLICANT: Skeky, Yasir A.W. APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. APPLICANT: Henderson, Robert A. APPLICANT: Houghton, Raymond L. APPLICANT: Houghton, Raymond L. APPLICANT: Wantals de Bassols, Carlota APPLICANT: Poy, Teresa APPLICANT: Wantanbe, Yoshihiro APPLIC	AP	PLICANT:						415 Argo
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APPLICANT: Fanger, Cary R APPLICANT: Wandenabe, Yoshihiro APPLICANT: Wandenabe, Yoshihiro APPLICANT: Wandenabe, Yoshihiro APPLICANT: Wandenabe, Yoshihiro APPLICANT: Wandenabe, Yoshihiro APPLICANT: Wandenabe, Yoshihiro APPLICANT: Wandenabe, Yoshihiro APPLICANTON: COMPOSITIONS AND METHODS FOR THE THERAPY AND FILE REFERENCE: 210121.427C27 CURRENT APPLICATION NUMBER: US/10/012,896 CURRENT APPLICANTON NUMBER: US/10/012,896 CURRENT APPLICANTON NUMBER: US/10/012,896 CURRENT APPLICANTON NUMBER: US/10/012,896 AND 1010 ANDHER OF SEQ ID NOS: 1011 ANDHER OF SEQ ID NO	AP .		Vinais de Bassois, Carlo Foy, Teresa	ota	·			1111 817 CCAC
APPLICANT: Meagher, Madeleine Joy TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER FILE REFERENCE: 210121.427C27 CURRENT APPLICATION NUMBER: US/10/012,896 CURRENT PAPLICATION NUMBER: US/10/012,896 NUMBER OF SEQ ID NOS: 1011 SEQ ID NO 1010 LENGTH: 1065 TYPE: DNA ORGANISM: Homo sapiens 10.012-896-1010 Matches: 211 God No:: 3.47e-80 Length: 1065 DTe: 947.00 Matches: 211 Crent Similarity: 75.348 Mismatches: 41 Indels: 33.104 Indels: 7 Cops. 593-793A-113 (1-553) x US-10-012-896-1010 (1-1065)	; AF	PLICANT: PLICANT:	Fanger, Gary R. Wantanabe, Yoshihiro					75 GlyG
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER CURRENT APPLICATION NUMBER: US/10/012,896 CURRENT APPLICATION NUMBER: US/10/012,896 CURRENT FILING DATE: 2001-12-10 NUMBER OF SEQ ID NOS: 1011 SEQ ID NO 1010 LENGTH: 1065 LENGTH: 1065 TYPE: DNA ORGANISM: Homo sapiens -10-012-896-1010 GRANISM: 3.47e-80 Matches: 21 cent Similarity: 75.34	; AF	PLICANT: TLE OF IN	Meagher, Madeleine Joy VENTION: COMPOSITIONS AN) METHODS FOR THE THERAE	PY AND			
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APPLICANT: Millon, Davin C.
APPLICANT: Mitcham, Jennifer Lynn
TITLE OF INVENTION: COMPOUNDS FOR IMMUNODIAGNOSIS OF
TITLE OF INVENTION: PROSTATE CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.428C6
CURRENT APPLICATION NUMBER: US/09/232,880
CURRENT FILIG DATE: 1999-01-15
NUMBER OF SEQ ID NOS: 338
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No. US20020182596A1
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Stolk, John A.

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Matches:
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Mismatches:
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10
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Publication No. US20020183251A1
GENERAL INFORMATION:
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APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqiu
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Marc W.
                                                                = A,T,C or
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919.00
96.50%
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                                              NAME/KEY: misc_feature
LOCATION: (1)...(789)
OTHER INFORMATION: n =
                        TYPE: DNA
ORGANISM: Homo sapien
                                                                                                            Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                        Alignment Scores:
Pred. No.:
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       CO ID NO 10
LENGTH: 789
                                        FEATURE:
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| LOCATION: 9, 380, 451, 565, 582, 716, 718, 758, 762, 765, 768, 771,
| LOCATION: 779, 783
| OTHER INFORMATION: n = A,T,C or G
| US-10-012-896-10
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APPLICANT: SUCIK, JOHN A.

APPLICANT: SUCIK, JOHN A.

APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel X.

APPLICANT: Li, Samuel X.

APPLICANT: Skeiky, Vasir A.W.

APPLICANT: Hepler, William T.

APPLICANT: Hural, John
APPLICANT: Hural, John
APPLICANT: Houghton, Raymond L.

APPLICANT: Wonell, Particia D.

APPLICANT: Vinals de Bassols, Carlota
APPLICANT: Fanger, Gary R.

APPLICANT: Fanger, Gary R.

APPLICANT: Wantanabe, Yoshihiro
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APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wantanabe, Yoshihiro
APPLICANT: Wasacher, Madeleine Joy
TITLE OF INVENTION: LOMPOSITIONS AND METHODS
FILE REFERRNCE: 210121.427C27

CURRENT FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 1011

SOFTWARET FILING DATE: FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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242 362 422 433 473 123 ATCCTGCCCTACACACTGGCCTCCTCTACCACCGGGAGAAGCAGGTGTTCCTGCCCAAA 182 493 494 IleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIle 513 481 533 541 553 900 303 CTCCCACCTCCACCCGCGCTCTGCGGGGCCTCTGCCTGTGATGTCTCCGTACGTGTGGTG IleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLysGlnValPheLeuProLys ValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCysLeuAspLeuAla 363 GTGGGTGAGCCCACCGANGCCAGGGTGGTTCCGGGGCCGGGGCATCTGCCTGGACCTCGCC 514 ValGlnLeuSerGlnSerValThrAlaTyrMetValSerAlaAlaGlyLeuGlyLeuVal LeuProProProAlaLeuCysGlyAlaSerAlaCysAspValSerValArgValVal Search completed: February 19, 2003, 05:16:48 Job time : 402 secs 454 474 482 394 ρp qq g q g Op Qγ à δ δ ŏ 셤 á

Pred. No. is the number of results predicted by chance to have a

GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nuc	OM protein - nucleic search, using frame_plus_p2n model
Run on:	February 19, 2003, 03:45:09; Search time 1694 Seconds (without alignments) 5286.956 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-593-793A-113 2861 1 MVQRLWVSRLLRHRKAQLLLAIXFATQVVFDKSDLAKYSA 553
Scoring table:	BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Ygapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
Searched:	16154066 segs, 8097743376 residues
Total number of	Total number of hits satisfying chosen parameters: 32308132
Minimum DB seq Maximum DB seq	Minimum DB seq length: 0 Maximum DB seq length: 200000000
Post-processing	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 100 summaries

Command line parameters:
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-WODEL-framet-p2n.model.-DEV=xlh
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-WODEL-framet-p2n.model.-DEV=xlh
-WODEL-F2D-CO-COMPA-F3000/V0S09593793/runat_13022003_161308_21565/app_query.fasta_1.711
-WODEL-G2D-COMPA-F3000/VOS09593793/runat_10.1-COOPCL-0.-LOOPEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX-blosum62 -TRANS=human40.cdi -LIST=100
-WOLALIGH-200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGEM-45 -MODE=LOCAL
-WOTFMT=pto -NORM=ext -HEAPSIZE=500 -MINIEN=0 -MAXLEN=2000000000
-USRE-US09593793_@CGN_1_1 959_@runat_13022003_161308_21565 -NCPU-6 -ICPU=3
-NO_XLDXY -NO_MMAP -LARGEQUERY -NGC_SCORES=0 -WAIT -LONGIAG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 gb_est2:*
gb_htc:*
gb_est3:*
gb_est4:*
gb_est5:*
em_estfun:* em_estba:* em_esthum:* em_estin:*
em_estmu:*
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em_estpl:*
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gb_est1:* EST:* 99... 110... 1112... 1122... 1144... 1159... 1169... 1169... 1169... 1169... 1169... 1169... 1169... 1169... 1169... 1169... 1169... Database:

em_gss_other:* em_gss_pro:* em_gss_rod:*

em_gss_inv:* em_gss_pln:*

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Matches:
Conservative:
Mismatches:
Indels:
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90.82%
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Query Match:
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                                                                                                                                                                                                                          BI107873 858 bp mRNA linear EST 26-JUN-2001 602901816F1 NCI_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5031771 5',
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Contact: Robert Strausberg, Ph.D.
Email: gapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.I.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11088 row: o column: 04
High quality sequence stop: 810.
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720 GGCATGCCCGGAACCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGCATGGCAACT 779
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                         285 uMetThrPheThrLeuPheTyr---ThrAspPheValGlyGluGlyLeuTyrGlnGlyVa
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                                                                                                                                                                                                                                                                                                 house mouse.
Mus musculus
Eukaryota, Metazoa; Chordata;
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1 (bases 1 to 858)
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BG242597 1116 bp mRNA linear EST 13-FEB-2001 602354010F1 NCI_CGAP_Maml Mus musculus cDNA clone IMAGE:4482362 5',
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Sciurognathi; Muridae; Murinae; Mus
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242 CysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHis
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
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HH-MCC http://mgc.ncl.nih.gov/.

National Institutes of Health, Mammallan

Unpublished (1999)
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Mammalia; Eutheria; Rodentia;
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BG242597
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Mus musculus
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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   Library Arrayed by: The I.M.A.G.E. Consortium |(LLNL)
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Mismatches:
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Matches:
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81.13%
76.82%
38.08%
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Best Local Similarity:
Query Match:
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Qy	448	AlaGlyGlySerGlyLeuLeuProProProAlaLeuCySGlyAlaSerAlaCysAsp 467 :::
δ	468	ValSerValArgVal-ValValGlyGluProThrGluAlaArgValValProGlyArgGl 487
qa	699	GTTTCCATGCGAGTGGGTGGTGGTGAGCCACCTTGGGGCCCCGGTTGTCCCGGGCCCGGGG 728
oy de	487	yIleCysLeuAspLeuAlaIleLeuAspSerÄlaPheLeuLeuSerGlnValAlaPro 506
	788	CCTGGCCCATGCACGCTGACACTCTGCACTGG 82
Qy	522	aTyrMetValSerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValVa 542
qq	821	CCATATGGGGATCAGTGCAGGCATGCTGTTGTTGTCGTTTTGACACCGGGACTGG 880
QQ QD	542 881	1Phe 543 GTC 884
RESULT 4 BE867241 LOCUS DEFINITION	4 41 rion	
ACCESS	NOI	mRNA sequence. BE867241
VERSION KEYWORDS	N	BE867241.1 GI:10316017
SOURCE ORGANISM	NISM	
REFERENC	NCE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 718)
AUTHORS	ORS	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	I NAL	Unpublished (1999) Contact: Robert Strausberg, Ph.D.
		Email: cgapbs-r@mail.nih.gov Tissue Procurement: ATCC
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at:
		nctp://imaye.iiii.gov Plate: LLAM9559 row: a column: 04
FEATURES		
<i>α</i>	source	O)
		/clone="IMAGE:8846411" /clone_lib="NIH_MGC_65"
		/tissue_type="adenocarcinoma" /lab host="DH10R (phane-resistant)"
		/note="Organ: Colon; Wester: pCMV'SPORT6; Site_1: NotI; /note="Organ: Colon; Wester: pCMV'SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primar: Oligo dT. Site_2: Sall; Cloned unidirectionally. Primars of the colon of the col
BASE CO	COUNT	Technologies. 1 168 t 1 others
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7	5	

Plate: LLAM10254 row: e column: 05 High quality sequence stop: 666. Location/Qualifiers 1. 786 1. 786 Jana Laxon: 1000" Ab_xref="taxon: 1000" Clone="lib="NOI" Ab_xref="taxon: 1000" Aclone="lib="NCI" Ab_xref="taxon: 1000" Aclone="lib="NCI" Ab_xref="taxon: 1000" Aclone="lib="NCI" Alab_host="lib" Alab_host="lib" Anote="Organ: mammary: Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NOII: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gibbert, Shith, NIH"	## BASE COUNT 121 a 246 c 234 g 185 t ORIGIN Alignment Scores: Alignment Scores: Fred. No.: Score: Scoret Similarity: Best Local Similarity: Best Local Similarity: Best Local Similarity: Best Local Similarity: Best Local Similarity: Best Local Similarity: 36.11% Mismatches: DB: US-09-593-793A-113 (1-553) x BG174399 (1-786)	Oy 104 ProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProArgProLeuGluLeuAla 123	Db 241 GGACACCAGGGTTCTGGCCCCTACCTGGGAAGAATGCCTCTTTGGCCTCCT 300 203 uThrLeuIlePheLeuThrCysValalaalaThrLeuIeuValalaGluGluAlaAlae 223
12 Gaps: 0 19-593-7934-113 (1-553) x BE867241 (1-718) 340 LeuValMetAspargLeuValGlnArgPheGlyThrArgAlaValTyrLeuAlaSerVal 35 1111111111111111111111111111111111	Qy 400 AlaSerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGly 419 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	400 LeuCystyAtaSerAtaCysAspValSerValArgValValValLili	RESULT 5 BG174399 LOCUS BG174399 LOCUS BG174399 LOCUS BG174399 LOCUS ACCESSION REAR Sequence. BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EST BG174399.1 GI:12681102 EVENTOR BG174399.1 GI:12681102 BG174399.1 GI:12681102 BG174399.1 GI:12681102 COMMENT EDMAIL: Gapbs-r@mail.nih.gov/. Tissue Procurement: Gilbert Smith, Ph.D. CONMENT EDMAIL: Gapbs-r@mail.nih.gov/ Tissue Procurement: Gilbert Smith, Ph.D. CONMENT EDMAIL: Gapbs-r@mail.nih.gov/ Tissue Procurement: Gilbert Smith, Ph.D. CONMENT EDMAIL: Gapbs-r@mail.nih.gov/ Tissue Procurement: Gilbert Smith, Ph.D. CONMENT EDMAIL: Gapbs-r@mail.nih.gov/ Tissue Procurement: Gilbert Smith, Ph.D. CONMENT EDMAIL: Gapbs-r@mail.nih.gov/ Tissue Procurement: Gilbert Smith, Ph.D. CONMENT EMAIL: Gapbs-r@mail.nih.gov/ Tissue Procurement: Gilbert Smith, Ph.D. CONMENT CONMENT EMAIL: Gapbs-r@mail.nih.gov/ Tissue Procurement: Gilbert Smith, Ph.D. CONMENT

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/note="vector: pCMV-SPORT6 (Life Technologies); Site_1:
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L. (Contact: Robert Strausberg, Ph.D. Email: capabs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

COntact: Robert Strausberg, Ph.D.

Email: capabs-remail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CONTact: Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium; (LNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://mage.llnl.gov

Plate: LLAM13611 row: b column: 08

High quality sequence stop: 615.

L. 1. 885
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IMAGE:6198823 5', mRNA sequence.
                                                                                                                   357
                                                                                                                                                 721 CTCATTG-----GACAGGCTGGCTCCCGAAATTTCGGGCCCACGGCCAGTTAATCTTGC 774
                                                                                                             -SerLeuValMetAspArgLeuValGlnArgPhe---GlyThrArgAlaValTyrLeuAl
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/clone_lib="Lupski_sciatic_nerve"
/sex="male"
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Mismatches:
Indels:
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/db_xref="taxon:9606"
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BQ948390.1 GI:22363868
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COMMENT
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MetValGlnArgLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu

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Tunor Gene Index
Unpublished (1997)
Other_ESTS: u078h02.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov |
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAR clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW412402 592 bp mRNA linear EST 08-FEB-2000 uo78h02.yl NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:2648691 5' similar to TR:Q39231 Q39231 SUCROSE-PROTON SYMPORTER. [1] ;, mRNA
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NCI-GGAP http://www.ncbi.nlm.hip.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
120
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                                                                ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro
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High quality sequence stop: 42
Location/Qualifiers
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AW412402.1 GI:6938274
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Site_2: NotI; cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs -r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAM9855 row; j column: 10

High quality sequence stop: 610.

High quality sequence stop: 610.

Albacation/Qualifiers

1. 929

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/db_xref="taxon:10090"

// Clone="Image: 140677"

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// Lab_host="DH10B (T1 phage-resistant)"

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NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 93.4)

NIH WGC http://mgc.nci.nih.gov/.

NITH MGC http://mgc.nci.nih.gov/.

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Fissue Procurement: The Cepko Laboratory

CDNA Library Preparation: Life Technologies, Inc.

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/clone="IMAGE:6396664"
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Site_2: SalI; Cloned unidirectionally, Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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AGENCOURT_8881033 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:6396364 5', mRNA sequence.
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 549)
Kargul,G.J., Dudekula,D.B., Olan,Y., Lim,M.K., Jaradat,S.A., Tanaka,T.S., Carter,M.G. and Ko,M.S.H.
Verification and initial annotation of NIA mouse 15K cDNA clone set Onpublished (2001)
Other_ESTS: H3066G04-3
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
                                                                                                                                                                        246 ATGATCCAGAGGCTGTGGGCCAGCCGTCTGCTACGGCACCGGAAAGCTCAGCTCCTGCTG
                                                                                                                                                                                                                                                                 101 PheLeuIleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArgProLeu
                                                                                                                                                                                                                                                                                                                                                                                                          744 CATTGACTGGGACACCAGCGTTCTGGGCCCCCTACCTGGGTACTCAGGGAAAAATGCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            200 -PheGlyLeu---LeuThrLeuIlePheLeuThrCysValAlaAlaThrLeu----Le
                                                                                                                                                                                                                                             61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              216 uValAlaGluGluAlaAlaLeuGlyProThn --- GluProAlaGluGly 231
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US-09-593-793A-113 (1-553) x BQ934815 (1-934)
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543 TGTGGG 548
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            )-Not primers. References include: (1) Genome-wide expression profiling of mid-gestation placenta and embryo using a 15,000 mouse developmental CDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale CDNA analysis reveals phased gene expression patterns during prelimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of 7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7: 1967-1978."
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details. Plate: H3066 row: G column: 04 Seg primer: -21M13 Reverse High quality sequence stop: 549
                                                                                                                                                                                                                                                                                                                   /note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/qonad) and one newborn ovary cDNA library. Average insert size 1.5 kb. All source libraries are cloned unidirectionally with Oligo(dT
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/db_xref="tanon:10090"
/clone="H3066G04"
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/sex="Clones arrayed from a variety of cDNA libraries"
/libraries"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TyrGlnGlyValProArgAlaGluProGlyThrGluAlaArgArgHisTyrAspGluGly 320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 ACCTITCCTGTGGCTGCCGCTGCCACTGCCCTGTCCCACAGCGTGGTAGTGACAGCC 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 SerTrpMetAlaLeuMetThrPheThrLeuPheTyrThrAspPheValGlyGluGlyLeu
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Matches:
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/organism="Mus musculus"
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                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                    /lab_host="DH10B"
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868.00
93.96%
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BG173136 -969 bp mRNA linear EST 06-FEB-2001
602335411F1 NCI_CGAP_Mam1 Mus musculus CDNA clone IMAGE:4458602 5',
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Email: cgapbs-rémail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.W.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
Plate: LLAM10257 row: e column: 03
                                                                                                                                                                                                                                                                                                                                                        AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLysProGlyAlaPro 440
                                                                                                                                                                                                                             1 (bases 1 to 969)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly
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/organism="Mus musculus"
/strain="FVB/N"
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Location/Qualifiers
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75.58%
29.99%
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Query Match:
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house mouse
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Best Local Similarity:
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                                                                                                                                     Alignment Scores
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clone IPCA-2
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Wararyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 482)

11 (bases 1 to 482)

Walker, W., Nohmuth, W., Sprinzak, E., Hodgson, D. and Klingler, T.

Prediction of gene function by genome-scale expression analysis:

prostate cancer associated genes
                                                                                                                                   240
                   425
                                                                                                              265
                                                                                                                                                          285
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                                                                                                                                                                                                                                                                                                                                                                                366 AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAla'LeuThr 385
 9
 1 AGCGTTCTGGCCCCCTACCTGGGTACTCAGGAAGAATGCCTCTTTGGCCTCCTCACCCTC
                                                                                                                        181 GTTGGCCTGGCTTTCCGGAATCTGGGTACCCTGTTTCCCCGGCTGCAGCAGCTGTGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             656 AGAAAGCCACTTGTTCCGGCCAAAT---AACGGAGGGACCCTGAAGCATGCCCGTGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                         406 -GluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAs
                                                                                                                                                         266 ArgMetProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeu
                                                                                                                                                                                                                                                           360 AGAGCCGAGCCAGGCACCGAGGC-CGGAGACACTATGATGAAGGCATTCGAATGGGCAGC
                                                                                                                                                                                                                                                                                                      246 AlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeuProArgLeuHisGlnLeuCysCys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Incyte Pharmaceuticals
3174 Porter Drive, Palo Alto, CA 94304, USA
co-expressed with known prostate-cancer genes.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Senome Res. 9 (12), 1198-1203 (1999)
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from multiple libraries and
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NIH-MGC http://mgc.nci.nih.gov/
National institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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Mismatches:
                                                                                                           assembly
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green,
                                                                                                                                           Ļ
                                                                                                                                                                                                          Length:
Matches:
             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IPCA 2"
/clone=lib="Homo sapiens pr
/tissue_type="prostate"
/dev_stage="adult"
/note="multiple clone assen
                                                                                                                                                                                                                                                                      Indels:
Gaps:
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TITLE
JOURNAL
COMMENT
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cDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM9803 row: p

High quality sequence start: 2

High quality sequence stop: 680.

Location/Qualifiers

1. 700

Accation/Qualifiers

1. 700

Accation-Type-Wiss musculus"

/strain-"FVBAN"
/Ab_ref="taxon:10090"
/clone-"IMAGE:4220415"
/clone-"IMAGE:4220415"
/clone-"IMAGE:4220415"
/lab_host="HH108 (T1 phage-resistant)"
/hote="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI: Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

110 a 227 c 197 g 166 t
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Conservative:
Mismatches:
Indels:
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1. 872
/ Organism="Mus musculus"
/ Strain="NMRI"
/ Ab_xref="taxon:10090"
/ Clone="Inhabe:#919513"
/ Clone="Inhabe:#919513"
/ Clone="Lib="NUI_CGAP_Mam4"
/ Lissue_Lype="tumor, gross | Lissue"
/ Alab_host="DH10B"
/ Alab_host="DH10B"
/ Alab_host="DH10B"
/ Alab_host="DH10B"
/ Alab_host="Cognism mammary; Vector: pcMV-SPORT6; Site_1: Sail; Site_2: Noti: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Growth and Differentiation 7, 3-11 (1996)."
                                                                                                                                                                                                                  BG2798469FI NCI_CGAP_Mam4 Mus musculus CDNA clone IMAGE:4919513 5', mRNA sequence.
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INIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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                      598 GGTAGTGACACCTCAGCTGC-CTCACCGGGTTCACCTTCTCGGC-TTGCAGATCCTG-- 653
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: LLAM10834 row.i column: 18
High quality sequence stop: 738.
Location/Qualifiers
aValValThrAlaSerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuPr
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Mismatches:
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house mouse.
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ProLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly 60 	ProvalLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHisTrpArgGly 80 	ArgTyrGlyArgArgArgProPhe11eTrpAlaLeuSerLeuGly11eLeuLeuSerLeu 100 	PheLeulleProArgAlaGlyTrpLeuAlaGlyLeuLeuCysProAspProArg 	GluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCys-GlyGln-ValCysP 140 	heThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysArgGlnA 160 	laTyrSer-ValTyrAlaPheMetIleSerLeuGlyGlyCysLeuGlyTyrLeuLeuPro 179 :::	AlaileAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGln 195 	BG469520 N 602532833FI NIH_MGC_15 Homo sapiens CDNA clone IMAGE:4660496 5', mRRA sequence. BG469520.1 GI:13401795 BG47695 BG47695 BG49695 BG49695 BG49695 BG49695 BG496965 BG496967 BG496967 BG496967 BG496967 BG496967 BG496967 BG496967 BG496967 BG496967 BG496967 BG496967 BG496967 BG496967 BG496967 BG49697 BG
41	460	81 520	101	121	140	160	180	RESULT 15 B0469520 LOCUS DEFINITION ACCESSION VERYWORDS SOURCE AUTHORS TITLE JOURNAL COMMENT FEATURES SOURCE
Qy Dp	Qy Db	Oy Db	9	Oy Dp	O.y Dp	O.y D.b	Oy Db	R S S S S S S S S S S S S S S S S S S S

901 bp mRNA linear EST 12-SEP-2001 Musimusculus cDNA clone IMAGE:5337073 5', Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 901)

11 (bases 1 to 901)

12 (bases 1 to 901)

13 (bases 1 to 901)

14 (bases 1 to 901)

15 (bases 1 to 901)

16 (bases 1 to 901)

17 (bases 1 to 901)

18 (bases 1 to 901)

18 (bases 1 to 901) Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov |
Issue Procurement: Lothar Hennighausen Ph.D., Chu-xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)" 272 c 264 g | 185 t 242 429 GlySerGlyLeuLeuProProProProAlaLeuCysGlyAlaSerAlaCysAspValSer 469 ValargValValValGlyGluProThrGluAlaArgValValProGlyArgGlyIleCys 489 509 362 62 490 -LeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPh 303 CCTGGACCTCGCCATCCTGGATAGTGCCTTCCTGCTGTGTCCCAGGTGGCCCCATCCCTGTT PheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSerGluAspSerLeuMetThr 894 163 0 2 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: US-09-593-793A-113 (1-553) x BG469520 (1-894) BI650119 603296208F1 NCI_CGAP_Mam3 mRNA sequence. B1650119 B1650119.1 GI:15564355 4.92e-66 796.00 98.19% 98.19% 27.82% 483 CCAAATACTCAGCG 496 laLysTyrSerAla 553 EST. house mouse. Percent Similarity: Best Local Similarity: Ø 173 Scores Query Match: RESULT 16 BI650119 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM BASE COUNT ORIGIN No.: AUTHORS TITLE JOURNAL COMMENT 410 470 Alignment 450 183 243 549 REFERENCE Pred. g g g g qq ρp qq Dp δ ò ö ò Qγ ò g à ò ò

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Alignment Scores:
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                        RESULT 17
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DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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                              http://image.llnl.gov
Plate: LLAM11855 row: p column: 02
High quality sequence stop: 778.
Location/Qualifiers
1. 901
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Mismatches:
Indels:
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781.00
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Best Local Similarity:
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//clone_lib="NIH_MGC_46"
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//tissue_type="leiomyosarcoma cell line"
//lab_host="DalloB (phage-registant)"
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//note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
//note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
//note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
//note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
//note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
//note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
//note="Organ: uterus; Vector: pOTB7; Site_1: XhoI; Site_2:
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1 (bases 1 to 850)

1 (bases 1 to 850)

1 (bases 1 to 850)

2 NIH-WGC http://mgc.ncl.nih.gov/.

3 NIH-WGC http://mgc.ncl.nih.gov/.

4 Unpublished (1999)

4 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-remail.nih.gov/

6 Contact: Robert Strausberg, Ph.D.

7 Tissue Procurement: ATCC

7 Tissue Procurement: ATCC

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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, M., Okazaki, Y., Okido, T., Saito, R., Sasai, C., Sano, H., Sasaki, D., Shibata, K., Shinaqawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., Unpublished (2001)

Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BB610495 RIKEN full-length enriched, adult male stomach Mus musculus cDNA clone 2210413P12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Computer based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Kondo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: genome_res@gsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Haydstsu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNas to
prepare [full-length cDNA libraries for rappid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Aswali,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC). Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                            496 AspSerAlaPheLeuLeuSerGlnValAlaProSerLeuPheMetGlySerIleValGln
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                                                                                                                                                          /note="Site_1: XhoI; Site_2: SstI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia
                                 /organism="Mus musculus"
Mp_xref="texon:10090"
/clone="2210413P12" |
/clone_lib="RIKEN full-length enriched, adult male
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                                                                                                                 /tissue_type="stomach"
/dev_stage="adult"
/lab_host="SOLR"
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Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K., Ishii, Y., Yonno, H., Kouda, M., Matsuyama, T., Yakamura, M., Nishi, K., Nomura, K., Numssaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasanishi, A., Muramatsu, M. and Hayashizaki, Y. RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. .. 10 (11), 1757-1771 (2000) Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
                                                                                                          EST 11-0CT-2001
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UKL:http://genome.gs.gsc.riken.go.jp,
Carninci,P., Shibata,Y., Hayasu,N., Sugahara,Y., Shibata,K., Itoh
'M., Konno,H., Okazakı,Y., Muramatsu,M. and Hayashizakı,Y.
Normalization and subrraction of cap-trapper-selected cDNAs to
prepare full-length.cDNA libraries for rapper selected cDNAs to
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penes. Genome Res. 10 (10), 1617-1630 (2000)
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Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
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Contact: Yoshihide Hayashizaki
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
T-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-922
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Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. Ist strand cDNA was
                                                                                                                                BB701488 RIKEN full-length enriched, in vitro fertilized eggs Musmusculus cDNA clone 7420429L15 3', mRNA sequence.
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/note="Site_1: Sal1; Site_2: BamH1; cDNA library was
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/clone="7420429L15"
/clone_lib="RIKEN full-length enriched, in vitro
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/sex="female"
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was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+); after bulk excision from Lambda FLC I. Cloning sites, 5' end: Sall; 3' end: BamHI" 168 c. 145 g. 128 t.
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GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTTVN 3'], CDNA was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 leAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThrGlnGluCluCysLeuPheG
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BM914562
BM914562.1 GI:19364941
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698.00
85.80%
82.25%
24.40%
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house mouse.
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Best Local Similarity:
Query Match:
DB:
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VERSION
KEYWORDS
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EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/And sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."
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           Contact: Robert Strausberg, Ph.D.
Email: gapbs-remain.nh.gov
Email: gapbs-remain.nh.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: McC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLCM2002 row: m column: 14
High quality sequence stop: 485.
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    National Institutes of Health, Mammalian Gene Collection (MGC)
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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 759)
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Tissue Procurement: Jeffrey El Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Their M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9810 row: 1 column: 07
High quality sequence start: 3
High quality sequence stop: 756.
Location/Qualifiers |
I. 756
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National Institutes of Health/ Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                               BF789072.1 GI:12094108
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660.00
90.24%
87.20%
23.07%
5', mRNA sequence.
BF789072
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BASE COUNT 148 a ORIGIN Alignment Scores: Pred. No.:	Score: Percent Similarity: Best Local Similarity: Query Match: DB:	US-09-593-793A-113 (1-55: Qy 403 TyrHisArgGluLys Db 457 THTPARCCCACCC		Oy 443 AsnGlyHisValGly 	Qy 463 AlaSerAlaCysAsF 	0y 483 ValProGlyArgGly 	Oy 503 GlnValAlaProSer 	Qy 523 TyrMetValSerAla 	Qy 543 PheaspLysSerast 	e o z	NEIWOUS EST. SOURCE human. ORCANISM Homo sapiens Eukaryota; Memmalla; Eut	ADTHORS NIH-MGC http: AUTHORS NIH-MGC http: TITLE National Institution of the contact: Robe COMMENT Contact: Robe Tissue Procur CDNA Lissue Procur	CDNA Library DNA Sequenci Clone distrit found through http://image http://mage Plate: LLCML FEATURES Locc
euAspPheCysGlyGlnValC; TGGACTTTGTGGCAGGTGT ArgAspProAspHisCysArg	Db 699 ACTCCATTGGAGGCTTACTCTCCGACTCTTCGGACCAGACATGGCGCAG 749 Qy 160 aTyrSerVal 163 :::: Db 750 CTTCTCTGT 759	RESULT 22 AZ418156/c LOCUS AZ418156 578 bp DNA linear GSS 03-OCT-2000 DEPINITION 1M0194E12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic	Clone UUGCIM0194E12 F, DNA sequence. ACCESSION A2418156 VERSION A2418156.1 GI:10542169 COUNCY COUNC	NISM		TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts JOURNAL Unpublished (2000)		Tel: 801 585 5606 Fax: 801 585 7177 Email: ddundgenetics.utah.edu Tnsert Lenoth: 10000 Std Error: 0 00	12 3CAGT 578.	FEATURES Course Continuo Conti	/ab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-" /note="Vector: PWD42nv; Purified genomic DNA from M. musculus C5/BL/51 (male) was obtained from the Jackson Laboratory Mouse DNA Resource /http://www.iax.org/resoinces/Angres/) The DNA	was hydrodynamically resources your minersylving was hydrodynamically lastered by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel	electrophoresals. Vector DNA was prepared from a derivative of pWDA2 (gil473114 gb AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

F "	148 a 156 c 174 g 100 t	Scores: 3.77e-53	-793A-113 (1-553) x AZ418156 (1-578)	TyrHisargGluLysGlnValPheLeuProLysTyrakgGlyAspThrGlyGlyAlaSer 422 :::::: TTTTATCCCACCTCAGGTGTTCCTGCCCAATACCGAGGGACGCTGGAGGTAGCAC 398	SerGluAspSerLeuMetThrSerPheLeuProGlyPtoLysProGlyAlaProPhebro 442 	AsnGlyHisValGlyAlaGlyGlySerGlyLeuLeuProProProAlaLeuCySGly 462 	AlaSerAlaCysAspValSerValArgValValValGiyGluProThrGluAlaArgVal 482 	ValProGlyArgGlyIleCysLeuAspLeuAlaIleLeuAspSerAlaPheLeuLeuSer 502 	GlnValAlaProSerLeuPheMetGlySerIleValGİnLeuSerGlnSerValThrAla 522 	TyrMetValSerAlaAlaGlyLeuGlyLeuValAlaI]eTyrPheAlaThrGlnValVal 542 	PheasplysSeraspleuAlaLysTyrSer 552 TTTGACAAGAACAACGCCAAATACGCG 8	BG469487 BG4
	BASE COUNT ORIGIN		-593		m /	e 7	e /			2 3	7 3	Z E

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Email: cgapbs-r@mail.nih.gov
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/clone_lib="NIH_MGC_15"
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/tissub_type="adenocarcinoma cell line"
/lab host="adenocarcinoma cell line"
/lab h
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.AG.E. Consortium (LLNL) NA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov. c column: 08 plate: LLAM10336 row: c column: 08 High quality sequence stop: 655.
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Konno, H., Fukuhishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashicaki, Y.

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                                                 BB627667 BIKEN full-length enriched, adult male urinary bladder Musmusculus cDNA clone 9530024M01 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome resegsc.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. . 10 (10), 1617-1630 (2000)
Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and
Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Yoshinide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
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                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Project of Genome Exploration Research Group in Riken
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/clone="9530024M01"
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/lab_host="DH10B"
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Fax: 81-45-503-9216
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RESULT 25
BB627667
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BI145201 630 bp mRNA linear EST 05-JUL-2001 602909395F1 NCI_CGAP_Li9 Mus musculus cDNA clone IMAGE:5050583 5',
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: Jeffrey B. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                   /db_xref="txxn:10090"
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/clone=lib="NCI_CGAP_Lib"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.9 kb. Constructed by Life
Average. Note: this is a NCI_CGAP Library."
a 180 c 199 g 137 t
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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           distribution informati
         Clone distribution: MGC clone distribution infor found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov n column: 24 High quality sequence start: 2 High quality sequence stop: 630. Location/Qualifiers
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Mismatches:
Indels:
DNA Sequencing by: Incyte Genomics, Inc.
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Matches:
                                                                                                              /organism="Mus musculus"/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                               (1-630)
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601.00
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TLE WashU Xenopus EST project, 1999
JRNAL Unpublished (1999)
JNA Contact: Sandy Clifton, Ph.D. Washington University School of Medicine
4444 Forest Park Parkway, Box (8501, St. Louis, MO 63108, USA Tax: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
Library constructed by Life Technologies. DNA Sequencing by:
Rashington University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: Info@lmage.llnl.gov
High quality sequence stop: 435.

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Location/Qualifiers

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/db_xref="taxon:8355"
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/note="Vector: pcW - spORPFs; Site_1: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: NotI; Site_2: Not
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Arakawa.T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Ohno, H., Kouda Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Tagawa, A., Takahashi, F., Takeda, Y., Tanaka, T., Toya, T., RIKEM Mouse ESTS (Arakawa, T., et al. 2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . Il (2), 281-289 (2001) Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                26-OCT-2001
bladder Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: genome-resignor.riken.go.jp,
URL:http://genome.gsc.riken.go.jp,
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Carninci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapper selected cDNAs to
prepare full-length cDNA libraries for rappid discovery of new
agi.K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Watahiki,M., Yoneda,Y., Ishikwa,T., Ozawa,K., Tanaka,T., Matsuura
Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
The Institute of Physical and Chemical Research (RIKEN)
Tel: 81-45-503-922
Fax: 81-45-503-9216
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                             388 ThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAlaSerLeuTyrHisArgGluLys 407
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                                                                                                                                                                                                                                                                                                           BB627844 RIKEN full-length enriched, adult male urinary musculus cDNA clone 9530042D02 5', mRNA sequence.
                                                                                                                                                                                                                                                                                   linear
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/clone="9530042D02"
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AA984323 348 bp mRNA linear EST 27-MAY-1998 am84a12.s1 Stratagene schizo brain S11 Homo sapiens cDNA clone IMAGE:1629790 3', mRNA sequence.
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1 (bases 1 to 348)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kizmann,D., Kucaba,T., Lacy,M., Lee,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schelnberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
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/lab_host="DH10B"
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Material obtained by Johnston N., Torrey, E.F., Yolken R., material obtained by Johnston N., Torrey, E.F., Yolken R., and the Stanley Neuropathology Consortium; Analysis of RNAs from the Brains of Individuals with Psychiatric Diseases (Unpublished) Stanley Neurovirology Laboratory, Johns Hopkins School of Medicine, Baltimore MD."
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                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: polyT not found Seq primer: -40ml3 fwd. FT from Amersham High quality sequence stop: 348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 AlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAlaSerAlaAlaLeuThr 385
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/tissue_type="schizophrenic brain S-11 frontal lobe"
/dev_stage="34 years old"
/lab_host="SOLR (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                1. 348 / Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address | Address
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
Fel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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        WashU-NCI human EST Project
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                                                                Contact: Wilson RK
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Best Local Similarity:
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5. GACTAGTTCTAGATCGCGACGGCCGCCCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary library, non-amplified Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                                                                                                                                                                                                               NIH-MGC http://mgc.nci.nih.gov/.

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James, R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13625_row: d_column: 14
                                                                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; (Catarrhini; Hominidae; Homo
1 (bases 1 to 959)
AGENCOURT_8842232 Lupski_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6204253 5', mRNA sequence.
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Mismatches:
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High quality sequence stop: 490.
Location/Qualifiers 1
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                                                                    BQ950805.1 GI:22366283
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Directionally cloned into EcoRI/XhoI sites using the
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGAGGG(G). Size-selected 550bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
                                                                                                                                               1035 bp mRNA linear EST 22-MAY-2001 602752813F1 NIH_MGC_17 Homo sapiens cDNA clone IMAGE:4905674 5', BG828841
                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (Dases 1 to 1035)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence start: 3
High quality sequence start: 3
High quality sequence start: 3
                40
 SerAlaAlaGlyLeuGlyLeuValAlaIleTyrPheAlaThrGlnValValPheAspLys
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                    SerAspLeuAlaLysTyrSerAla 553
                                                                                                  308 AGCGACTTGGCCAAATACTCAGCG 331
                                                                                                                                                                                                                                         BG828841.1 GI:14176428
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Best Local Similarity:
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AUTHORS
TITLE
JOURNAL
 526
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                                                                                                                                                                                                                        ACCESSION
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dias Neto,E., García Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtmi2.pl?tl=RC66£t2=RC6-FN0202-271000-011-A03£t3=2000-10-27£t4=1)
Seq primer: puc. 18 forward High quality sequence start: 12 High quality sequence stop: 321.
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                                                                                        135 sGly-----GlnValCysPheThrProLeuGluAlaLeuLeuSerAspLeu----- 150
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09
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  41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 322)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 ------PheArgAspProAspHis---CysArg | 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 TGGGGCCAAGGAGTGGTGCATTCACATCCAACATGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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us-09-593-793a-113.rst

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Homo saplens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 342)

Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,

Chissoe,S., Dietrich,N., Duduque,T., Favello,A., Gish,W., Hawkins
,M., Hultman,M., Kucabb,T., Lacy,M., Le,M., Le,N., Mardis,E.,
B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T 23-DEC-1997
CDNA clone
; Site_2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196.716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: estewatson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
                                                                                                                                                                                                                                                                                                                                                                          483
                                                                                                                                                                                                                                                                                                                                              261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   484 ProGlyArgGlyIleCysLeuAspLeuAlaIle-LeuAspSerAlaPheLeuLeuSerGl 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 TCTGCCTGTGATGTCTCCGTACGTGTGGTGGTGGTGAGCCCCCCGAGGCCAGGGTGGTT
                                                                                                                                                                                                                                                                                                            HisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGlyAlaSerSer
                                                                                                                                                                                                                                                                                                                              320 CACCGGGAGAAGCAGGTGTTCCTGCCCAAATCCCGAGGGGACACTGGAGGTGCTAGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464 SerAlaCysAspValSerValArgValValGlyGluProThrGluAlaArgValVal
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4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                322
1 999
1 0 1 0 0
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Matches:
Conservative:
Mismatches:
Indels:
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497.00
93.46%
92.52%
17.37%
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314 286 1810
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Fax:
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AA112573/c
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KEYWORDS
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BE914848 1037 bp mRNA linear EST 29-SEP-2000 601667874F1 NCI_CGAP_Mam1 Mus; musculus cDNA clone IMAGE:3967818 5',
Thus, the origin of this clone is uncertain. This caution should be kept in mind should you use this clone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I (bases 1 to 1037)

NIH-WGC http://mgc.nci.nih.go/,
National Institutes of Health, Mammalian Gene Collection (MGC)
                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 307.
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107
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Mismatches:
Indels:
Gabs:
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BE914848
BE914848.1 GI:10413891
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496.00
96.46%
94.69%
17.34%
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Mus musculus
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Best Local Similarity:
Query Match:
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BE914848
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AUTHORS
TITLE
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Db 733 CCGCTITCTCTTGTTCGC		M Mus	REFERENCE (The Control of the Contro	found through the I http://image.llnl.g plate: LLAM10989 r	High quality sequent FEATURES Location/Q Source 1564 / Organism= //Strain="ref" //Ab_xref="information" //Clone="INformation" //Cl	/lab_nost= /note="org	Site_2: Sa Average in Technologi BASE COUNT 95 a 156 c	ent Scores: No.:	Score: 485.00 Percent Similarity: 94.59% Best Local Similarity: 90.99% Query Match: 16.95%	DB: . US-09-593-793A-113 (1-553) x BG	Qy 442 ProAsnGlyHisValGlyAla			Qy 502 SerGlnValAlaProSerLeu	Qy 522 AlaTyrMetValSerAlaAla
	COMMENT Contact: Robert Strausberg, Ph.D. Email: cgapbs-rémail.nih.gov Tissue Procurement: Gilbert Smith, Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MC clone distribution can be		/organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone_lib="NCI_CGAP_Mam1" /tissue_type="tumor, blopsy sample" /dev_stage="10 months, virgln" /lab_host="Organ: manmary; Vector: pCWV-SPORT6; Site_l: Sall; Site_2: Not!; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator	providing samples: Gilbert Smith, NIH" BASE COUNT 202 a 289 c 310 g 234 t 2 others ORIGIN	Alignment Scores: 3.13e-36 Length: 1037 Pred. No.: 487.50 Matches: 124 Score: 79.65% Conservative: 13 Percent Similarity: 72.09% Mismatches: 28 Query Match: 17.04% Indels: 3 DB: Core Score Conservative: 13 Conservative: 13 Conservative: 13 Conservative: 13 Conservative: 13 Conservative: 13 Conservative: 13 Conservative: 13 Conservative: 13 Conservative: 13 Conservative: 13	US-09-593-793A-113 (1-553) x BE914848 (1-1037)	Qy 1 MetValGlnargLeuTrpValSerArgLeuLeuArgHisArgLysAlaGlnLeuLeuLeu 20	Qy 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaalaGlyIleThrTyrValPro 40	Qy 41 ProLeuLeuLeuGluValGluValGluGluLysPheMetThrMetValLeuGlyIleGly 60 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 61 ProValLeuGlyLeuValCysValProLeuLeuGlySerAlaSerAspHis-TrpArgG1 80	y ArgTyrGlyArgArgArgProPhelleTrpAlaLeuSerLeuGlylleLeu-LeuSerL 	IleProArgAlaClyTrp-LeuAlaClyLeuLeuCysProAsp-ProAr 	Oy 118 gProLeuGluLeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnVa 138	Oy 138 lCysPheThrProLeuGluAlaLeuLeuSerAspLeuPheArgAspProAspHisCysAr 158	<pre>gGlnAlaTyrSerValTyrAlaPheMet 167 ::: ::: ::::: </pre>

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564 bp nRNA linear EST 12-JUN-2001
3AP_CO24 Mus musculus cDNA clone IMAGE:4984191 5',
                                                                                                                                                                                                     E Strausberg, Ph.D.

(email.inh.gov
nent: Jeffrey E. Green, M.D.

Preparation: Life Technologies, Inc.

Arrayed by: The I.M.A.|G.E. Consortium (LLNL)
ty by: Incyte Genomics, Inc.

Atton. MGC clone distribution information can be
                                                                                                                                        Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                         c.nci.nih.gov/.
es of Health, Mammalian Gene Collection (MGC)
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101
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Mismatches:
Indels:
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Matches:
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ence stop: 563.
/Qualifiers
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SCGCTTATG 757
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Contact: Yoshihide Hayashizaki
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
Mus musculus
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Query Match:
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COMMENT
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BB707065
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Verification and initial annotation of NIA mouse 15K cDNA clone set Verification and initial annotation of NIA mouse 15K cDNA clone set Unpublished (2001)

Other_ESTS: H3066G04-5
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdne@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/15k.html for details.
Plate: H3066 row: G column: 04
Seq primer: -21M13 Forward
High quality sequence stop: 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not1; This clone is among a rearrayed set of 15,247 clones from 11 embryo cDNA libraries (including preimplantation stage embryos from unfertilized egg to blastocyst, embryonic part of E7.5 embryos, extraembryonic part of E7.5 embryos, and E12.5 female mesonephros/gonad) and one newborn ovary CDNA library. Average insert size 15 kb. All source libraries are cloned unidirectionally with Oligo(dT) -Not primers. References include: (1) Genome-wide expression profilling of mid-gestation placenta and embryousing a 15,000 mouse developmental CDNA microarray, 2000, Proc. Natl. Acad. Sci. U S A, 97: 9127-9132; (2) Large-scale CDNA analysis reveals phased gene expression patterns during preimplantation mouse development, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of the contraction contraction and patterns during preimplantation mouse develolpment, 2000, Development, 127: 1737-1749; (3) Genome-wide mapping of unselected transcripts from extraembryonic tissue of
                                                                                                                                     466 bp mRNA linear EST 26-JAN-2001
H3066G04-3 MIA Mouse 15K cDNA Clone Set Mus musculus cDNA clone
BG068547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5-day mouse embryos reveals enrichment in the t-complex and under-representation on the X chromosome, 1998, Hum Mol Genet 7:1967-1978."

1 138 c 126 g 81 t
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="H3066604"
/clone_1b="NTA Mouse 15K cDNA Clone Set"
/sex="Clones arrayed from a variety of cDNA libraries"
/dev_stage="Clones arrayed from a variety of cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    466
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Mismatches:
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/db_xref="taxon:10090"
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Matches:
                 1. .466
/organism="Mus musculus"
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468.00
96.08%
93.14%
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                                                                                                                      RESULT 36
BG068547/c
                                                                                                                                                                                              DEFINITION
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                               ACCESSION
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KEYWORDS
SOURCE
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FEATURES

COMMENT

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia;|Sclurognathi; Muridae; Murinae; Mus.
1 (bases I to 317)
Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiradka, T., Hirozane, T., Imotani, K., Ishli
'Y., Ito, M., Kawai, J., Kojina, Y., Kondo, H., Matsuyama, T.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T.,
Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K.,
Shibeta, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa
'A., Takahashi, F., Takaku-Akhira, S., Tanaka, T., Tomaru, A., Toya, T.,
Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BB707065 RIKEN full-length enriched, in vitro fertilized eggs Mus musculus cDNA clone 7420496101 3', mRNA sequence.
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wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahlki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Marsuura Hayashizaki,Y.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ků, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9226
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URL:http://genome.gsc.riken.go.jp/
Carninci.P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., It
M., Konno,H., Okazaki,Y., Muramatau,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
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81 ArgTyrGlyArgArgPro 87
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10 (11), 1757-1771 (2000)
Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugah, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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90
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Mismatches:
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                                                                                          Location/Qualifiers
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455.00
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86.54%
15.90%
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Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
FOR PRIMERS
FORWARD: AGGAAACAGCTATGACCAT 09-JUL-2000 Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W. Design and use of two pooled tissue normalized cDNA libraries for Euteleostomi; 16; Site_1: NotI; Site_2: SalI; tissue from day 11, 13, 15, 20, 455 515 336 GTTAACCTGCTGACGTTCGGCCTGGAGGTGTGCCTGGCCGCAGGCATCACCTACGTGCCA 395 20 40 9 80 21 ValAsnLeuLeuThrPheGlyLeuGluValCysLeuAlaAlaGlyIleThrTyrValPro 41 ProLeuLeuLeuGluValGlyValGluGluLysPheMetThrMetValLeuGlyIleGly EST Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Losses 1 to 537)
Pahrenkrug,S.C., Freking,B.A., Rohron of the control of t 5', mRNA sequence. linear 537 85 1 0 0 EST discovery in swine Unpublished (2000)
Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA TPL: 402 762 4366
Fax: 402 762 4366 Conservative: Mismatches: mRNA Length: | Matches: /note="Vector: pcMv SPORT6; Library made from pooled tis and 30 embryos." Indels: /organism="Sus scrofa" /db_xref="taxon:9823" /clone_lib="MARC lpIG" /tissue_type="pooled" /lab_host="DH10B" US-09-593-793A-113 (1-553) x AW787124 (1-537) AW787124 120845 MARC 1PIG Sus scrofa cDNA BACKWARD: GTTTTCCCAGTCACGACG Plate: 45 row: C column: 12 Seq primer: ATTTAGGTGACACTATAG. pig. Sus scrofa Eukaryota; Metazoa; Chordata; Location/Qualifiers 186 9 AW787124 GI:7843900 EST. 7.88e-32 437.00 98.85% 97.70% 1. 537

us-09-593-793a-113.rst

EST 24-NOV-2000

linear

533

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1. .265
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCO-FN0140-040800-023-h03 FN0140 Homo sapiens CDNA, mRNA sequence.
BF371417 GI:11333442
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 265)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                    182 GCCCACCGAGGTCCAGGTGGTTCCGGGCCGGGGCATCTGCTCTGGATCCTCGCCATCCTG 241
                                                                                                                                                                  515 -GlnLeuSerGln-SerValThrAlaTyrMetValSerAlaAla-GlyLeuGlyLeuVal
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/lab_host="DH10B (phage-resistant)"
/note="Organ: spleen; Vector: poTB7; Site_i: XhoI; Site_2: CoCRI; coNR made by voligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAGGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
                                                                                                                                        bp mRNA linear .EST 15-MAY-2001 sapiens cDNA clone IMAGE:4850347 5',
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bammanla: Eutheria; Primates; Catarrhini; Hominidae; Homo.
(Dases 1 to 717)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs.refmail.nlh.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium:(LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Matches:
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602723976F1 NIH_MGC_113 HOMO
                                                                                                                                                                                         mRNA sequence.
BG745565
BG745565.1 GI:14056218
  516 CGCTATGGTCGCCGGAGGCCC 536
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82.43%
14.59%
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match:
                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.:
                                                                                                                                                               DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
                                                                                 RESULT 39
                                                                                                                                                                                                                         ACCESSION
                                                                                                           BG745565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
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265 83 1 3

DB:	12		Nationa , 7000 E
- 560-6	93A-113 (1-553) x BF3/141/ (1-265)	BASE COUNT 102 a ORIGIN	146 c 170 c
122 1	LeuAlaLeuLeuIleLeuGlyValGlyLeuLeuAspPheCysGlyGlnValCysPheThr 141 :::	ent Scores: Vo.:	.16-29
142 1	ProteuglualaLeuLeuSeraspLeuPheargaspProaspHisCysargglnalaTyr 161 	ore: ccent Similarity: st Local Similarity: ery Match:	405.00 96.39% 95.18% 14.16%
162 9	ServalTyralaphemetileSerLeuGlyGlyCysLeuGlyTyrLeuLeuProAlaile 181 	DB: US-09-593-793A-113 (1-553	10 (1-553) x AW822644 (
		Qy 1 MetValGlnArgLeuTrpValSerArgLe ::	TrpValSerArgLe GGGCCAGCCGTCT
		Oy 21 ValAsnLeuLeuThrPheGlyLeuGluVe 	PheGlyLeuGluVa
	AW822644 523 bp mRNA linear EST 17-MAY-2000 uq13905.y1 Ren Stubbs mouse thymus Mus musculus cDNA clone	Qy 41 ProLeuLeuGluValGlyValGluGl 	ValGlyValGluG
ACCESSION VERSION KEYWORDS	ro	453 CCAGTGCTAC	
SOURCE		Of ALSTREAM 83 	
REFERENCE AUTHORS	<pre>bundarious, metazoa; Choldata; Velleblada; Velleblada; Butharia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 523) Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Thelsing,B., Allen,M., Bowers,Y., Person B. Staller F. Gibbons M. Barron, M. Schurt, P. Ditter</pre>	RESULT 42 CNS05OVL LOCUS COSOSOVL DEPINITION Tetradoon nigroviridis gen	10: roviridis gend
TITLE JOURNAL COMMENT	/E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. The WashU-NCI Mouse EST Project 1999 Upubblished (1999) Other_ESTs: uq13q05.x1 Contact: Marra M/WashU-NCI Mouse EST Project 1999	Sequence. ACCESSION AL341178 VERSION AL347178.1 GI:8240948 KEWORDS GSS; genome survey sequence SOURCE Tetraodon nigroviridis. ORGANISM Tetraodon nigroviridis	GI:8240948 survey sequence groviridis. groviridis
	Washington university school of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1800 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@lmage.llnl.gov) for further information.	EUKATYOTA; METAZOA; CINCTGA ACTINOPLETYGII; NeOPLETYGII ACANTHOMOTOPIA; ACANTHOPLEY; TETRACCONTIGAE; TETRACCON. TETRACCONTIGAE; TETRACCON. AUTHORS ROEST-CTOLLIUS, H., Jaillon, BERNOL, A., Fizames, C., WINC	tazoa; Chorda; 1; Neopterygi; 3; Acanthopter; 5; Tetraodon. 5;H., Jaillon zames,C., Winc
FEATURES Source	MGI:10419 Seq prime High qual	Saurin, W. and Weissenbach, TITLE Human gene number estimate Tetracdon nigroviridis DNA JOURNAL Unpublished REFERENCE 2 (bases 1 to 1020) AUTHORS Roest-Crollius, H., Jaillon,	nd Weissenbach, unmber estimate igroviridis DNA to 1020) tus, H., Jaillon
	/strain="C3H" //db.xref="Laxon:10090" /clone="IMAGE:2802392" /clone=lib="Ren Stubbs mouse thymus" /sex="mixed" /dev_stage="3 weeks"	Bouneau, L., Billault, A., Qu Weissenbach, J. TITLE Charaterization and repeat freshwater pufferfish Tetra JOURNAL Unpublished REFERENCE 3 (bases 1 to 1020)	, Billault,A., Q. hh,J. ation and repeat pufferfish Tetri d to 1020)
	/lab_nost="DHIOB" //note="Organ: thymus; Vector: pT7T3D-Pac; Site_1: Not1; Site_2: Pac1; 1st strand cDNA was primed with an oligo(dT) primer; double-stranded cDNA was ligated using 5' linker ggcogctat and 3' linker aactggaagcttaatt. Library is size-selected >2.5 kb and average insert size is 3.5 kb. Clones were arrayed from primary plating; non-amplified. Library constructed by X. Ren and L. Stubbs (Lawrence	Genos Direc Submi This scale genom	tope. tt Submission tted (12-ARR-2000) sequence is a single r clone-end sequencing e. For more informatic /www.genoscope.cns.fr Location/Qualifier

read and was generated as part of a large g project of the Tetraodon nigroviridis ion, please take a look at fr/Tetraodon. DNA linear GSS 26-MAY-2000 sy sequence T7 end of clone higroviridis, genomic survey ata; Craniata; Vertebrata; Buteleostomi; ii; Teleostei; Buteleostei; Neoteleostei; rygii; Percomorpha; Tetraodontiformes; n,O., Dasilva,C., Bouneau,L., Fisher,C., ncker,P., Brottier,P., Quetier,F., e provided by genome wide analysis using A sequence n,O., Dasilya,C., Fizames,C., Fisher,C., Quetier,F., Saurin,W., Bernot,A. and nal Laboratory and DOE Joint Genome East Ave, L-453, Livermore, CA 94550)." t analysis of the compact genome of the raodon nigroviridis LeuLeuArgHisArgLysAlaGlnLeuLeuLeu 523 79 1 3 0 0 Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps: 020 bp DNA nome survey s Tetraodon nig (1-523)9

<pre>source 11020 /organism="Tetraodon nigroviridis" /db_xxef="taxon:99883" /clone="106H14" /clone=lib="C"</pre>	REFERENCE AUTHORS TITLE
#Genoscope sequence ID : C0BC006DD07c1-end : T7" BASE COUNT 201 a 289 c 256 g 251 t 23 others ORIGIN	JOURNAL
Alignment Scores: 8.28e-27 Length: 1020 Fred. No.: 389.50 Matches: 93 Score: 389.50 Matches: 93 Percent Similarity: 58.18% Conservative: 35 Best Local Similarity: 42.27% Mismatches: 52 Query Match: 13.61% Indels: 5 DB: 17.61% Gaps: 5	
US-09-593-793A-113 (1-553) x CNSO5OVL (1-1020)	FEATURES
Qy 155 AspHisCysArgGlnAlaTyrSerValTyrAlaPheMetIleSerLeuGlyGlyGlySbeu 174	eo Inos
Qy 175 GlyfyrLeuLeuProAlaIleAspTrpAspThrSerAlaLeuAlaProTyrLeuGlyThr 194 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	
Oy 195 GInGluGluCysLeuPheGlyLeuLeuThrLeuIlePheLeuThrCysValAlaaThr 214	
Oy 215 LeuLeuValAlaGluGluAlaAlaLeuGlyProThrGluProAlaGluGlyLeuSerAla 234 ::: :::	
Qy 235 ProserLeuSer 238	· · · BASE COUNT ORIGIN
Db 235 ACCTCCACCAGCCTGGAACTGGGCGCCGGGCGGGCGGCGGCGGCGGCGGCGTGCCN 294	Alignment S
Oy 239ProHisCysProCysArgAlaArgLeuAlaPheArgAsnLeuGlyAlaLeuLeu 257	Score: Percent Simi Best Local S
Qy 258	Query Match DB:
Db 354 TGTCTGCTGAGGACCTGCTGGTCCATGACTGCCATCTACAGGAGTTACTGCCACGTG 413	US-09-593-7
Oy 268 ProArgThrLeuArgArgLeuPheValAlaGluLeuCysSerTrpMetAlaLeuhetThr 287	Qy 1 Me
	20
Db 473 TTCATCTGTTCTACACGGACTTTGTGGGGGAAGTCCTGTACGAGGGCGTGCCCAGGGC 532	11 DD 370 TC
Oy 308 GluproGlyThrGluAlaArgArgHisTyrAspGluGlyValArgMetGlySerLeuGly 327	Oy 40 rd
Db 533 CTGCCGGGAAGTGCCCCAGGCAAAGATACGAGGAAGGT	Db 430 CC
Oy 328 LeuPheLeuGlnCysAlaIleSerLeuValPheSerLeuValMetAspArgLeuvalGln 347	Qy 58 y1 Db 490 CA
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×	Db 550 TC
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/clone='InAGE:429170"
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/lab_host="DH10B (T1 phage-resistant)"
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Site_1: Sfil (ggccgctcggcc); Site_2: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggccgtcggcc); Site_2: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggccgtcggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggccgtcggccgc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_1: Sfil (ggcattatggcc); Site_
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhin1; Hominidae; Homo. I (bases 1 to 906)
NIH-MGC http://mgc.ncl.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                         DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. consortium/LLNL at:
http://mage.llnl.gov
Plate: LLCM150 row: n column: 19
High quality sequence stop: 564.
I. 906
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Email: cgapbs-remail.nih.gov
Irissue Procurement: CLONETECH Laboratories, Inc.
cDNA Library Preparation: CLONETECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coProLeuLeu--LeuGluVal----GlyValGluGluLysPheMetThrMetValLeuGl
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Matches:
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Mismatches:
Indels:
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71.60%
65.68%
13.46%
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| Similarity:
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400 9

us-09-593-793a-113.rst

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11 a 111 c 137 g 68 t lothers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 428)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M'A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
                                                                                                                                                                                                                                                                                                                                                                                                                             BF854834 1inear EST 16-JAN-2001
RC6-FN0202-271000-011-E04 FN0202 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtm12.pl?tl=RC6&t2=RC6-FN0202-271000-011-E04&t13=2000-10-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 20
High quality sequence start: 20
High quality sequence stop: 423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                                                                                                                    361 AlaPheProvalAlaAlaGlyAlaThrCysLeuSerHisSerValAlaValValThrAla
                          1 GCTTTCCCTGTGGCTGCCGGTGCCACATGCCTGTCCACAGTGTGGCCGTGGCGGGCACACAGCT
                                                                                               SerAlaAlaLeuThrGlyPheThrPheSerAlaLeuGlnIleLeuProTyrThrLeuAla
                                                                                                                                                                                          SerLeuTyrHisArgGluLysGlnValPheLeuProLysTyrArgGlyAspThrGlyGly
                                                                                                                                                                                                                                                                                    421 AlaSerSerGluAspSerLeuMetThrSerPheLeuProGlyProLys 436
                                                                                                                                                                                                                                                                                                             428
76
7
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Matches:
Conservative:
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381.50
77.57%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human.
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 45
BF854834/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
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COMMENT
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                                                                                                                                                                                                                                                                                  AA112574 23-DEC-1997 zm28c12.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:526966 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: est@watson.wustl.edu
WARNING: There is evidence that suggests that the 384-well parent
plate of this clone contains both human and mouse derived clones.
Thus, the origin of this clone is uncertain. This caution should be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 228)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: -40Ml3 fwd. from Amersham.

Location/Qualifiers
670 TGTGCCTGATCCCAGGGCCCTGGGAGGCTAGGACTTGTCA-----ATCCTGGGTTTGGG 723
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4444 Forest Park Parkway, Box 8501, St. Louis, MO
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Fax: 314 286 1810
Email: est@watson.
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TITLE JOURNAL MEDLINE COMMENT

Alignment Scores:

Pred. No.:

BASE COUNT

ORIGIN

FEATURES

Query Match:

human.

ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS

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RESULT 44 AA112574

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Best Local Similarity: 71.03% Query Match: 13.33% DB: 13.33% DB: 12.00-593-793A-113 (1-553) x BF8 Oy 22 AsnLeuLeuThrPheGlyLeuG S:: :: ::	: 1/71 secs
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